RCMI2024

2024 RCMI CONSORTIUM NATIONAL CONFERENCE

April 29 – May 1, 2024 • Bethesda, MD • #RCMIconf

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The views expressed in written conference materials or publications and by speakers and the moderators do not necessarily reflect the official policies of the Department of Health and Human Services; nor does mention by trade names, commercial practices, or organizations imply endorsements by the U.S. Government.

Dear Colleagues:

On behalf of the Research Centers in Minority Institutions (RCMI) Conference Organizing Committee, the RCMI Principal Investigators, Faculty and Staff, and the National Institute on Minority Health and Health Disparities (NIMHD) Leadership, Program Officers, and Project Scientists, we welcome you to the 2024 RCMI Consortium National Conference. The Conference will highlight RCMI contribution to national science advances, including innovations in data science and artificial intelligence. RCMI U54 Centers presentations, oral and poster presentations will showcase the best science across the RCMI Consortium.

Following opening remarks by NIMHD Director Dr. Eliseo Pérez-Stable, NIH institutes and Center Directors will discuss strategic initiatives and funding opportunities that RCMI investigators are uniquely positioned to lead. The RCMI Consortium Keynote and Panel Discussion will feature "Artificial Intelligence-Safely, Ethically, Responsibly".

Plenary Session IV will provide an update on NIMHD evaluation of the RCMI Program, and data collection standards by RCMI Coordinating Center for the annual evaluation of RCMI U54 Centers. Plenary Session V will discuss effective strategies and approaches in promoting meaningful collaboration between RCMI investigators and the NIH funded programs from COSWD, NIDA, All of Us, ODSS, CFAR/NIAID.Plenary Session VI Lunch & Conversation will highlight NIMHD Training, Other Opportunities and Resources for Health Disparities Research.

Concurrent workshops will feature RCMI Consortium collaboration on investigator development, research administration, community engagement, research infrastructure, data science, and artificial Intelligence:

Workshop A: Investigator Development Consortium

Workshop B: Community Engagement Consortium

Workshop C: Research Infrastructure/Capacity Consortium

Workshop D: EQBMED– Equitable Breakthroughs in Medicine Development (RCMI-CC / PhRMA Foundation Collaboration)

Workshop E: National Research Mentoring Network (NRMN) Strategic Empowerment Tailored for Health Equity Investigators (SETH)

Workshop F: RCMI Administrators share best practices

Workshop G: RCMI Clinical Research Network for Health Equity (CRN-HE) Multi-Site Collaboration – UG3 / UH3

Workshop H: Artificial Intelligence and Machine Learning for Health Disparities Research

Plenary Session VII is the Second Annual Sidney A. McNairy, Jr, PhD, DSc Awards Ceremony to recognize Outstanding RCMI Young Investigator (s), Mentor and Senior Investigator, and to present the RCMI Coordinating Center Outstanding Service Awards to our colleagues who work tirelessly behind the scenes, toward excellence that is inclusive.

Poster Sessions are a great way to network and foster career long collaborations. Get to know the work of each U54 Center by joining cutting edge scientific presentations by all twenty-two U54 Centers.

RCMI Deputy Director, Monica Webb Hooper, PhD, will bring the Closing Charge, to remind us about why this work matters.

We thank the RCMI Conference Organizing Committee consists of all RCMI Centers Principal Investigators who have worked collaboratively under the leadership of the RCMI Coordinating Center Contact and Multi-Principal Investigators, and in close coordination with NIMHD Program Officials and Project Scientists.

We are grateful to the RCMI U54 Centers Principal Investigators and Abstract Review Committee, chaired by Dr. Monica Esquivel, for an efficient review process that ensured the presentation of the best science from across the RCMI Consortium.

Our thanks to, Dr. Rina Das, Dr. Rada Dagher and other NIMHD Program Officials; Speakers, Moderators and Abstract Presenters; RCMI Coordinating Center staff and volunteers: Dr. Tandeca King Gordon; Geannene Trevillion; Mohamad Malouhi; Dr. Muhammed Idris, Pam Bullard; Dr. Adam Townes; Jada Holmes; Chanelle Harris; and the RCMI U54 Centers Principal Investigators, their respective core directors, and staff. Special thanks to 1Joshua Group for their outstanding Conference Management Services.

Finally, we thank you, our attendees, for your commitment, dedication, and contribution to the success of this program, and to the RCMI theme of Inclusive Excellence!

Yours Sincerely, and on behalf of the RCMI Conference Organizing Committee:

Elizabeth Ofili, MD, MPH, Conference Chair and Contact PI, RCMI Coordinating Center
Emma Fernández-Repollet, PhD, Chair, Steering Committee, RCMI Consortium
Vivek R. Nerurkar, D.M.L.T., M.Sc., Ph.D., Multi-PI, RCMI Coordinating Center
Paul B. Tchounwou, ScD, Multi-PI, RCMI Coordinating Center
Daniel F. Sarpong, PhD, Multi-PI, RCMI Coordinating Center
Monica K. Esquivel PhD RDN CSSD, Chair, Abstract Review Committee, RCMI Conference

Sincerely,

Elizabeth Ofili, MD, MPH, FACC

GENERAL INFORMATION

RCMI CONSORTIUM GOAL STATEMENT

The RCMI Coordinating Center works closely with key personnel at all RCMI U54 Specialized Centers and with NIMHD leaders and staff to help the centers collectively achieve their objectives to: (1) enhance institutional research capacity within the areas of basic biomedical, behavioral, and/or clinical research; (2) enable all levels of investigators to become more successful in obtaining competitive extramural support, especially from NIH, particularly on diseases that disproportionately impact minority and other health disparity populations; (3) foster environments conducive to career enhancement with a special emphasis on development of early career investigations; (4) enhance the quality of all scientific inquiry and promote research on minority health and health disparities; and (5) establish sustainable relationships with community-based organizations that partner with RCMI Centers.

OVERALL OBJECTIVE

The RCMI Program Grantees Conference will bring together RCMI U54 Centers PI/PDs and other senior scientists from each center, research project leaders, pilot project awardees, key community partners, NIH leaders, and staff to exchange information and discuss opportunities for collaboration and strategies for solving shared challenges in:

- Project administration and coordination among sites
- Research resources to support scientific and multi-site projects
- Early-stage investigator development and mentoring
- Community engagement

ACCREDITATION

The Morehouse School of Medicine is accredited by the Accreditation Council for Continuing Medical Education to provide continuing medical education for physicians.

Credit Designation

The Morehouse School of Medicine designates this live activity for a maximum of up to **9.0** ***AMA PRA Category 1 credit(s)***™. **Physicians should only claim credit commensurate with the extent to their participation in the activity.**

At the close of this activity, participants will be able to:

- Describe the process in the coordination and evaluation of the RCMI U54 Centers to leverage the expertise and member resources to accelerate research on diseases that disproportionately affect underserved people and communities;
- Detail collaboration and funding information to promote successful grant applications and funding opportunities with NIH Institutes and Centers; and
- Describe clinical and scientific discovery, research development, and implementation processes that highlight best science across the RCMI Consortium.

Disclosure Statement

Morehouse School of Medicine (MSM) in accordance with ACCME guidelines required instructors, planners, managers, and other individuals who are in a position to control the content of this activity to disclose any real or apparent conflict of interest they may have as related to the content of this activity. All identified conflicts of interest are thoroughly vetted by MSM for fair balance, scientific objectivity of studies mentioned in the materials or used as the basis of content, and the appropriateness of patient care recommendations. Full disclosure of speaker relationships will be made at this activity.

Resolution of Conflicts of Interest

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   a. The system will attempt to locate an existing account using the email you enter.
   b. Enter your last name and phone number, click submit.
   c. Account not Found will appear. Click **CONTINUE**

4. Follow all prompts and enter requested information.
5. Click **Save Profile** to complete your account

START HERE IF YOU HAVE AN ACCOUNT

6. In the left navigation area, click **My Portal** and then select **Claim Credit**
7. Enter Activity code _____Click **Submit**
8. The Survey Monkey evaluation will display. Make your selections on the survey and Click **Done**
9. You are directed to the Certificate Preparation Page. The type and amount of credit that matches your test profile is displayed. Attest to the amount of credit you wish to claim and Submit.
10. Your certificate is now displayed. Your profile is now registered and credited for the activity.

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Click Credit History & Past Certificate from the left navigation menu. Locate the event from the listing and click Print Certificate. This is a reprint of the certificate that you just received. The reprint will stay with your record and be available for re printing when needed.

GENERAL INFORMATION

Disclaimer

The information provided at this CME activity is for continuing education purposes and is not meant to substitute for the independent medical judgement of a healthcare provider relative to a diagnostic and treatment options of a specific patient's medical condition.

RCMI STEERING COMMITTEE BOARD OF DIRECTORS

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Chairperson

Elizabeth O. Ofili, MD, MPH
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Daniel F.K. Sarpong, PhD
PI Director – Community Engagement Domain

Vivek R. Nerurkar, MLT, MSc, PhD
PI Director – Investigator Development Domain

Paul B. Tchounwou, ScD
PI Director – Research Infrastructure Domain

CAPT Antoinette Percy-Laurry, DrPH, MSPH
Project Scientist (Voting)

Rada K. Dagher, PhD, MPH
Project Official (Non-Voting)

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Morehouse School of Medicine

Mohamad Malouhi
Morgan State University

Adam M. Townes, PhD
Morehouse School of Medicine

Geannene Trevillion
Morehouse School of Medicine

ABSTRACT COMMITTEE CHAIR

Monica K. Esquivel, PhD, RDN, CSSD

ORGANIZER

1Joshua Group, LLC
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Elizabeth Williamson

GENERAL INFORMATION

VENUE

Hyatt Regency Bethesda Hotel
One Bethesda Metro Center
7400 Wisconsin Ave.
Bethesda, MD 20814
+1 301.657.1234

CONFERENCE REGISTRATION CHECK-IN INFORMATION

Hotel Lobby

Sunday, April 28, 2024	3:00 PM – 7:00 PM
Monday, April 29, 2024	7:00 AM – 5:00 PM
Tuesday, April 30, 2024	7:00 AM – 7:00 PM
Wednesday, May 1, 2024	7:00 AM – 12:00 PM

NAME BADGES

Identification badges will be provided to all registered participants, speakers, and special guests and are **REQUIRED** for participation in ALL conference activities. There is a **$50 replacement fee** for all badge reprinting. Badges are printed based on information entered at time of registration.

POSTER / EXHIBIT HOURS *

Chesapeake Suites • Meeting Room Level (MR) and Terrace • 2nd Floor

Monday, April 29, 2024	4:30 PM – 6:30 PM
Tuesday, April 30, 2024	7:00 AM – 8:00 AM
	7:00 PM – 9:00 PM
Wednesday, May 1, 2024	7:00 AM – 8:00 AM

SPEAKER READY HOURS

Executive Board Room • Meeting Room Level (MR)

Sunday, April 28, 2024	3:00 PM – 7:00 PM
Monday, April 29, 2024	7:00 AM – 5:00 PM
Tuesday, April 30, 2024	7:00 AM – 6:00 PM
Wednesday, May 1, 2024	7:00 AM – 8:00 AM

SOCIAL MEDIA

Please post about your experience at the RCMI Consortium National Conference on social media sites using the hashtags **#RCMIConf** and **#1JGCollabs**.

DISCLAIMER NOTICE

Please be aware that by entering the conference areas, you consent to your voice, name, and/or likeness being used without compensation, in films and tapes for exploitation in any and all media, whether known or hereafter devised, for eternity, and you release Morehouse School of Medicine, its agents, successors, assigns, and licenses from any liability whatsoever of any nature.

FUNDING

Funding for this conference was made possible [in part] by Grant Number 24MD015970 from the National Institute on Minority Health and Health Disparities (NIMHD), National Institutes of Health (NIH), Department of Health and Human Services (HHS). The views expressed in written conference materials or publications and by speakers and moderators do not necessarily reflect the official policies of the Department of Health and Human Services, nor does mention of trade names, commercial practices, or organizations imply endorsement by the U.S. Government.

ADDITIONAL SUPPORT

1Joshua Group, LLC

PROGRAM-AT-A-GLANCE

SUNDAY, APRIL 28, 2024

4:00 PM — 6:00 PM | **Welcome Reception**
Meeting Rooms Foyer (MR)

6:00 PM — 8:00 PM | **Principal Investigators' Association Meeting [Closed]**
Cabinet / Judiciary (MR)

6:00 PM — 8:00 PM | **Hands-On Training: RCMI Collaboration Tools & Data Collection Portal — p. 18**
Diplomat / Ambassador (MR)

MONDAY, APRIL 29, 2024

7:00 AM — 8:00 AM | **Continental Breakfast**
Regency Foyer (BR)

8:00 AM — 11:00 AM | **Plenary Session I & Opening — p. 19**
RCMI Collaboration and Partnership Opportunities with NIH Institutes and Centers and the Center for Scientific Review
Regency Ballroom (BR)

11:00 AM — 12:45 PM | **Lunch**
Regency Foyer (BR)

11:30 AM — 1:00 PM | **RCMI Presidents Lunch Meeting with NIMHD Leadership [Closed]**
Cabinet / Judiciary (MR)

1:00 PM — 2:00 PM | **Plenary Session II — p. 20**
RCMI Consortium Keynote & Panel Discussion
Regency Ballroom (BR)

2:15 PM — 4:15 PM | **Plenary Session III — p. 21**
U54 Centers Presentation Session I
Regency Ballroom (BR)

4:30 PM — 6:30 PM | **Poster Networking Reception 1 & Exhibits**
Visit p. 38 for Abstract Categories and Presentation Information
Chesapeake Suites (MR) & Terrace (2nd Floor)

PROGRAM-AT-A-GLANCE

TUESDAY, APRIL 30, 2024

7:00 AM — 8:00 AM
Poster Networking Breakfast 1 & Exhibits
Visit p. 38 for Abstract Categories and Presentation Information
Chesapeake Suites (MR) & Terrace (2nd Floor)

8:00 AM — 9:45 AM
Plenary Session IV — p. 22
RCMI Consortium Program Evaluation
Regency Ballroom (BR)

10:00 AM — 11:00 AM
Plenary Session V — p. 23
RCMI Collaborations and Administrative Supplements and Funding Opportunities
Regency Ballroom (BR)

11:30 AM — 1:00 PM
Plenary Session VI — p. 24
Lunch & Conversation featuring NIMHD Training and Other Opportunities from Collaborating NIH ICs
Regency Ballroom (BR)

11:30 AM — 1:00 PM
RCMI Administrators Working Lunch [Closed] — p. 25
Old Georgetown Room (MR)

1:30 PM — 3:00 PM
Concurrent Workshops A-D — pp. 26-29
A: Regency I/II (BR); B: Regency III/IV (BR); C: Cabinet/Judiciary (MR); D: Diplomat/Ambassador (MR)

3:15 PM — 4:45 PM
Concurrent Workshops E-H — pp. 30-33
E: Diplomat/Ambassador (MR); F: Cabinet/Judiciary (MR); G: Regency I/II (BR); H: Regency III/IV (BR)

6:00 PM — 7:00 PM
Plenary Session VII — p. 34
Sidney A. McNairy, Jr., PhD, DSc Awards Ceremony
Regency Ballroom (BR)

7:00 PM — 9:00 PM
Poster Networking Reception 2 & Exhibits
Visit p. 38 for Abstract Categories and Presentation Information
Chesapeake Suites (MR) & Terrace (2nd Floor)

PROGRAM-AT-A-GLANCE

WEDNESDAY, MAY 1, 2024

7:00 AM — 8:00 AM
Poster Networking Breakfast 2 & Exhibits
Visit p. 38 for Abstract Categories and Presentation Information
Chesapeake Suites (MR) & Terrace (2nd Floor)

7:00 AM — 8:00 AM
RCMI PI/PD Beakfast Meeting with [Closed]
Cabinet / Judiciary (MR)

8:00 AM — 11:55 AM
Plenary Session VIII — p. 35
RCMI U54 Centers Presentations Session II
Regency Ballroom (BR)

12:00 PM — 1:00 PM
Plenary Session IX & Closing — p. 36
NIMHD Closing Charge
Regency Ballroom (BR)

RCMI2024

SHUTTLE SERVICE

Complementary shuttle services between the Hyatt Regency Bethesda (Conference Hotel) and Marriott Bethesda North will transport in 60-minute increments.

SUNDAY, APRIL 28

DEPART MARRIOTT	DEPART HYATT
3:00 PM – 8:00 PM	3:30 PM – 8:30 PM

MONDAY, APRIL 29

DEPART MARRIOTT	DEPART HYATT
6:30 AM – 9:30 AM	7:00 AM – 10:00 AM
5:00 PM – 8:00 PM	5:30 PM – 8:30 PM

TUESDAY, APRIL 30

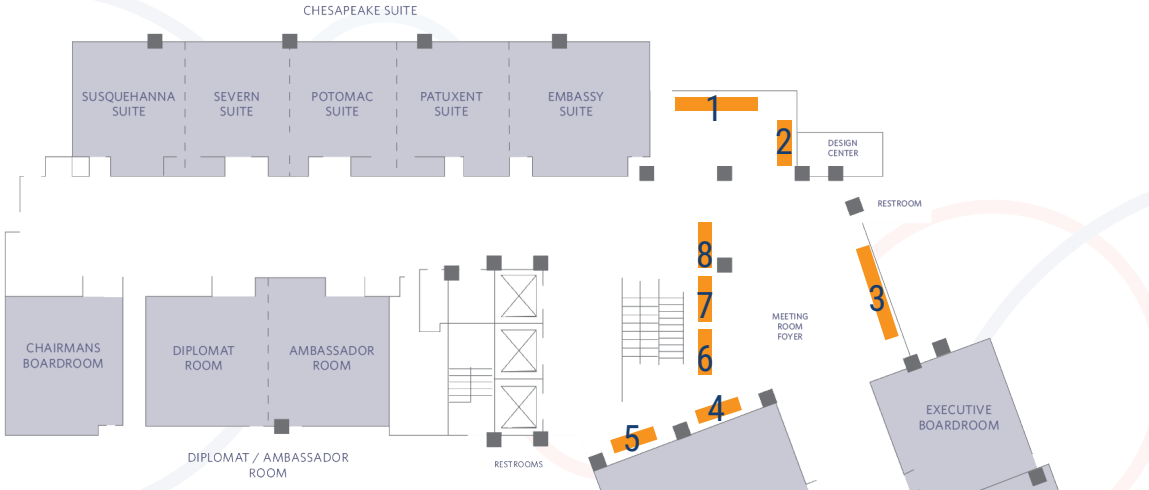
DEPART MARRIOTT	DEPART HYATT
6:30 AM – 9:30 AM	7:00 AM – 10:00 AM
5:00 PM – 7:00 PM	5:30 PM – 9:30 PM

WEDNESDAY, MAY 1

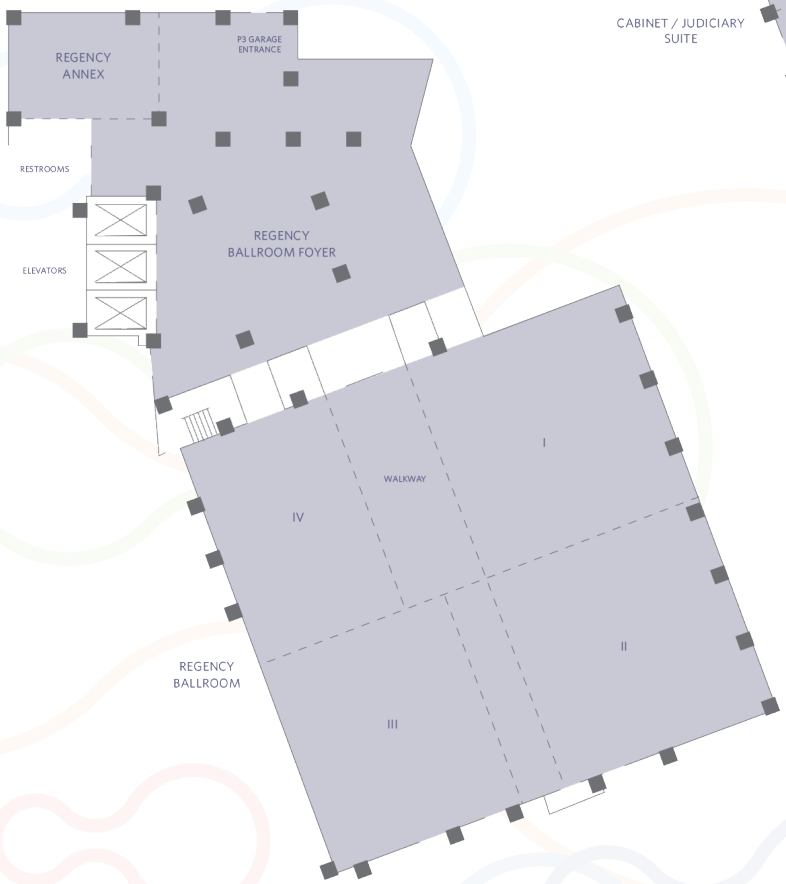
DEPART MARRIOTT	DEPART HYATT
6:30 AM – 9:30 AM	7:00 AM – 10:00 AM
	1:30 PM – 2:30 PM

VENUE FLOOR PLAN

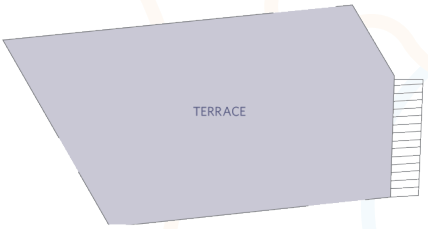
CONFERENCE LEVEL (MR)



BALLROOM LEVEL (BR)



2ND FLOOR



VENUE FLOOR PLAN

SPEAKER READY
Executive Boardroom (MR)

PLENARY SESSIONS
Regency Ballroom (BR)

BREAKOUT SESSIONS
Regency I/II (BR)
Regency III/IV (BR)
Cabinet / Judiciary (MR)
Diplomat / Ambassador (MR)

POSTER SESSIONS & EXHIBITS
Chesapeake Suite (MR)
Terrace (2nd Floor)

EXHIBITORS
Conference Level (MR)

1. RCMI Coordinating Center
2. University of Puerto Rico Medical Sciences Campus
3. Howard University
4. Morehouse School of Medicine Clinical Research Center
5. Morehouse School of Medicine Center of Excellence for the Validation of Digital Health Technologies & Clinical Algorithms
6. Piestar
7. Meharry Medical College
8. Texas Southern University

Please be aware that by entering the conference areas, you consent to your voice, name, and/or likeness being used, without compensation, in films and tapes for exploitation in any and all media, whether now known or hereafter devised, for eternity, and you release Xavier University of Louisiana, its agents, successors, assigns, and licenses from any liability whatsoever of any nature.

We would really like to be a resource to the RCMI Consortium!

COME JOIN US AT NAACFRC 2024 CER!

NAACFRC 2024

COMMUNITY-ENGAGED RESEARCH CONFERENCE

ATLANTA | JUNE 6, 2024

CER PATHWAYS TO EQUITABLE PROGRAMS AND POLICIES

The NAACFRC 2024 Community-Engaged Research (CER) Conference: CER Pathways to Equitable Programs and Policies will share community-engaged research including innovative research approaches, stories of successful research collaborations, and lessons learned from research within the following program tracks: Temporary Assistance for Needy Families (TANF), Head Start/Early Head, or Childcare Assistance.

Attending the conference provides an opportunity to build your professional network and share knowledge, experiences, and ideas. While this is a hybrid conference, we truly encourage in-person attendance to gain the full experience.

Register at: naacfrc.org/annual-conferences/

MOREHOUSE SCHOOL OF MEDICINE

NAACFRC National African American Child and Family Research Center

This project is supported by the Administration for Children and Families (ACF) of the United States (U.S.) Department of Health and Human Services (HHS) as part of a financial assistance award (Grant #: 90PH0031-01-00) totaling $1.8 million with 100 percent funded by ACF/HHS. The contents are those of the author(s) and do not necessarily represent the official views of, nor an endorsement, by ACF/HHS, or the U.S. Government. For more information, please visit the ACF website, Administrative and National Policy Requirements: *acf.hhs.gov/administrative-and-national-policy-requirements*

RCMI Institutions & Principal Investigators

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Clark Atlanta University
Daqing Wu, PhD

Delaware State University
Sangeeta Gupta, MD
Melissa Harrington, PhD

Florida A&M University
Karam F.A. Soliman, PhD

Florida International University
Eric Wagner, PhD

Howard University
William M. Southerland, PhD

Jackson State University
Joseph Whittaker, PhD

Meharry Medical College
Samuel E. Adunyah, PhD
James E.K. Hildreth, PhD, MD

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Timothy Turner, PhD

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Jerris R. Hedges, MD, MS, MMM
Noreen K. Mokuau, DSW

University of Houston
Bettina M. Beech, DrPH, MPH

University of Puerto Rico - Medical Science Campus
Emma Fernandez-Repollet, PhD

University of Texas at El Paso
Robert A. Kirken, PhD

Xavier University of Louisiana
Gene D'Amour, PhD
Christopher Williams, PhD

AGENDA

SUN. APR. 28

6:00 PM – 8:00 PM **Regency Ballroom (BR)**

Hands-On Training

RCMI Collaboration Tools & Data Collection Portal

The goal of this hands-on workshop is to introduce and onboard RCMI-Investigators to the All of Us (AoU) Researcher Workbench. This workshop is designed for those with little to no experience with AoU. The workshop will include a presentation of the AoU program and the Public Data Browser followed by a customized “data treasure hunt.”

Moderator

Muhammed Y. Idris, PhD

Morehouse School of Medicine

AGENDA

MON. APR. 29

8:00 AM –11:00 AM **Regency Ballroom (BR)**

Plenary Session I & Opening

RCMI Collaboration and Partnership Opportunities with NIH Institutes and Centers

NIH leaders will engage RCMI Investigators on strategic initiatives and funding opportunities that address workforce diversity and collaborative research on health disparities. This session will highlight collaborative opportunities that RCMI investigators are uniquely positioned to lead.

Welcome, and Introduction of the RCMI Consortium
Elizabeth O. Ofili, MD, MPH
Contact PI
Morehouse School of Medicine

Emma Fernandez-Repollet, PhD
Chair, Steering Committee
University of Puerto Rico, Medical Sciences Campus

Opening Remarks
Eliseo Perez-Stable, MD
Director, NIMHD

NIH Workforce Diversity Initiatives and Funding Opportunities
Marie Bernard, MD
Chief Officer, Scientific Workforce Diversity

National Institute of General Medical Sciences
Jon R. Lorsch, PhD
Director, NIGMS

National Heart, Lung, and Blood Institute
George A. Mensah, MD
Director, Center for Translation Research and Implementation Science
NHLBI

National Institute on Drug Abuse
Wilson Compton, MD, MPE
Deputy Director, NIDA

National Cancer Institute
Douglas R. Lowy, MD
Principal Deputy Director, NCI

Center for Scientific Review
Noni Byrnes, PhD
Director, CSR

Moderated Panel Discussion / Q&A
Jay Vadgama, PhD
Charles R. Drew University of Medicine & Science

Omonike Olaleye, PhD, MPH
Texas Southern University

K. Sean Kimbro, PhD
Morehouse School of Medicine

AGENDA

MON. APR. 29

1:00 PM – 2:00 PM **Regency Ballroom (BR)**

Plenary Session II

RCMI Consortium Keynote and Panel Discussion

This session will highlight RCMI contribution to national science advances and innovation in data science and artificial intelligence, “Artificial Intelligence-Safety, Ethically, Responsibly.”. The interactive session is designed to foster collaboration.

Moderators

Jerris R. Hedges, MD, MS, MMM
University of Hawaii at Manoa

Deepak Kumar, PhD
North Carolina Central University

Keynote

Bradley Malin, PhD
Accenture Professor of Biomedical Informatics,
Biostatistics and Computer Science
Vanderbilt University Medical Center

Panelists

Jamboor .K. Vishwanatha, PhD
University of North Texas Health Science Center

Lang Wu, PhD
University of Hawaii at Manoa

AGENDA

MON. APR. 29

2:15 PM – 4:15 PM **Regency Ballroom (BR)**

Plenary Session III

RCMI U54 Centers Presentation Session I

Highlight RCMI contribution to national science advances and innovation to national science advances and innovation in NIH priorities on Health Disparities

Moderators
Gabriel Lai, PhD
NIMHD

Christine F. Hohmann, PhD
Morgan State University

Howard University
Valencia Perry, PhD

University of Texas, El Paso
Bibiana Mancera, PhD
Yong Qin, PhD

Morehouse School of Medicine
Leanne Burnham, PhD
K. Sean Kimbro, PhD

Ponce Health Sciences University
Melissa Marzan-Rodrigues, DrPH
Eliut Rivera-Segarra, PhD
Marcos J. Ramos, PhD
Wilfredo De Jesus-Rojas, MD

San Diego State University
Emily Schmied, PhD

University of Puerto Rico Medical Sciences Campus
Osmarie Martinez, PhD

Clark Atlanta University
Bekir Cinar, PhD

AGENDA

TUE. APR. 30

8:00 AM – 9:45 AM Regency Ballroom (BR)

Plenary Session IV

RCMI Consortium Program Evaluation

The primary goal of the RCMI Coordinating Center's Evaluation is to stress increased scientific and community collaborations, scientific productivity, development of new and early-stage investigators, and engagement of diverse groups of scientists in mitigating health disparities.

The RCMI tracking and Evaluation Consortium worked to achieve consensus on best practices for evaluation, standardization, and harmonizing evaluation data across the U54 RCMI programs, establish common metrics for evaluation, and provide input into the design and development of a centralized database management system to streamline the collection, management, analysis, and reporting of evaluative data for the RCMI U54 Center and the RCMI Coordinating Center.

Session Objectives:

- Present an update on the RCMI Program Evaluation by NIMHD.
- Provide updates on Common Metrics, Common Data Elements, Data Collection and Harmonization.
- Highlight RCMI Community Engagement Consortium Signature Programs.

Moderators

Emma Fernandez-Repollet, PhD
University of Puerto Rico, Medical Sciences Campus

Julie A. Baldwin, PhD
Northern Arizona University

Update on RCMI Program Evaluation

Elizabeth O. Ofili, MD, MPH
Morehouse School of Medicine

RCMI U54 Centers Evaluation, Data Collection, and Harmonization

Daniel F.K. Sarpong, PhD
Yale University Center for Health Equity

RCMI Community Engagement Consortium Signature Programs

Daniel F.K. Sarpong, PhD
Yale University Center for Health Equity

AGENDA

TUE. APR. 30

10:00 AM – 11:00 AM **Regency Ballroom (BR)**

Plenary Session V

RCMI Collaborations and Administrative Supplements and Funding Opportunities

This session will share information with RCMI Investigators on NIH programs, resources, funding opportunities and promote collaborations in effectively supporting training and research activities that address health disparities in the communities RCMI program serves.

Session Objectives:

- Discuss effective strategies and approaches in promoting meaningful collaboration between RCMI investigators and the NIH funded programs from COSWD, NIDA, All of Us, ODSS, CFAR/NIAID.
- Share NIH Program resources and funding opportunities with RCMI grantees.

Moderators

Rina Das, PhD
NIMHD

Samuel E. Adunyah, PhD
Meharry Medical College

Programs and Funding Opportunitites at COSWD

Jean H. Shin, PhD
Deputy Director, COSWD OD

Programs and Funding Opportunities at NIDA

Aria Crump, ScD
Director, ODHD, NIDA

All of Us Research Program Resources and Funding Opportunities

Martin Mendoza, PhD
Director, Health Equity

Office of Data Science Strategy (ODSS) Data Science Resources and Funding Opportunities

Raphael Isokpehi, PhD
Program Director, TWICE

Centers for AIDS Research (CFAR) Program and Funding Opportunities

Eric Refsland, PhD
Team Lead, CFAR, DAIDS, NIAID

AGENDA

TUE. APR. 30

11:30 AM –1:00 PM **Regency Ballroom (BR)**

Plenary Session VI

Lunch & Conversation

Featuring NIMHD Training, Other Opportunities, and Resources for Health Disparities Research

Session Objectives:

- Share NIMHD training opportunities to promote independent funding relevant to RCMI grantees.
- Share other NIMHD funding opportunities relevant to RCMI grantees.
- Share tools and resources to conduct health disparities research.

Moderator

Rina Das, PhD
NIMHD

Training Opportunities at NIMHD

Dorothy Castille, PhD
NIMHD

SBIR/STTR Opportunities and Loan Repayment Programs

CDR Michael Banyas, USPHS, MPA, MA
NIMHD

The PhenX Toolkit SDOH Collection

Nancy L. Jones, PhD
NIMHD

HD Pulse: A Resource for Health Disparities Research

Tilda Farhat, PhD
NIMHD

AGENDA

TUE. APR. 30

11:30 AM – 1:00 PM **Old Georgetown Room (MR)**

RCMI Administrators Working Lunch [Closed]

RCMI Program Administrators and Program Managers Association

This session will share best practices on effect research administration and research compliance.

Moderators

SeTonia Cook
Meharry Medical College

Geannene Trevillion, CRA
Morehouse School of Medicine

An Overview of NIH Grants Management

Michelle Phillips, PhD, CRA
NIMHD

Checklists for Cores and Projects

Claudia Alberico, PhD
North Carolina Central University

AGENDA

TUE. APR. 30

1:30 PM – 3:00 PM Regency Ballroom I/II (BR)

Concurrent Workshop A

Investigator Development Consortium

This session will foster transdisciplinary collaboration and mentorship across the RCMI Consortium. This science speed-dating workshop will allow basic biomedical, clinical, community and behavioral researchers the opportunity to engage with others who may not be familiar with their research area. This session will consist of rotating small group roundtable discussions to enable participants to share their research ideas and needs. By introducing their research and discussing their needs, participants will establish new collaborative and mentoring networks, as well as gain insights into research fields that they previously knew nothing or very little about.

Session Objectives:

- Explore new collaborative and mentoring partnerships.
- Gain insights into research across the network.
- Learn about research cores and other resources.

Facilitator

Vivek R. Nerurkar, DMLT, MSc, PhD
University of Hawaii at Manoa

Moderators

Zhenbang Chen, PhD
Meharry Medical College

Marc Cox, PhD
University of Texas, El Paso

Stacey Gorniak, PhD
University of Houston

Georges Haddad, PhD
Howard University

Christine F. Hohmann, PhD
Morgan State University

Eun-Sook Lee, PhD
Florida A&M University

Temesgen Samuel, DVM, PhD
Tuskegee University

Jonathan K. Stiles, PhD
Morehouse School of Medicine

Nicolette Teufel-Shone, PhD
Northern Arizona University

AGENDA

TUE. APR. 30

1:30 PM – 3:00 PM **Regency Ballroom III/IV (BR)**

Concurrent Workshop B

Community Engagement Consortium

This session will promote and strengthen academic and community partnerships in effectively supporting behavioral, clinical, and translational research that address diseases that disproportionately impact RCMI.

Session Objectives:

- Share community engagement transfer employed in underserved communities and communities of color.
- Discuss effective strategies and approaches in promoting meaningful collaboration between investigators and the community – Academic-Community Research Partnership.
- Introduce the role of the RCMI Community Engagement Consortium in the Learning phase of the Equitable Breakthroughs in Medicine Development (EQBMED)

Moderator
Nancy Jones, PhD
NIMHD

Science of Community Engagement, Particularly on Assessing of Measuring the Impact
Selina Hernandez, MPH
University of California, Riverside

Moderators
Carla Williams, PhD
Howard University

Donna Antoine-LaVigne, PhD
Jackson State University

Community Partners
Nicole Rowan, BBA, MSM
Meharry Medical College

Sara Sanders
San Diego State University

AGENDA

TUE. APR. 30

1:30 PM – 3:00 PM Cabinet / Judiciary (MR)

Concurrent Workshop C

Research Infrastructure Consortium

This session will facilitate communication about research resources at RCMI U54 Centers in order to enhance effectiveness and efficiency of core facilities and promote innovative practices for collaborative and interdisciplinary research.

Session Objectives:

- Share up-to-date information and highlight novel technological developments and their application to innovative research aimed at improving minority health and reducing and/or eliminating health disparities.
- Discuss issues and best practices in core facilities management and operations.
- Share practical information to enhance the optimization and implementation of technologies and techniques within core facility and biomolecular laboratory settings.
- Brainstorm strategic solutions to challenges and impediments to the cost-effective management of RIC/RCC facilities.

Moderators

Renato Aguilera, PhD
University of Texas, El Paso

Abiel Roche-Lima, PhD
University of Puerto Rico, Medical Sciences Campus

Catherine Propper, PhD
Northern Arizona University

Wendy Jai Men Huang, PhD
San Diego State University

Jacqueline Stevens
Jackson State University

Welcome and Workshop Overview

Paul B. Tchounwou, ScD
Morgan State University

Artificial Intelligence Program and the STRIDES Initiative at the National Institutes of Health

Laura Biven, PhD
Office of Data Sciences Strategy, NIH

Artificial Intelligence and Machine Learning as Service and Training at RCMI Coordinating Center

Muhammed Y. Idris, PhD
Morehouse School of Medicine

Single Cell Approaches (e.g RNAseq, ATACseq, DNAseq) to Explore Tumor Microenvironment in Relation to Health Disparity

Sergei Nekhai, PhD
Howard University

Panel Discussion on Challenges, Solutions, and Best Practices for Improving Operational Efficiency and Cost-Effective Management of RCI/ RCC Facilities

Pranab Dutta, PhD
Charles R. Drew University of Medicine and Science

Fatima Merchant, PhD
University of Houston

Kinfe Redda, PhD
Florida A&M University

James Wachira, PhD
Morgan State University

AGENDA

TUE. APR. 30

1:30 PM – 3:00 PM **Diplomat / Ambassador (MR)**

Concurrent Workshop D

EQBMED: Equitable Medicines Development RCMI-CC / PhRMA Foundation Collaboration

Equitable Breakthroughs in Medicine Development (EQBMED), led by Yale School of Medicine, Morehouse School of Medicine, the RCMI Coordinating Center (RCMI-CC) at Morehouse School of Medicine, and Vanderbilt University Medical Center, is a partnership bringing clinical trial sites closer to the community to further equity and access for diverse populations. EQBMED has selected the first four Learning Phase sites, moving the needle closer to a scalable and sustainable clinical trial model in historically underserved communities.

Session Objectives:

- Describe the objectives of the Learning Phase of the EQBMED Initiative.
- Present the RCMI-CC framework to expand industry sponsored clinical trial sites to RCMI institutions and affiliated health system partners.
- Describe the Learning Phase clinical trial sites at Grady Health Systems / Morehouse School of Medicine, Meharry Medical College / Vanderbilt University Medical Center, and Texas Southern University / RCMI Coordinating Center.

Moderators

Robert A. Kirken, PhD
University of Texas, El Paso

Tandeca King Gordon, EdD
Morehouse School of Medicine

Welcome and Overview on behalf of EQBMED Network Partners

Elizabeth O. Ofili, MD, MPH
Morehouse School of Medicine

Panelists

Tesheia Johnson, MBA
Yale Center for Clinical Investigation

Priscilla E. Pemu, MD, MS
Morehouse School of Medicine

Veronica Ajewole, PharmD
Texas Southern University

Rajbir Singh, MBBS
Meharry Medical College

AGENDA

TUE. APR. 30

3:15 PM –4:45 PM **Diplomat / Ambassador (MR)**

Concurrent Workshop E

National Research Mentoring Network (NRMN) Strategic Empowerment Tailored for Health Equity Investigators (SETH)

This session will provide an overview of the NRMN-SETH mock study section for early-stage investigators; NRMN alumni, coaches, developers, and mentors share lessons learned and best practices.

Session Objectives:

- Describe the timeline and goals of the NRMN-SETH mock study section
- Describe common proposal challenges and solutions identified during NRMN-SETH mock study section
- Hear from NRMN Alumni, coaches, developers, and mentors.
- Discuss the potential to adapt the NRMN-SETH program mock study section model for RCMI early-stage investigator initiated inter-institutional research projects, including RCMI-CC pilot project proposals.

Who should attend:

- RCMI early-stage investigators, who are planning to submit a RCMI-CC inter-institutional pilot project proposals, and/or who recently submitted an NIH research proposal (e.g. R or K applications) and received a summary statement.
- NRMN alumni (scholars, coaches, developers).
- RCMI mentors and RCMI IDC core directors.

Moderators

Yulia A. Levites Strekalova, PhD
University of Florida, Gainesville

Jonathan K. Stiles, PhD
Morehouse School of Medicine

Welcome and Overview

Elizabeth O. Ofili, MD, MPH
Morehouse School of Medicine

NRMN-SETH Scholars NIH Awarded Projects

Felicite Noubissi, PhD
Jackson State University

Ricky Camplain, PhD
Northern Arizona University

Hongmei-Wang, PhD
Texas Southern University

Monica Esquivel, PhD, RDN
University of Hawaii at Manoa

Stacey Gorniak, PhD
University of Houston

NRMN-SETH Coaching Model

Yulia A. Levites Strekalova, PhD
University of Houston

Georges Haddad, PhD
Howard University

NRMN-SETH Developer Model

Jonathan K. Stiles, PhD
Morehouse School of Medicine

Adriana Baez, PhD
University of Puerto Rico, Medical Sciences Campus

Priscilla E. Pemu, MD, MS
Morehouse School of Medicine

NRMN-SETH Mock Study Section Model

Mohamed Mubasher, PhD
Morehouse School of Medicine

Closing Remarks

Elizabeth O. Ofili, MD, MPH
Morehouse School of Medicine

AGENDA

TUE. APR. 30

3:15 PM –4:45 PM **Cabinet / Judiciary (MR)**

Concurrent Workshop F

RCMI Administrators

This session will engage consortium-wide RCMI U54 Center Administrators to share best practices on effective research administration and research compliance. Optimize data collection for reporting and evaluation of U54 Centers.

Session Objectives:

- Optimize data collection for reporting and evaluation of U54 Centers.
- Provide fiscal and administration session for program managers and research administrators of the RCMI consortium.
- Participants will be able to improve their work efficiency, make better decisions based on data, and make it easier for their institutions to successfully implement AI technology.
- Provide insights on how to educate users about new AI-enhanced functionalities and accurately interpret AI-driven insights.

Moderators

SeTonia Cook
Meharry Medical College

Geannene Trevillion, CRA
Morehouse School of Medicine

AI in Research Administration

Stacey McRae
Howard University

Pre-Award & Budget Development

Tamara Hill, PhD, CRA
Morehouse School of Medicine

Data Collection and Evaluation

Daniel F.K. Sarpong, PhD
Yale University Center for Health Equity

AGENDA

TUE. APR. 30

3:15 PM –4:45 PM Regency Ballroom I / II (BR)

Concurrent Workshop G

RCMI Clinical Research Network for Health Equity (CRN-HE) Multi-Site Collaboration
UG3 / UH3

The goal of the NIMHD funded RCMI Clinical Research Network for Health Equity (CRN-HE) is to leverage community-based clinicians and/or healthcare delivery systems to conduct research addressing health care for populations that experience health disparities including the diverse clinicians providing health services.

Session Objectives:

- The PIs/MPIs from the RCMI CRN-HE at the University of Hawaii at Manoa, San Diego State University, North Carolina Central University, and Howard University will describe their program's UG3 goals, milestones, and progress to UH3 submission.
- Daniel Sarpong, RCMI-CC MPI, will describe RCMI Consortium Common metrics and data standards that will guide data collection across RCMI CRN-HE
- Alexander Quarshie, Informatics Director, and Eva Lee, Senior Data Scientist, will share challenges with operationalizing EMR data for research, and outline data governance model.
- Kesley D. Holmes, DHA, MA, CCRP, Director, Clinical Trials Office (CTO) and Research Operations will briefly outline the CTO support of the CRNHE awardees for the RCMI-CC.

Moderator
Welcome & Overview
Rada K. Dagher, PhD, MPH
NIMHD

Speakers
Cecilia M. Shikuma, MD
University of Hawaii at Manoa

Guadalupe X. Ayala, PhD, MPH
San Diego State University

Deepak Kuman, PhD
North Carolina Central University

Mark S. Johnson, MD, MPH
Howard University

Daniel F.K. Sarpong, PhD
Yale University Center for Health Equity

Alexander Quarshie, MD, MS
Morehouse School of Medicine

Eva Lee, PhD
Morehouse School of Medicine and
Georgia Institute of Technology

Kesley D. Holmes, DHA, MS, CCRP
Morehouse School of Medicine

Closing Remarks
Rada K. Dagher, PhD, MPH
NIMHD

AGENDA

TUE. APR. 30

3:15 PM –4:45 PM Regency Ballroom III / IV (BR)

Concurrent Workshop H

AI / ML for Health Disparities

This concurrent session will present findings from Data Science Collaboration NOSIs and original research from AI/ML for Health Equity projects. We will also have a general presentation on funding opportunities related to two flagship NIH programs: the All of Us Researcher Workbench as well as the Artificial Intelligence / Machine Learning Consortium to Advance Health Equity and Researcher Diversity (AIM / AHEAD).

Session Objectives:

- Dr. Idris will provide an overview / introduction to current trends, applications, and opportunities around AI / ML in Health Disparities Research
- Showcase examples of Artificial Intelligence / Machine Learning Applications in Health Disparities Research across the RCMI Network
- Dr. Odom will lead a discussion on data science training opportunities, particularly around upskilling trainees from non-technical backgrounds

Moderators

Muhammed Y. Idris, PhD
Morehouse School of Medicine

Gabriel J. Odom, PhD
Florida International University

AI/ML for Health Disparities Research Focused on Hispanics

Abel Roche-Lima, PhD
University of Puerto Rico, Medical Sciences Campus

Machine Learning Analysis of Mixed Metals and Clinical Measures in Pediatric Populations

Carmen Dickinson-Copeland, PhD, MSCR
Morehouse School of Medicine

CardioGPT: Addressing Imbalanced Learning Commonly Encountered in ECG Classification Using NLP

Jianwei Zheng, PhD
Charles R. Drew University of Medicine and Science

Identifying Multi-Factor Combinations of Clinical and Socio-Demographical Data to Predict Cervical Dysplasia Outcomes Using Machine Learning Algorithms to Tackle Health Disparities Among Different Races / Ethnicities

Eduardo L. Tosado Rodríguez, PhD, MSc
University of Puerto Rico, Medical Sciences Campus

AGENDA

TUE. APR. 30

6:00 PM –7:00 PM **Regency Ballroom I / II (BR)**

Plenary Session VII

Sidney A. McNairy, Jr., PhD, DSc Awards Ceremony

The Sidney A. McNairy Jr Awards for Inclusive Excellence were established in 2023 by the RCMI Consortium to honor the legacy of Dr. McNairy in advancing inclusive excellence and service to the RCMI Program at the National Institutes of Health.

2023 Inaugural Award Recipients for Inclusive Excellence

- Inaugural Visionary Award Recipient: Sidney A. McNairy, Jr., PhD, DSc
- Young Investigator Award Recipient: Patricia Mendoca, PhD – Florida A&M University
- Extraordinary Leadership in Academic Community Partnership Award Recipient: Priscilla E. Pemu, MD, MS – Morehouse School of Medicine
- Extraordinary Leadership in Academic Community Partnership Award Recipient: Rev. Leland Jones, MDiv, DMin – Greater New Light Missionary Baptist Church, Atlanta, GA
- Extraordinary Mentorship Award Recipient: Jonathan K. Stiles, PhD – Morehouse School of Medicine
- Extraordinary Leadership Award Recipients: Shafiq A. Khan, PhD – Clark Atlanta University; Richard Yanagihara, MD, MPH – University of Hawaii at Manoa

Moderators

Emma Fernández-Repollet, PhD
University of Puerto Rico Medical Sciences Campus

Noreen Mokuau, DSW
University of Hawaii at Manoa

Selina Darling-Reed, PhD
Florida A&M University

Melissa Harrington, PhD
Delaware State University

Greetings

Sidney A. McNairy, Jr., PhD, DSc

2024 Award Categories
Young Investigator Awards

Teri Platt, PhD
Clark Atlanta University

Sourav Roy, PhD
University of Texas, El Paso

Outstanding Mentor Award

Paul B. Tchounwou, ScD
Morgan State University

Outstanding Senior Investigator Award

Cecilia M. Shikuma, MD
University of Hawaii at Manoa

RCMI Coordinating Center Outstanding Service Awards

Tandeca King Gordon, EdD, MEd
Morehouse School of Medicine

Mohamad Malouhi, MS
Morgan State University

Pamela L. Bullard
University of Hawaii at Manoa

Geannene Trevillion, CRA
Morehouse School of Medicine

Vivek R. Nerurkar, DMLT, MSc, PhD
University of Hawaii at Manoa

1Joshua Group Team
Kermit G. Payne; Melanie T. Hill, MBA;
Kimberly L. Brown, and Darren E. Baylor, JD

AGENDA

WED. MAY 1

8:00 AM – 12:00 PM **Regency Ballroom (BR)**

Plenary Session VIII

RCMI U54 Centers Presentation Session II

Highlight RCMI contribution to national science advances and innovation to national science advances and innovation in NIH priorities on diversity, equity, and inclusion.

Moderators
Larissa Aviles-Santa, MD
NIMHD

William M. Southerland, PhD
Howard University

K. Sean Kimbro, PhD
Morehouse School of Medicine

Morgan State University
Nicole Arnold, PhD

Meharry Medical College
Sanika S. Chirwa, MD, PhD

Florida A&M University
Selina Darling-Reed, PhD
Syreeta Tilghman, PhD
John S. Luque, PhD

Florida International University
Diana Azzam, PhD

Texas Southern University
Hongmei Wang, PharmD, PhD
Kehinde A. Idowu, PhD

University of Hawaii at Manoa
Jerris R. Hedges, MD, MS, MMM
Nicholas James, PhD
Nani Morgan, MD

Charles R. Drew University of Medicine & Science
Yong Wu, PhD

Jackson State University
Joseph Whittaker, PhD

North Carolina Central University
Vijay Sivaraman, PhD

Northern Arizona University
Emily Cope, PhD

Tuskegee University
Bedi Deepa, MD, PhD
Timothy Turner, PhD

Delaware State University
Shaidul Islam, PhD
Chase Stratton, PhD

University of California, Riverside
Selina Hernandez, MPH

University of Houston
Bettina M. Beech, DrPH, MPH

Xavier University of Louisiana
Gene D'Amour, PhD
Christopher Williams, PhD

AGENDA

WED. MAY 1

12:15 PM – 1:15 PM **Regency Ballroom (BR)**

Plenary Session IX & Closing

NIMHD Charge

Moderators

Nathan Stinson, Jr., PhD, MD, MPH
NIMHD

Richard Noel, Jr., PhD
Ponce Health Sciences University

Closing Charge

Monica Webb Hooper, PhD
Deputy Director, NIMHD

Closing Remarks

Elizabeth O. Ofili, MD, MPH
Morehouse School of Medicine

Emma Fernandez-Repollet, PhD
University of Puerto Rico, Medical Sciences Campus

Meharry Medical College, is one of the nation's oldest and largest historically black academic health science centers dedicated to educating physicians, dentists, researchers, and health policy experts. Founded in 1876, Meharry was the first medical school in the South for African Americans. Today, Meharry includes a medical school, dental school, graduate school, physician assistant program, and applied computational sciences school. Meharry is also a leading producer of African Americans with Ph.Ds. in biomedical sciences.

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ABSTRACTS

Posters are Presented in the Chesapeake Suites (MR) and Terrace (2nd Floor)

ABSTRACTS

Basic and Applied Minority Health and Health Disparities Research

Cancer Health Disparities Research

01.01.01 – Poster Session 2 · Chesapeake Suites (MR)

THE REGULATION AND TARGETING OF HISTONE METHYLATION SIGNALING IN PROSTATE CANCER

Guoliang Li, Sherly I. Celada, LaKendria K. Brown, Samuel E. Adunyah, Robert J. Matusik and Zhenbang Chen
Meharry Medical College, and Vanderbilt University Medical Center

Prostate cancer (PCa) is the most common non-cutaneous cancer in American men. In addition, PCa disproportionately strikes African American men more than other ethnic groups. The molecular mechanism of PCa progression remains elusive, and castration resistant prostate cancer (CRPC) is not curable. Therefore, new targets and more effective treatment strategies are urgently needed to achieve better clinical outcomes. Literature shows that aberrant histone modifications, including methylation, are associated with the development and progression of PCa. Deregulation of the trimethylation of lysine 4 and lysine 27 on histone H3 (H3K4me3 and H3K27me3) is frequently observed in advanced PCa and CRPC. Histone methylation is a reversible dynamic process that is tightly controlled by histone methyltransferases and demethylases to regulate biological functions in cells. EZH2 (Enhancer of zeste homolog 2)-the histone H3K27 methyltransferase and KDM5B (Lysine demethylase 5B)-the histone H3K4 demethylase are upregulated in human PCa and CRPC. Our data showed that the levels of EZH2 and KDM5B are significantly increased in several human PCa cell lines and prostate tumors of Pten mutant mice. We investigated the anti-cancer effects of KDM5B/EZH2 inhibition in both human PCa cells and mouse models. We found that combined inhibition of KDM5B and EZH2 to disrupt H3K4me3 and H3K27me3 effectively suppressed PCa growth in human PCa cells and mouse models. Mechanistically, KDM5B and EZH2 regulated AKT signaling pathways in human PCa cells and mouse models. Combined inhibition of KDM5B and EZH2 abrogated AKT signaling and induced in senescence in a synergistic manner. Our data support the concept that the combination inhabitation of KDM5B/EZH2 is a novel and effective therapeutic strategy against PCa including CRPC.

01.01.02 – Poster Session 1 · Chesapeake Suites (MR)

ANALYSIS OF TRANSCRIPTOME-WIDE DIFFERENCES AMONG THE AFRICAN AMERICAN AND WHITE PARTICIPANTS WITH TRIPLE-NEGATIVE BREAST CANCER

Kumaraswamy Naidu Chitrala
University of Houston (KNC)

Breast cancer is known to be the second most common cancer type among women in the United States. According to the National Cancer Institute, cancer stat facts there were 297,790 estimated new cases in 2023. Among the breast cancer subtypes, triple-negative breast cancer (TNBC) is highly heterogeneous with a poor prognosis and accounts for 15%-20%. Specifically, African American females are known to develop TNBC more compared to White females. In this study, we assessed the differences in the transcriptome profiles of the samples from African American (AA) and White patients with TNBC. We have isolated the samples and performed RNA sequencing experiments. We used CASAVA to perform quality control analysis followed by the alignment with the reference genome using the tools HISAT2, and TOPHAT2. Mapped genome results were visualized using the Integrative Genomics Viewer. DeSeq2 was used to perform the differential gene expression (DEG) analysis. Pathway enrichment analysis was performed using DAVID. Our results showed that 692 genes were uniquely expressed among the AA patients and 855 genes were uniquely expressed among the White patients. Deseq2 analysis showed that 5 genes were differentially expressed at a significant p-value< 0.01 and p-value adjusted (padj) <0.01. Among them, the genes CXCL8II (-3.29), CCDC163 (-2.92) were found to be down-regulated, and the genes LINC01291 (9.31), ZNF683 (1.90), SCARB1 (1.34) were found to be upregulated. Pathway enrichment analyses showed that up-regulated genes were significantly enriched in plasma lipoprotein assembly, remodeling, and clearance, binding and uptake of ligands by scavenger receptors, scavenging by class B receptors, transport of small molecules, vesicle-mediated transport, HDL clearance, plasma lipoprotein clearance pathways. Downregulated genes were significantly enriched in cytokine signaling in the immune system, signal transduction, immune system, cellular responses to stress, senescence-associated secretory phenotype, cellular senescence, signaling by GPCR, chemokine receptors, signaling by Interleukins, interleukin signaling, cellular responses to stimuli pathways. In conclusion, our results will be useful in further studies on elucidating the transcriptome level disparities among AA and white patients with TNBC.

Research reported in this publication was supported by the National Institute on Minority Health and Health Disparities of the National Institutes of Health to the University of Houston under Award Number U54MD015946. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

01.01.03 – Poster Session 2 · Chesapeake Suites (MR)

DISPARITIES IN PRESCRIPTION OPIOIDS AMONG A NATIONAL SAMPLE OF ADULT CANCER PATIENTS, 2012-2021.

RW Algatan; BK Smith; SB Weaver; LT Wingate
Howard University Hospital, Howard University College of Pharmacy

OBJECTIVES: Cancer is a major public health problem worldwide and is the second most common cause of death in the United States after heart disease. Pain remains a serious sequela of cancer and many treatments rendered to patients with cancer are designed to treat pain. This study aimed to determine whether racial and ethnic differences exist in rates of opioid prescriptions for adults diagnosed with cancer in the United States.

METHODS: This serial cross-sectional study included adults diagnosed with cancer who participated in the Medical Expenditure Panel Survey (MEPS) from 2012-2021. Descriptive statistics were used to characterize the baseline characteristics of the sample. Multiple logistic regression models were used to estimate the relationships between race/ethnicity and receipt of opioid prescription for adult cancer patients. All estimates were adjusted for the complex probability survey design of MEPS using sampling weights, stratification, and clustering to provide nationally representative estimates.

RESULTS: Out of 21753 adult respondents with a cancer diagnosis only 5151 respondents had an analgesic prescription on their profile, which are weighted to represent 5,799,878 cancer patients present in the United States between 2012-2021. Among cancer patients with an opioid prescription, 90.03% were White, 6.13% were Black, 1.17% were American Indian/Alaskan Natives, and were 0.89% Asian/Native Hawaiians. Based on multivariable regression results, Black respondents (OR = 0.68, 95% CI: 0.55-0.85) and Asian or Native Hawaiian respondents (OR = 0.45, 95% CI: 0.26-0.76) were significantly less likely than White respondents to obtain opioid prescriptions after controlling for other covariates. American Indian/Alaskan Native respondents had significantly higher adjusted odds of obtaining opioid prescriptions (OR = 4.35, 95% CI: 1.57-11.53) compared to White respondents.

CONCLUSIONS: There are disparities in opioid prescriptions by race and ethnicity for patients undergoing cancer treatment.

ABSTRACTS

01.01.04 – Poster Session 1 · Chesapeake Suites (MR)

MODULATION OF THE TRANSCRIPTOME OF TRIPLE NEGATIVE BREAST CANCER BY TRYPANOSOMA CRUIZI EXTRACTS

DD Ball; KJ Rayford; A Cooley; PN Nde; and AM Sakwe
Department of Biomedical Sciences, School of Graduate Studies, Meharry Medical College Nashville, TN (DDB, AMS, KJR, AC, PNN)

PURPOSE: Patients diagnosed with triple negative breast cancer (TNBC) are often resistant to conventional treatments resulting in poor prognosis and relapse of more aggressive tumors. Therefore, an urgent need for nonconventional therapeutics to antagonize highly aggressive tumors has become a major necessity. Substantial evidence supports the notion that Trypanosoma cruzi, an intracellular protozoan, has anti-tumor properties, including inhibition of cell proliferation, immune evasion, and metastasis, in breast and colon cancer models. However, the molecular mechanisms underlying the T. cruzi induced anti-tumor activities remain poorly understood. METHODS: In this study, we evaluated the transcriptomic profiles of two morphologically distinct TNBC lines following treatment with cytosolic and crude membrane extracts of T. cruzi (Tuhaluen strain, clone MMC20A). We isolated total RNA for RNA-seq, performed in silico analysis, and validated mRNA expression of selected differentially expressed genes by RT-qPCR. RESULTS: Although both cytosolic and membrane extracts attenuated TNBC cell viability in a cell type dependent manner, the basal-like MDA-468 cells were more sensitive to membrane extracts of T. cruzi compared to the mesenchymal-like BT-594 TNBC cells. T. cruzi extracts significantly affected the expression of 1138 and 1277 mRNAs in MDA-468 and BT-594 TNBC cells, respectively. We observed that in both cell lines, the membrane extracts were more potent than the cytosolic extracts: 977 versus 421 genes in MDA-468 cells and 1027 versus 862 genes in BT-549 cells, respectively. Gene ontology and KEGG pathway analysis revealed substantial enrichment of MAPK, Cytokine-Cytokine Receptor signaling, and proinflammatory signaling pathways. Of the 86 genes validated by RT-PCR, proinflammatory genes such as JUNB, JUND, FOSB and tumorigenic biomarkers such as EGR1 and RAGE were found to be upregulated. CONCLUSION: Taken together, our study provides evidence of anti-tumor properties of T. cruzi protein extracts, which can be exploited to identify novel biotherapeutic interventions for patients with aggressive TNBC.

This project was supported, in part, by NIH/NIGMS SC1GM139814, NIH U54MD007586 and an Education Gift from Dr. Bernard Crowe.

01.01.08 – Poster Session 2 · Chesapeake Suites (MR)

POTENTIAL THERAPEUTIC EFFECTS OF KAEMPFEROL ON TRIPLE-NEGATIVE BREAST CANCER CELLS

S Kaur; P Mendonca; KFA Soliman
College of Pharmacy and Pharmaceutical Sciences, Institute of Public Health (CoPPS, IPH), Florida A&M University, Tallahassee, FL (PM; SK; KFAS)

Triple-negative breast cancer (TNBC) is one of the most known aggressive subtypes of breast cancer. It affects African American women disproportionally in comparison to Caucasian women. Due to the lack of estrogen, progesterone, and human epidermal growth factor receptors (HER-2), it poses direct challenges to the efficacy of standard hormonal therapies. The current TNBC treatments present higher toxicity and multiple side effects. An alternative would be using natural compounds that have emerged as potential anticancer agents. Kaempferol is a flavonoid aglycone found in many fruits, vegetables, and herbs. PURPOSE: this work aims to investigate the differential effect of kaempferol on cell toxicity, cell growth, and underlying mechanisms in inducing cell cycle arrest in genetically different TNBC cells from Caucasian (MDA-MB-231) and African American (MDA-MB- 468) women. METHODS: cytotoxic assays, cell cycle, and RT-PCR assays. RESULTS: kaempferol significantly inhibited cell growth in both the cell lines with a more profound effect against MDA-MB-231 (IC50: 43.86 µM) compared to MDA-MB-468 cells (IC50: 53.47 µM). Similarly, kaempferol treatment induced cell cycle arrest at S-phase in both the cancer cell subtypes. The MDA-MB-231 cells showed kaempferol effect at lower concentrations (6.25µM and 12.5µM), while MDA-MB-468 cells showed the same effect at higher concentrations (25µM and 50µM). Kaempferol also modulated CDK gene expression associated with cell cycle progression in breast cancer cells. The inhibition at S-phase is important in cancer treatment because it targets the highly proliferative nature of cancer cells which are characterized by uncontrolled cell division. CONCLUSION: This study indicates that, by inducing cell cycle arrest at the S-phase, kaempferol may interfere with cancer cell growth and proliferation, inhibiting DNA replication, and offering potential therapeutic benefits. This approach could reduce side effects and increase treatment efficacy, offering hope for more effective interventions in the fight against TNBC.

National Institute of Minority Health and Health Disparities of the NIH U54 MD007582

01.01.11 – Poster Session 1 · Chesapeake Suites (MR)

PREXASERTIB INDUCES DNA REPAIR DEFICIENCY AND SYNERGIZES WITH ADRM1 INHIBITOR IN QNBC CELLS

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Breast cancer persists as one of the deadliest forms of cancer affecting women. Within its diverse subtypes, quadruple-negative breast cancer (QNBC) stands out as the most aggressive, predominantly affecting African American patients and challenging to treat. Mechanistically, heightened DNA repair and activation of cell cycle checkpoints stand as primary factors contributing to QNBC tumors' resistance to chemotherapy and recurrence of the disease. We examined the influence of DNA damage checkpoint kinase 1 (CHK1) inhibition using prexasertib on regulation of homologous recombination (HR) proteins as single agent and in combination with ADRM1-specific inhibitor Up284.. Interestingly, our data indicate an important cross-talk between DNA damage response and ADRM1 signaling, which contributed to cell cycle dysregulation and synergistic lethality in QNBC cells. We assessed HR efficiency and DNA damage through Dr-GFP report and comet assays, respectively. Additionally, we examined DNA morphology and DNA repair foci through immunofluorescence analysis. Furthermore, we conducted bioinformatics analysis on QNBC patients and KmPlot to assess RAD51 expression and survival probability across various parameters such as tumor stage, subtype, and race in breast cancer patients.

Our findings demonstrate that inhibition of CHK1 by prexasertib promotes downregulation of BRCA1 and RAD51 proteins. Consistently, QNBC cells treated with prexasertib exhibited significant reduction in HR efficiency compared to control cells. These results led us to hypothesize that prexasertib treatment induces homologous recombination deficiency (HRD) and therefore could synergize with ADRM1 inhibitor Up284 in QNBC cells. Notably, there existed a contrast in RAD51 expression among racial cohorts, with African-American breast cancer patients exhibiting higher RAD51 levels compared to Caucasian counterparts.

Correspondingly, African-American QNBC patients displayed diminished survival rates. These findings suggest RAD51 as a potential biomarker for aggressive QNBC and for racial discrepancies in breast cancer outcomes. The in vitro preclinical data presented herein offers further mechanistic understanding for the prospective assessment of combining prexasertib and ADRM1 inhibitor Up284, aiming for enhanced outcomes and decreased racial disparity in QNBC.

U54-MD007585 32

01.01.12 – Poster Session 2 · Chesapeake Suites (MR)

EXPLORING DNA METHYLATION MARKS AND CLINICAL APPLICATIONS IN PROSTATE CANCER DISPARITIES

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Abstract: Prostate cancer exhibits significant racial and ethnic disparities in both incidence and mortality rates, stemming from a complex interplay of factors including structural, socioeconomic, socio-environmental, behavioral, and biological influences. However, comprehensive genomic studies to investigate factors contributing to prostate cancer etiology and progression, has predominantly focused on populations of European origin, leaving a notable gap in understanding the disease among African American and other minority populations. Epigenetic alterations, particularly DNA methylation changes, are prevalent in early prostate carcinogenesis, i.e., during the transition from benign prostate epithelium to inflammatory lesions called proliferative inflammatory atrophy and premalignant prostatic intraepithelial neoplasia lesions in most prostate cancers and presents a promising avenue for biomarker discovery. In this study, we employed sodium bisulfite conversion followed by sequencing of genomic DNA on biospecimens from African American and European American men, including benign and cancer samples from radical prostatectomies, tissue biopsies, and cell-free circulating tumor DNA from blood. Our results reveal differential DNA methylation patterns associated with high-grade and/or advanced-stage disease, as well as with disease recurrence and disparities in aggressive subtypes such as neuroendocrine and metastatic prostate cancers. These findings underscore the potential of epigenetic DNA methylation marks as biomarkers for various clinical applications, including screening, diagnosis, risk stratification, active surveillance, and treatment monitoring. Addressing the critical need for novel biomarkers in prostate cancer management, this study highlights the utility of exploring epigenetic mechanisms to mitigate prostate cancer disparities and improve patient outcomes across diverse populations.

2U54MD007597

01.01.13 – Poster Session 1 · Chesapeake Suites (MR)

HER2 EXPRESSION IN BLACK MEN WITH PROSTATE CANCER

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PURPOSE: Patients with prostate cancer (PCa) initially respond to androgen deprivation therapy. However, relapse is inevitable and lethal. For this reason, inhibiting androgen-independent signaling pathways—such as human epidermal growth factor receptor 2 (HER2)—is a promising area of investigation. HER2 overexpression in PCa tumors correlates with worse prognosis, but HER2 has not been evaluated in Black men. We hypothesize that HER2 overexpression correlates with West African genetic ancestry (WAA) in Black PCa patients and worsens outcomes. METHODS: We quantified HER2/ERBB2 with RNAseq analysis of prostate tissue samples collected from Black patients (n=36) and assessed a correlation with WAA through single nucleotide polymorphism genotyping of genomic DNA. We conducted immunohistochemistry on primary PCa tissue collected from 10 Black PCa patients. We quantified HER2/ERBB2 mRNA expression in Black and non-Hispanic white (NHW) PCa cell lines. We determined the effect of HER2 blockade on migration and cell viability. We used Pathway Studio to identify top-ranked HER2-associated genes in the MDA-PCa-2b cell line. RESULTS: RNAseq analysis suggests a positive correlation between HER2/ERBB2 and WAA (r=0.1593). Thirty percent (3/10) of the Black tissue specimens show moderate HER2 staining. We detected HER2/ERBB2 mRNA in our cell lines. When treated with 20 nM trastuzumab, migration was not reduced in NHW cell lines. When treated with 20 nM trastuzumab, we only observed significantly reduced viability in Black cell lines. Targeted analyses in MDA-PCa-2b using Pathway Studio revealed statistically significant genes EGFR, LTBP3, TGF-A, HBEGF, GLO1, MYC as well as HER2/ERBB2. CONCLUSION: HER2/ERBB2 expression is correlated with WAA in prostate tissue, and primary PCa tumors of Black patients have detectable HER2 protein expression before metastasis. Inhibition of HER2 with 20 nM trastuzumab alters migration and cell viability differentially by race. HER2 interacts with at least 25 proteins involved in PCa genesis & metastasis.

Research reported in this poster is supported by the National Institutes of Health/National Institute on Minority Health and Health Disparities Research Centers in Minority Institutions (RCMI) (2U54MD007602) (LWB), the Department of Defense Prostate Cancer Research Program (W81XWH2110038) (LWB), the Prostate Cancer Foundation (20YOUN04) (LWB), the Georgia Clinical Translational Science Alliance KL2 Scholars Program (KL2TR002381) (LWB), and the National Institute of General Medical Sciences of the National Institutes of Health RISE (R25GM058268) (JM).

01.01.14 – Poster Session 2 · Chesapeake Suites (MR)

COOPERATIVE YAP/TEAD AND NF-KAPPA B SIGNALING IN PROSTATE CANCER

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PURPOSE: Metastatic prostate cancer poses a substantial health challenge, particularly affecting African American men, due to the poorly understood disease mechanism and lack of therapy that prolongs patient survival. The objective of this study is to investigate direct YAP/TEAD and NF-kappa B/RELA interactions that synergically contribute to the aggressiveness of prostate cancer.

METHODS: The interaction of RELA with YAP1 and TEAD was visualized by co-immunoprecipitation and proximity ligation assay. We assessed YAP1, TEAD, and RELA protein levels in tissues using immunohistochemistry and mRNA levels with quantitative PCR. Cell migration was evaluated using a scratch-wound assay. Cell growth was assessed utilizing a CCK-8 kit. Subcutaneous xenograft assays were conducted to evaluate prostate tumor growth in vivo. Algorithms built in TIMER and cBioportal helped visualize the correlative expression patterns of YAP1, TEAD, and RELA transcripts in human prostate tumor samples.

RESULTS: We demonstrated that YAP1/TEAD-RELA protein interaction occurs in prostate tumor cells regulated by androgens and cytokines and inhibited by genistein. YAP1 and TEAD knockdown reduced cell migration, while ectopic RELA expression failed to reverse this effect. Furthermore, genistein attenuated YAP1, TEAD, and RELA expression in prostate tumor cells and tissues. TED-347, a potent YAP1/TEAD inhibitor, diminished cell growth ex vivo. Also, TED-347 or genistein significantly reduced prostate tumor growth in vivo, which coincided with decreased YAP1 and RELA protein levels, suggesting that TED-347 and genistein are portent YAP1/TEAD inhibitors. We observed a robust positive correlation between YAP1, TEAD3, and RELA expression in human prostate tumors. We are also conducting quantitative analysis of YAP1 and RELA in prostate cancer race disparity tissues.

CONCLUSION: These findings unveil novel insights into the crosstalk between the Hippo/YAP and NF-kappa B pathways crucial for prostate cancer progression. Targeting this axis holds promise for developing innovative therapeutic strategies to improve patient outcomes in cancer management.

NIH/NIMHD/RCMI U54MD007590

ABSTRACTS

01.01.15 – Poster Session 1 · Chesapeake Suites (MR)

FRACTIONATED OCIMUM GRATISSIMUM LEAF EXTRACTS INHIBIT THE PROLIFERATION AND INDUCE APOPTOSIS OF A549 LUNG ADENOCARCINOMA (A549) CELLS

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PURPOSE: Leaf extracts of Ocimum gratissimum (Og) have been used in West African folk medicine for centuries. Previous in-vitro studies in our laboratory demonstrated that fractionated ethyl acetate (P2) and water- (PS/PT1) soluble extracts of Og (OGFEs) inhibit the proliferation of prostate cancer cells. It has been reported that the crude aqueous extract induces apoptosis in lung adenocarcinoma cells, however, the efficacy of fractionated extracts of Og on these cancer cells remains unclear. In the present study, we hypothesized that OGFEs inhibition of cell growth and induction of apoptosis is associated with the activation of pro-apoptotic proteins and induction of DNA condensation in A549 cells.

METHODS: To test the above-stated hypothesis, Og was cultivated and its leaves were harvested, extracted and fractionated to produce fraction P2 in ethyl acetate and fraction PS/PT1 in water. Anti-proliferative activity was assessed by direct cell count using a hemocytometer. For morphological characterization of apoptosis induction by OGFEs, nuclear staining was performed using 4',6-diamidino-2-phenylindole (DAPI). Western blot analysis was performed to evaluate the apoptotic activity of OGFEs.

RESULTS: Data generated from anti-proliferation studies indicated that P2 significantly inhibits cell proliferation in a concentration-dependent manner, while cells treated with PS/PT1 showed a gradual decrease in viability with significant effects occurring at 500µg/mL DAPI staining revealed induction of apoptosis as evidenced by chromatin condensation and formation of apoptotic bodies in treatment with 200 and 400 µg/mL of OGFEs. An increase in the levels of pro-apoptotic proteins was observed as the concentration OGFEs increased. CONCLUSION: These results suggest that P2 and PS/PT1 fractionated extracts of Ocimum gratissimum leaves induce growth inhibition and apoptosis of A549 cells.

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01.01.16 – Poster Session 2 · Chesapeake Suites (MR)

S-NITROSYLATION OF P53 UNDER NITROSATIVE STRESS IN MELANOMA CELLS

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Our analyses and previous studies showed that melanoma tumors expressed significantly higher induce nitric oxide synthase (iNOS) than most tumors and normal tissues. Nitric oxide (NO) is known to modify protein structure and plays a critical role in supporting tumor growth, metastasis, and resistance to therapy. One physiological influence of nitric oxide (NO) is exerted directly through the post-translational modification of crucial signaling proteins by S-nitrosylation (SNO). Previous studies showed that the function of p53 could be regulated by nitrosative stress via inducing protein conformation changes in cancer cells. To date, it remains unclear whether nitrosative stress can cause dysfunction of p53 in cancer cells. Herein, we examined the effects of different levels of NO donors on the growth of melanoma cells. Our in vitro studies showed that low levels of nitrosative stress (< 20 µM NO donors, S-nitrosoglutathione (GSNO) or diethylenetriamine (DETA) NONOate) did not suppress melanoma cell growth but slightly increased melanoma cell growth. Our biotin switch assays showed that the treatment with GSNO or DETA NONOate significantly increased total S-nitrosylated proteins in melanoma A375 and SB2 cells. p53 was confirmed to be S-nitrosylated in melanoma cells under nitrosative stress by the biotin switch assay and mass spectrometry. Proteomic characterization identified Cys242, Cys275, and Cys277 as the SNO sites of p53. The structural analysis demonstrated that the SNO of Cys277 and Cys242 could disrupt p53 conformation and its DNA-binding ability, further confirmed by the electrophoretic mobility shift assay. Our results describe an important mechanism of how nitrosative stress modifies crucial cysteines of p53 and alters p53 DNA-binding activities through SNO. Herein, we first present how the post-translational SNO of p53 alters its structure and DNA binding activities under nitrosative stress, which sheds light on a potential mechanism of nitrosative stress regulating p53 function in various inflammatory tumors.

The Border Biomedical Research Center (BBRC) Pilot Projects at UTEP; The Lizanell and Colbert Coldwell Foundation Research Award

01.01.17 – Poster Session 1 · Chesapeake Suites (MR)

PROTEOLYSIS-TARGETING CHIMERAS TO TREAT NON-SMALL CELL LUNG CANCER

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PURPOSE: Non-small cell lung cancer (NSCLC) accounts for the majority (~82%) of all lung cancer diagnoses and can be caused by several distinct mechanisms. One such mechanism is an inversion in Chromosome 2p leading to fusion of the tyrosine kinase domain of the Anaplastic Lymphoma Kinase (ALK) gene with the coiled-coil domain of the echinoderm microtubule-associated protein-like 4 gene (EML4), leading to dimerized, constitutively active tyrosine kinase. While the FDA has approved competitive ALK inhibitors, spontaneous suppressor mutations in the ALK active site limit their efficacy, with 11-month median duration of response.

METHODS: To address this, we developed a series of proteolysis-targeting chimeras (PROTACs) to induce the degradation of the EML4-ALK protein. These heterobifunctional PROTACs are small molecules containing an EML4-ALK targeting motif coupled to an E3 ubiquitin ligase-recruiting ligand. This complex induces the ubiquitination and subsequent proteasome-mediated degradation of the target protein.

RESULTS: Through a series of iterative synthesis and testing, we have developed a series of early stage, lead PROTAC compounds. In cellular assays, we see that single nanomolar concentrations of our PROTACs induce degradation of transformed, NSCLC-causing EML4-ALK fusions, as well as EML4-ALK with suppressor mutations that block the efficacy of currently approved therapeutics. Importantly, we observe EML4-ALK degradation for concentrations at or lower than those used for current inhibitors. In an NSCLC mouse xenograft model, oral doses of 10 mg/kg induced complete tumor regression, with a shorter time course to regression and at lower doses than a currently approved inhibitor. In closely monitored mice, we observe no acute toxicity, weight loss, or lethargy in treatment regimens matching tumor regression levels.

CONCLUSION: Here we present ongoing cellular studies of further optimization of our lead compounds against EML4-ALK and drug-resistant ALK suppressor mutations.

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01.01.18 – Poster Session 2 · Chesapeake Suites (MR)

HORMONE RECEPTOR-POSITIVE BREAST CANCER DRUG DISCOVERY

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PURPOSE In the United States, breast cancer is the leading type of cancer for women, with over 310,000 new cases and over 42,000 deaths projected in 2024. Disparities in breast cancer are evidenced by a 10% lower 5-year survival rate for the Black population when compared to the White population. 70-80% of cases are hormone receptor (HR)-positive and have approved treatment modalities known as endocrine therapy. Despite its success, resistance to endocrine therapy eventually develops in most patients and results in progression to advanced stages of the disease. This project aims to address endocrine therapy resistance and reduce health disparities in breast cancer by discovering novel small molecule compounds.

METHODS An artificial intelligence-assisted high throughput virtual screen (HTVS) was conducted using over one billion small molecules targeting the estrogen receptor alpha (ERα). Feature importance analysis of the deep neural network model used during the HTVS was performed to gain insights into molecular substructures correlated with predicted ligands. To validate the top scoring hits of the HTVS, molecular dynamics simulations were performed with the docked ligands and ERα. Future studies include the experimental screening of the top scoring hits in HR-positive breast cancer cell line models.

RESULTS/EXPECTED RESULTS A targeted subset of the one billion compounds predicted by the deep learning model were docked and scored by free energy change. Molecular dynamics simulations supported docked poses predicted during the HTVS. Feature importance analysis of the deep neural network revealed molecular characteristics that are central to ERα ligands. Experimental screening of the top 20 lead compounds is underway.

DISCUSSION/CONCLUSION The number of commercially available small molecule compounds has increased into the range of tens of billions over the past few years and has broadened drug discovery opportunities. This project aims to explore this expanded chemical space for novel therapeutics in breast cancer.

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01.01.19 – Poster Session 1 · Chesapeake Suites (MR)

INVESTIGATING SMR PEPTIDE INTERACTIONS WITH BREAST CANCER-ASSOCIATED PROTEINS

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Background: Breast cancer (BC) is the second leading cause of cancer deaths in the US. Understanding the underlying mechanisms of BC is essential to improve survivability and reduce metastasis [1]. Our previous research examining the role of Nef in exosome mediated chronic immune activation demonstrated [2] that the Secretion Modification Region (SMR) peptide (Nef domain) interacts with specific proteins (mortalin, vimentin) key to tumorigenesis, and in published work shows it inhibits tumorosome extracellular vesicle (tEV) release, arrests the cell cycle, and restores complement-mediated cell death [2-5]. These findings suggest that the SMR targets important protein regulators of Epithelial Mesenchymal Transition (EMT) [2-5]. Objective: In this study we used SPR to show that the SMR peptide interacts specifically with its protein targets, and to compare the binding affinity and kinetics of the SMR peptide with the full Nef protein. Methods: In previous published work we showed that the SMR peptide interacted with the cellular protein mortalin [2]. In follow up co-IP assays and biological analysis research we have identified Vimentin as another binding target for the SMR peptide. Results: The SPR results further supported the interactions between Nef or the SMR peptide and VIM and mortalin showing Nef had a high affinity for binding to vimentin, and mortalin proteins. Discussion: Co-IP is a method that allows us to identify protein complexes and determine protein–protein interactions. In Co-IP, we use antigen-antibody interactions to isolate proteins. The protein of interest is “pulled down” from a cell lysate using antibody. Co-IP can be followed by SPR to gain deeper insights into interactions, but SPR directly measures binding kinetics, while Co-IP identifies protein complexes. Conclusion: The findings from this study underscore the potential of the SMR peptide as a tool to explore exosome mediated EMT pathways, and as a BC therapeutic.

NIH/2U54/MD007602-36, NIH/5U54/MD007602-35, NIH/2U54/MD007602-31A1, NIH/ RCMI/U54 CTRHD Pilot Grant

ABSTRACTS

01.01.21 – Poster Session 2 · Chesapeake Suites (MR)

EXPLORING SIGNALING PATHWAYS OF TUMOR-NERVE INTERACTIONS IN PROSTATE AND BREAST CANCER

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PURPOSE: A significant portion of prostate cancer (PCa) and breast cancer (BCa) patients develop bone metastatic disease. In some cases, cancer spreads through the nervous system, a process known as perineural invasion (PNI). Neurite outgrowth is believed to be a precursor to PNI. Snail is an important gene which regulates the epithelial-mesenchymal transition (EMT) process in which tumor cells at the invasive front undergo this transition to promote invasion, migration, and subsequent metastasis. We hypothesize that Snail expression will stimulate neurite outgrowth in both PCa and BCa cells through extracellular vesicles from cancer cells interacting with neurons.

METHODS: We collected conditioned media from PCa and BCa cells and isolated exosomes. Exosomal markers were detected using western blot. Additionally, we used Transmission Electron Microscopy (TEM) to observe the secretion of exosomes. Proteomics was performed to analyze proteins expressed within exosomes of LNCaP Snail overexpressing or C4-2 Snail knockdown cells. Our results showed that Snail-expressing cells secrete exosomes containing Talin1. Talin1 has previously been associated with neurite outgrowth. Neurite outgrowth assays were then performed using conditioned medium collected from C4-2 cells with Snail knockdown and MCF-7 cells with Snail overexpression.

RESULTS: Increased neurite outgrowth is observed in PC-12 cells and NPC (Induced Pluripotent Stem Cells differentiated neuronal progenitor cells) when cultured with conditioned medium collected from PCa and BCa cells expressing high levels of Snail. AKT activation was observed in the neuronal cells in response to conditioned media from Snail-expressing cells. Furthermore, we found that mH4, a proprietary small molecule inhibitor of Talin1, reduces Snail-mediated neurite outgrowth and AKT activation (p-AKT Thr308 and Ser473).

DISCUSSION/CONCLUSION: We have uncovered a pathway whereby Snail transcription factor promotes secretion of exosomes containing Talin1 which promotes AKT signaling in neuronal cells and neurite outgrowth. Talin1 small molecule inhibitor shows promise for therapeutic targeting of tumor-nerve interactions.

GRANT SUPPORT: The authors acknowledge the use of core facilities supported by the National Institute on Minority Health and Health Disparities through grant number 5U54MD013376 and 1U54GM128729-01-DaCCoTA Scholars Program (PI: Rezvani) National Institute of General Medical Sciences (NIGMS).

01.01.22 – Poster Session 1 · Chesapeake Suites (MR)

HMGA2 REGULATION OF OXIDATIVE STRESS AND FERROPTOSIS

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PURPOSE: Prostate cancer (PCa) remains a significant global health burden, and increase in oxidative stress is associated with cancer progression. High Mobility Group A2 (HMGA2), a chromatin architectural protein associated with PCa progression, increases oxidative stress and promotes sensitivity to ferroptosis inducers, however, the mechanism is unknown. GPX4 expression increases with PCa to protect against ferroptosis. We hypothesized that HMGA2 regulates GPX4 expression/activity to impact cellular responses to oxidative stress and ferroptosis sensitivity.

METHODS: We utilized RWPE1 (prostate normal) and a panel of PCa cell lines, including LNCaP, C4-2B, C4-2B MDVR (an enzalutamide-resistant cancer cell line), DU145, 22RV1 PC3, and MDA-PCa-2b. We conducted western blot analysis for HMGA2 and GPX4. Bodipy assays were performed to analyze lipid peroxide levels. MTS cell viability assays were performed to examine ferroptosis induction in the presence of RSL3, plus or minus ferroptosis inhibitor, ferrostatin-1 (Fer-1).

RESULTS: An inverse relationship between HMGA2 and GPX4 expression is observed together with higher lipid peroxide levels in more aggressive cells with higher endogenous levels of HMGA2. Knockdown of endogenous HMGA2 increases GPX4 expression, while overexpression of HMGA2 in LNCaP cells coincides with reduced GPX4 expression, leading to heightened oxidative stress and susceptibility to RSL3-mediated ferroptosis; this is antagonized by Fer-1. Interestingly, enzalutamide-resistant C4-2B MDVR cells display higher HMGA2 levels compared to C4-2B cells, as well as increased GPX4 expression which may serve to protect cells from ferroptosis. However, these cells are still susceptible to RSL3-mediated ferroptosis.

CONCLUSION: Our study reveals the novel roles of HMGA2 in down-regulating GPX4 expression, which is associated with higher lipid peroxide levels; this makes cells more susceptible to RSL3-induced ferroptosis. Thus, ferroptosis sensitivity offers promising insights for the development of targeted therapeutic interventions for aggressive PCa.

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01.01.24 – Poster Session 2 · Chesapeake Suites (MR)

SYNTHESIS OF POLYAMINE POLYISOPRENYLATED CYSTEINYL AMIDE INHIBITORS: POTENT EFFECTS AGAINST TRIPLE-NEGATIVE BREAST CANCER PROGRESSION PHENOMENA

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Triple-negative breast cancer (TNBC) accounts for 15-20 % of all newly diagnosed breast cancers resulting in 5% of all annual cancer-related deaths. Due to loss-of-function mutations of the RAS-GAP, RASA1, over 70% of TNBC cases have aberrantly hyperactive G-proteins such as KRAS. Polyisoprenylated cysteinyl amide inhibitors (PCAIs) were designed to suppress hyperactive G-proteins in cancer. Here, we designed and synthesized a series of polyamine PCAIs with improved aqueous solubility over previous PCAIs. Of the polyamine PCAIs, NSL-AB-51 was the most potent with EC50 values of 1.8 μM and 1.9 μM against MDA-MB-231 and MDA-MB-468, respectively. At 2 μM and 3 μM NSL-AB-51, the proliferation of MDA-MB-231 was impeded by 53% and 94% and in MDA-MB-468 by 54% and 97%, respectively. The ratios of dead to live cells in MDA-MB-231 and MDA-MB-468 compact 3D spheroids were 68% and 63% upon treatment with 5 μM of NSL-AB-51 while 10 μM treatments of NSL-AB-51 showed dead to live cell ratios of 73% and 79%, respectively, which further implicates NSL-AB-51 in inducing apoptosis. Migration was inhibited by 78% and 68% in MDA-MB-231 and MDA-MB-468 cells by 3 μM of NSL-AB-51, respectively. NSL-AB-51 (5 μM and 10 μM) inhibited MDA-MB-231 cell invasion through Matrigel by 38% and 53%, respectively. Additionally, filamentous actin was suppressed by 72% in MDA-MB-231 and 85% in MDA-MB-468 cells when treated with 2 μM of NSL-AB-51. The increased potency and significantly diminished hydrophobicity of the polyamine PCAIs bode well for their desired therapeutic application for the effective management of cancers with hyperactive G-proteins.

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01.01.26 – Poster Session 1 · Chesapeake Suites (MR)

INVESTIGATING HER2 IN PROSTATE CANCER/DIABETES DISPARITIES

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Burnham Morehouse School of Medicine (NM, JM, FK, KSK, LWB)

PURPOSE: African American (AA) men suffer the greatest prostate cancer (PCa) disease burden and higher rates of co-occurring type-2-diabetes (T2D) than non-Hispanic White (NHW) men. T2D, as a comorbidity in PCa patients, complicates treatment and reduces survival outcomes. PCa treatments increase the risk of T2D development, while managing T2D with antidiabetics increases mortality for PCa patients. We need to better understand the PCa/T2D comorbidity mechanisms to expand current PCa treatment options that do not worsen diabetes. We investigate human epidermal growth factor receptor 2 (HER2)—as a promising druggable target in AA PCa patients. HER2 promotes PCa metastasis and treatment resistance; and it enhances T2D oxidative stress-related metabolic pathways. We hypothesize that diabetes—high glucose (HG)—may upregulate key genes and proteins associated with HER2 signaling and PCa aggressiveness, which may alter cellular response to anti-HER2 trastuzumab (TZ) treatment. METHODS: We investigated HG's impact on clonogenicity, migration, and spheroid formation in AA and NHW PCa cells. We evaluated HG's impact on mRNA and protein expression of seven HER2 signaling-related genes, with and without TZ treatment in cells and spheroids. Lastly, we investigated HG's impact on TZ's ability to mitigate clonogenicity, migration, and spheroid formation. RESULTS: TZ kills AA but not NHW PCa cells. HG modulates mRNA and protein expression of HER2-related genes in AA and NHW cells. HG differentially modulates clonogenicity, migration, and spheroid formation in AA vs NHW cells. Lastly, HG differentially alters the cell viability, clonogenicity, migration, and spheroid formation of AA and NHW cells and spheroids in response to TZ. CONCLUSION: This study contributes to our understanding of the PCa/diabetes relationship and the role of HER2 and related genes in the diabetes-driven mechanisms that promote PCa aggression in AA men, as well as how T2D impacts response to anti-HER2 agents in PCa.

National Institutes of Health/National Institute on Minority Health and Health Disparities Research Centers in Minority Institutions (RCMI) (2U54MD007602) (NM, JM, FK, KSK, LWB), the Department of Defense Prostate Cancer Research Program (W81XWH2110038) (LWB), the Prostate Cancer Foundation (20YOUN04) (LWB), the Georgia Clinical Translational Science Alliance KL2 Scholars Program (KL2TR002381) (LWB), and the National Institute of General Medical Sciences of the National Institutes of Health R.I.S.E. (R25GM058268) (JM).

01.01.27 – Poster Session 2 · Chesapeake Suites (MR)

FUNCTIONAL SIGNIFICANCE OF BAI1 INHIBITION IN BREAST TUMOR GROWTH

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PURPOSE Although 90% of cancer-related deaths are mostly attributable to metastatic dissemination, the mechanisms driving metastasis are still not well understood. Our goal is to delineate a mechanism of breast cancer metastasis that involves Bai1-dependent breast cancer cell fusion. Bai1 is a phosphatidylserine (PtdSer) receptor that was shown to activate the Elmo/ Dock180/ Rac signaling to promote myoblasts fusion. This process was found to be stimulated by apoptosis. Our previous study showed that apoptotic cells could also promote breast cancer cells fusion with mesenchymal/multipotent stem/ stromal cells (MSCs) to produce heterogeneous hybrids with an increased ability to migrate and invade. Moreover, breast cancer cells could fuse with other cells in vivo and accumulate in lung metastases. Since activation of the ELMO/Dock180/Rac signaling pathway was also associated with breast cancer metastasis, we hypothesized that apoptotic cells generated in hypoxic conditions could stimulate fusion between breast tumor cells and cells of the tumor microenvironment by a mechanism activating Bai1 signaling to promote tumor progression. Our objective is to determine the effect of Bai1 in tumor development and progression.

METHODS We inhibited Bai1 in breast cancer cells MDA-MB-231, MDA-MB-157 and determined their ability to fuse and induce tumor growth when co-injected with MSCs into the breast of immunocompromised mice. Hybrids were identified by using the cre/ loxp-stop-loxp-GFP system.

RESULTS We found that inhibition of Bai1 in breast cancer cells significantly reduced their ability to induce tumor growth in mice when co-injected with MSCs ($P<0.05$). This reduction in tumor growth was associated with a low level of hybrids in breast tumors as determined by GFP expression ($P<0.05$).

DISCUSSION/CONCLUSIONS This suggests that Bai1 inhibition reduces tumor growth in part by preventing hybrid formation between breast tumor cells and MSCs and therefore reducing tumor heterogeneity. Additional studies will determine the impact of Bai1 inhibition on metastasis development.

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ABSTRACTS

01.01.28 – Poster Session 1 · Chesapeake Suites (MR)

TARGETING NUDT5 IN THERAPEUTIC-RESISTANCE PROSTATE CANCER

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Introduction: In the United States, prostate cancer (PCa) is one of the most common types of cancer in men. Most PCa patients respond well to androgen deprivation therapy (ADT) and chemotherapy; however, many men relapse and develop therapeutic resistance. It is urgent to discover the mechanism of resistance in PCa patients and develop new treatments to overcome drug resistance. NUDIX hydrolase 5 (NUDT5) has been linked to key processes in nucleotide metabolism and cancer. We aimed to unveil the role of NUDT5 in PCa, particularly therapeutic-resistant PCa.

Design: 1. NUDT5 siRNA Knockdown: We employed NUDT5 siRNA to investigate its knockdown effect on NUDT5 expression in chemoresistant cell line C4-2B TaxR. 2. Additionally, we tested the same knockdown approach in ADT-resistant cell line RV1. 3. NUDT5 Inhibitor Evaluation: We further assessed the effect of an NUDT5 inhibitor (Th5427) in C4-2B TaxR and RV1 cell lines. 4. NUDT5 Expression in Human Tissues: We examined NUDT5 expression in human prostate and prostate cancer (PCa) tissues using immunohistochemistry (IHC). We utilized a tissue microarray (TMA) comprising 96 cases/192 cores of normal prostate tissues, adjacent non-cancerous tissues, and PCa samples.

Results: 1. Knockdown of NUDT5 expression in C4-2B TaxR cells led to the inhibition of cell proliferation. 2. Similarly, knockdown of NUDT5 expression in RV1 cells resulted in decreased cell proliferation. 3. Th5427 treatment inhibited cell growth in the C4-2B TaxR and RV1 cell lines in a dose-dependent manner. 4. IHC analysis of a human prostate TMA revealed a significant association between NUDT5 expression and higher Gleason scores.

Summarization: This study showed that NUDT5 may play a key role in PCa progression toward therapeutic-resistance. Targeting NUDT5 could be a new strategy to overcome drug resistance.

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01.01.29 – Poster Session 2 · Chesapeake Suites (MR)

DEVELOPING ESTROGEN RECEPTOR PROTACS FOR BREAST CANCER TREATMENT

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Xavier University of Louisiana (MM, BK, SZ, AH, PM, SG, JL, TW, XP, FP-S, GW)

PURPOSE Estrogen receptor (ER) signaling is closely associated with the development and progression of breast cancer. The conventional endocrine therapies to treat breast cancer include the use of aromatase inhibitors (AIs) and antiestrogens, such as selective ER modulators (SERMs) and selective ER degraders (SERDs). Proteolysis-targeting chimeric (PROTAC) technology has become a powerful targeted protein degradation tool in recent years. The main purpose of this study is to develop novel PROTAC based ER degraders for the treatment of breast cancer.

METHODS We synthesized several PROTAC molecules using tamoxifen as the warhead for the target protein (ERα) and VHL ligand as the E3 ubiquitin ligase recruiting ligand, tethering them with various linker molecules. Compounds were characterized using the 1H NMR, 13C NMR, MS, and elemental analysis. All the compounds were tested for ERα dependent antiproliferative activity and ERα degradation in MCF-7 cells. In silico models of protein ligand complexes and PROTAC mediated ternary complexes consisting of ERα, VHL E3 ligase and PROTAC molecules were also generated.

RESULTS/ EXPECTED RESULTS Several PROTAC molecules exhibited >90% ERα degradation and showed good antiproliferation effect towards the breast cancer MCF-7 cells. A few compounds displayed sub-nanomolar inhibitory effect, which could be evaluated for preclinical studies. The ternary complex model enabled us to better understand the interaction of PROTAC molecules with the target protein and E3 ligase.

DISCUSSION/CONCLUSION We developed PROTAC molecules that can selectively degrade ERα by hijacking the ubiquitin-proteasome system. Overall, a couple of PROTAC molecules exhibited outstanding degradation potency against breast cancer, and be considered as promising preclinical candidates.

This study was supported by the National Institute on Minority Health and Health Disparities: NIMHD-RCMI grant number U54MD007595, and in part by the Louisiana Cancer Research Consortium (LCRC).

01.01.31 – Poster Session 1 · Chesapeake Suites (MR)

1 DAY ACUTE VS 7-11 DAY CHRONIC INFLAMMATION AND THE EVOLUTION OF IMMUNE EXHAUSTION/TOLERANCE

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While a causal relationship has been observed between 1)chronic inflammation and cancer initiation and 2)tolerance which limit efficacy of synthetic lipoglycans anti-tumor therapies; the mechanism of both remain poorly understood. These findings suggest that both are one in the same and reflect a pro-active negative feedback response. METHODS: Phenotype changes were documented (RNA-Seq,proteins) in resting vs. 1 day (acute) vs. 7&11 day (chronic) induced by TLR4/LPS antigen stimulation in macrophages with a controlled product free environment. RESULTS: The data establish 4 patterns; 1) acute induced-chronic sustained or induced only during chronic: Significant Gains: Checkpoints (Membrane + Receptors: PDL1,HAVCR2/TIM-3,SPP1,C3ar1,CD73,IL1RN,LILRbs,CD14,CD204,S100A8,CD83,CD87, ALCAM, Ms4a7,Fcgr1+,Msr1+),(Cyto-chemokines: IL-10,CCL2,CCL7),(Proteases: CthpL,D, Adam8), (Migratory Adhesives: TSPAN3,QSOX1,PDPN,ITGA5),(Glycolysis/ROS: CD36+, COX2, NOS2,GLrx,Hmox1),(Others:PLK2,NT5E, ADGRE1, CLEC4D, CALM1, TPI1, SRGN, PCNA,OD1,ANAX5,ERM,MSN,SPRRs,StfA3).These align with tumor suppressive M2 TAMS,MDSCs,dysfunctional NK and T cells and poor response to ICIs. 2) Acute-repressed and chronic sustained repressed or repressed only during chronic: Significant Losses:(Antigen Recognition;Histocompatibility:H2-Q4, H2-Q6, H2-T23, H2-D1, H2-T22, H2-Q4, H2-T23, H2-T24, H2-T22,H2-K1, H2-Q5),(Interferon Signaling: ISG15, IFI[27,30,44,44I,25,203,202b,204, 205,207,209,211,213,2712a] IFIT [1,2,3,3b,m2], Irf2bp2,Ifrd1,Ifngr1,Ifih1,IRFs [5,7],Igtp,Isg20,Ly6e,XBP1),(Xenobiotic: Gstm1),(Protease inhibitor: Cyst3),(OXHPHOS/ROS: Mt-Cytb,Nd2,Atp6, ND4,Nd6,SOD2,ACOD1/IRG1 (Itaconate)),(Anti-viral/bacterial:Lyz1,Lyz2, Card19, Ninj1),(Autophagy:p62/ SQSTM1) and 3) Tolerance, LPS response lost during chronic : (Interferon Type 1 Anti-viral: BST2,ISG15, USP18 ,IRF7,RSAD2/ Viperin),(Receptors: TLR2,CD53),(Cytokines:IL-6,G-CSF,CCL5),(Anti-bacterial: SAA3, SP140) (IL-1/TLR/TNF signaling:TNF, CLEC4, Il1a, Il1b),(humoral: LPXN,SP140) (Others: SRGN, ATF4, ATF3).CONCLUSION: The data align well with known ICI targets and suggests that chronic inflammation/tolerance involve provocation of immune negative feedback controls.

This project was supported by the FAMU Center of Health disparities research grant, RCMI 5U54MD007582 from NIH.

01.01.32 – Poster Session 2 · Chesapeake Suites (MR)

ORAL PROTEOME IN HIV AND HPV INFECTION: BIOMARKERS OF CANCER RISK

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PURPOSE Oral HPV has been linked to approximately 71.7% of all oropharyngeal squamous cell cancers (OSCC). The prevalence of oral HPV among people with HIV (PWH) is high, particularly in Puerto Rico, thus making Puerto Ricans disproportionately vulnerable to OSCC. Therefore, it is crucial to determine factors that can explain disparities in OSCC development. Here, we characterized the proteomic profile of Puerto Rican PWH with and without oral HPV 18 infection (HPV18+) with the hypothesis that there will be a differential proteomic profile by HPV status related to tissue integrity and oncogenesis.

METHODS The proteomic profile was characterized by tandem mass spectrometry (RCMI Translational Proteomics Center) from 10 saliva samples collected from Puerto Rican PWH with and without HPV18+. Statistical differences between groups were evaluated using Proteome Discover. Enrichment and protein-protein networks of the differentially abundant proteins ($p<0.1$) were performed using STRING.

RESULTS HPV18+ showed significant decrease ($p\leq0.05$) of desmoplakin (DSP), methionine sulfoxide reductase A (MSRA), leukocyte elastase inhibitor (SERPINB1), heat shock protein 90 (HSP90AA1), glutathione S-transferase pi 1 (GSTP1), and glutamate dehydrogenase 1 (GLUD1). Decreased abundance of DSP, GSTP1, MSRA has been associated with loss of tissue integrity, perturbed ROS homeostasis, altered protein repair and inefficient protein folding, respectively. Additionally, decreased GLUD1 and SERPINB1 have been identified as biomarkers for other cancers. The cellular component most significantly impacted in HPV18+ was the secretory granule (adj. $p<0.001$). Protein-protein interaction network showed 2 major clusters with the proteins HSP90AA1 and carcinoembryonic antigen-related cell adhesion molecule 6 as central hubs.

CONCLUSION We identified a specific proteomic profile in saliva associated with oral HPV18 that may represent potential biomarkers for OSCC prevention in Puerto Rican PWH.

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01.01.33 – Poster Session 1 · Chesapeake Suites (MR)

MSH3: AN UNDERESTIMATED DNA MMR GENE IN COLORECTAL CARCINOGENESIS AND POTENTIAL ROLE IN DISPARITY

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The maintenance of DNA sequence integrity is critical to avoid accumulation of cancer-causing mutations. Inactivation of DNA Mismatch Repair (MMR) genes is common among many cancers, including colorectal cancer (CRC) and is the driver of classic microsatellite instability (MSI) in tumors. Somatic MSH3 alterations have been linked to a specific form of MSI called elevated microsatellite alterations at selected tetranucleotide repeats (EMAST) that is associated with patient poor prognosis and elevated among African American (AA) CRC patients. Genetic variants of MSH3 and their pathogenicity vary among different populations, like AA, which are not well-represented in publicly available databases. To analyze unique and novel AA CRC MSH3 mutations to predict true pathogenic variants using specific in silico prediction tools and confirmed by in vivo knock-in CRISPR-Cas9 approach. Targeted exome sequencing of MSH3 among AA CRC samples followed by computational bioinformatic pipeline and molecular dynamic simulation (MDS) analysis approach confirmed six identified nonsynonymous, novel MSH3 variants that corresponds to MSH3 amino-acid changes (p.E413K; p.S466N; p.S920F; p.E976K; p.H1010Y; p.E1081K) were pathogenic, showed loss or gain of hydrogen, ionic, hydrophobic, disulfide bonding and affecting ATP hydrolysis and MSH3-MSH2 interacting domain, suggests deleterious effect on the structure and stability especially ATPase and MSH3-MSH2 interacting domain compared to wild type MSH3 structure. Furthermore, a reduction in both mutant MSH3 transcripts and protein levels led to increased resistance to 5-fluorouracil when compared to the wild-type SW620 cells. This indicates that a loss of MSH3 is correlated with resistance to 5-fluorouracil, providing cancer cells with a survival advantage. This phenomenon is likely to play a role in the emergence of resistance to CRC in AA patients. Our data showed that, six MSH3 non-synonymous mutations are deleterious as they affect important sites within MSH3-MSH2 interactive and ATPase domain. Assessing the real frequency of these mutations in large cohort and their specific effect on function may shed light on EMAST phenotype, high prevalence, and overall poor prognosis in the AA population. In vitro functional assays are underway to mimic these mutations phenotype.

United States Public Health Service (R01 CA258519)

ABSTRACTS

01.01.35 – Poster Session 2 · Chesapeake Suites (MR)

TOMM40 OVEREXPRESSION IN BREAST CANCER: IMPLICATIONS FOR ETHNIC DISPARITIES AND TUMOR SUBTYPES

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BACKGROUND: The precise role of TOMM40 in breast cancer pathogenesis remains elusive despite its established involvement in mitochondrial function. TOMM40, responsible for encoding the pore-forming subunit (TOM40) of mitochondrial protein-transport channels, is pivotal in maintaining mitochondrial functionality. Although the TOM complex, which encompasses TOM40, has been implicated in various diseases, including cancer, the specific impact of TOMM40 dysregulation on breast cancer pathogenesis remains incompletely understood. Prior investigations suggest TOMM40 as a potential biomarker in tumorigenesis, particularly concerning obesity-related breast cancer susceptibility. Nevertheless, further elucidation is required regarding the mechanisms underlying TOMM40 dysregulation in breast cancer initiation and progression.

OBJECTIVE: This study aims to investigate TOMM40 expression in breast invasive carcinoma (BRCA) and its association with ethnic disparities and tumor subtypes.

METHODS: TOMM40 expression was analyzed using the TCGA breast cancer database and CDU's Integrated Clinical and Tissue Biomarker Database Program (ICTBP) samples. Cell models (AA-HMEC, MCF10A TP53-/-, hTERT-HME1-BRCA1-/-) were used to assess TOMM40's functional role. Proteomic analysis was conducted to identify associated protein changes using BioID and TMT-based quantitative proteomic analysis.

RESULTS: Analysis of the TCGA breast cancer database and CDU ICTBP samples revealed significantly higher TOMM40 expression in breast invasive carcinoma tissues than in normal tissues. TOMM40 expression was particularly elevated in African Americans and triple-negative breast cancer subtypes. In cell models, TOMM40 overexpression promoted cell proliferation and colony formation. Additionally, TOMM40 significantly increased UVC irradiation-induced γ-H2AX (DNA damage marker) expression but inhibited apoptosis in AA-HMEC (AG11132), MCF10A TP53-/-, and hTERT-HME1-BRCA1-/- cell models. Proteomic analysis identified significant expression changes associated with TOMM40 overexpression.

CONCLUSION: Our findings suggest TOMM40's crucial role in BRCA, particularly in ethnic disparities and tumor subtypes. Further exploration may reveal therapeutic targets for personalized treatment.

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01.01.37 – Poster Session 1 · Chesapeake Suites (MR)

PERIPHERAL DNA METHYLATION IN OBESITY-RELATED BREAST CANCER

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PURPOSE: DNA methylation (DNAme) is a stable epigenetic mark, usually associated with a reduced gene expression. However, genome-wide DNAme profile is susceptible to disease. In this study, we profiled leukocyte DNAme in African-American and Latinx women with or without obesity and breast cancer. Our goal is to find specific genetic DNAme that could potentially serve as prognostic markers, addressing health disparity associated with breast cancer and obesity. METHOD: We used 12 African-American (AA) women and 7 Latinx (LX) women with confirmed breast cancer diagnosis and Body Mass Index (BMI) > 25 (Overweight or Obese). DNA was extracted from the buffy coat of peripheral blood using Qiagen DNA extraction kits. We used the next-generation sequencing technology to perform reduced presentation bisulfite sequencing (RRBS) and sequenced the libraries on a NextSeq 550 at our Precision Medicine Unit. Single-end 75bp reads were generated and processed using Bismark and mapped against the GRCh38 human genome, and differentially methylated regions (DMR) were derived using MethylKit using a 1kb window. Gene Ontology and Disease association studies were conducted using DAVID. RESULTS: Our results show obesity-associated breast cancer DNAme profiles vary significantly between African-American and Latinx women. 52 % of hypermethylated genomic regions in African-American and 45% in Latinx samples regions showed promoter association, respectively. The differential DNAme regions were associated with obesity and inflammation along with cancer. Gene ontology showed enrichments in RNA pol II transcription, WNT, and Hippo pathways. Genes such as hypermethylated genes in AA vs. LX were 8-oxo guanine DNA glycosylase1, AKT1, GNAS complex locus, ephrin B1 and estrogen receptor 1. CONCLUSION: Our study suggests that a distinct peripheral DNA methylation profile is associated with minority women suffering from both cancer and obesity with association to gene transcription, Wnt, and Hippo signaling.

This work was supported by grants from NIH-NIMHD U54MD007598 to J.V. Vadgama

01.01.39 – Poster Session 2 · Chesapeake Suites (MR)

A NOVEL GARLIC ORGANOSULFIDE ATTENUATES B[AP]-INDUCED PROGRESSION OF PREMALIGNANT BCC ABROGATING EMT

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The chemopreventive and chemotherapeutic effects of the garlic organosulfide, diallyl trisulfide (DATS), are well documented. Previous studies in our lab demonstrated that DATS attenuates benzo[a]pyrene (B[a]P)-induced cancer initiation in MCF-10A breast epithelial cells by inducing cell cycle arrest, preventing DNA strand breaks, and inhibiting lipid peroxide production. Given the ubiquitous nature of B[a]P in fossil fuels and its ability to act as a complete carcinogen we decided to examine the preventative impact of DATS on B[a]P-induced progression using premalignant MCF-10AT1 breast cancer cells. We hypothesize that DATS attenuates the B[a]P-induced progression through abrogating cancer stem cell formation and EMT in premalignant breast cancer cells. To test this hypothesis, wound healing, invasion, spheroid formation, immunoblotting, and immunofluorescence studies were performed on premalignant MCF-10AT1 breast cancer cells treated with DMSO (vehicle), 1 µM B[a]P, 40 µM DATS, and B[a]P/DATS co-treatment. Following 24-48 hr exposure, DATS prevented the migratory and invasive behavior of the cells by > 90% and 97%, respectively, while cotreatment exacerbated the response. Spheroids were also monitored for 90 days and were significantly decreased in the presence of DATS or co-treatment. Putative breast CSC markers measured by immunoblotting showed DATS decreased the B[a]P induction of CD24 and CD44. Interestingly, DATS and B[a]P alone significantly increased CD44 expression, but cotreatment decreased its expression. Similar results were observed with immunofluorescent staining of CD24/CD44. When EMT markers were examined, cotreatment decreased vimentin, and ß-catenin indicated for the first time the potential of DATS to prevent the induction of EMT in premalignant cells. These results suggest that DATS can inhibit B[a]P-induced CSC formation in premalignant cells, which can attenuate cell migration and invasion.

01.01.40 – Poster Session 1 · Chesapeake Suites (MR)

BIOPSYCHOSOCIAL PREDICTORS OF TUMOR-ASSOCIATED INFLAMMATION

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PURPOSE To investigate if exposure to social-environmental adversity exacerbates the biopsychosocial stress response to social stressors, leading to depression symptoms and inflammation-driven cancer progression.

METHODS Our cohort consisted of 175 Hispanic/Latinx women (>21 years old) who underwent surgery for tumor removal and were diagnosed with breast cancer in the last four years. Psychological assessments were performed using PHQ-8, GAD-7, PLC, and ACE. At each visit (baseline, 3, 6, and 12 months), questionnaires were administered, and blood was collected to assay for cytokines and stress hormone levels. Nude mice were subjected to restraint stress before and/or after breast cancer inoculation. Murine serum was analyzed for cytokines, while brain samples were assayed for BDNF and microglia.

RESULTS Study participants exhibited higher depression and anxiety symptoms than those reported in the literature. A quarter of participants reported four or more ACE events. Symptoms of depression, anxiety, and PTSD in participants with a history of chronic lifetime trauma were inversely correlated with resilience. In addition, significant associations were found between depression and anxiety symptoms with inflammatory cytokines. In tumor-bearing mice, restraint stress decreased BDNF levels and increased microglia in the hippocampus.

DISCUSSION The data generated by this study served as the foundation for several NIH-funded projects. For example, our group is developing a community-based intervention to increase access to mental health care for cancer patients and explore if these strategies help address psychological distress resulting from cancer and its treatment. In addition, we are investigating the effects of chronic social stress on the development of ovarian cancer and assessing if anti-inflammatory medications could abrogate this effect. Moreover, we are examining the role of emotional regulation and social support in grief, depression, and inflammation markers in breast cancer patients. Finally, we are dissecting the role of psychological distress in periodontal health among breast cancer survivors.

U54 MD007579

01.01.42 – Poster Session 2 · Chesapeake Suites (MR)

TOXICITY AND INHIBITORY EVALUATIONS OF OPTIMIZED GMC-1 ANALOGUES AS POTENTIAL REGULATORS OF HORMONAL

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PURPOSE Prostate cancer (PC) is a proliferative disorder characterized by abnormal cell growth that originates in the prostate gland. An effective way of treating PC is androgen deprivation therapy (ADT). However, at an advance stage, PC stops to respond to ADT, and this is referred to as castrate-resistant prostate cancer (CRPC). Earlier research reported GMC1 effectively inhibit androgen receptor (AR) and glucocorticoid receptor (GR) activities in a variety of PC lines. However, poor solubility of GMC1 in water and lipid has made it desirable and necessary to design and develop new pharmacophores/analogues with suitable water solubility, liquid stability, and therapeutically potent against PC.

METHOD This study is aimed at designing and developing new analogues of GMC1, and this study employed both computational and in vitro methods (using luciferase induction assay against AR and GR in MDA cells) to identified compounds with inhibitory potentials against CRPC related proteins and PC cells.

RESULT A structural optimization of analogues of GMC1 (RJ11 and RJ13) led to identification of 18 analogues. In vitro evaluation of the EC50 of the 18 compounds (25 µM) showed that compounds RMC1, 2, 3, 4, 5, and 10 had between 45 – 90% inhibition against GR, and compound RMC2 exhibited 60% inhibition against AR. The result of toxicity evaluation of the six compounds showed the compounds lowered the reporter's expression by 80%.

DISCUSSION/CONCLUSION The toxicity assay showed the six compounds lowered the reporter's expression at 25 µM, thereby suggesting the reported inhibition might be because of toxicity. Further evaluation and optimization of the analogues are on-going.

This project is sponsored by NIH-RCMI (U54MD007605) and CTTP (RP210043) Grants.

ABSTRACTS

01.01.43 – Poster Session 1 · Chesapeake Suites (MR)

IN VITRO INVASION OF TNBC CELLS WITH DIFFERENT CD44 ISOFORMS

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Cancer cell migration and invasion are essential processes for tumor progression and metastasis and the CD44 cell membrane receptor has been associated with both phenotypes in cancer cells. The objective of this study is to explore the migration and in vitro invasion capabilities of two triple negative breast cancer cell lines derived from African-American women, HTB-132 and HCC1806 and a potential role of CD44 in such cellular behavior. We hypothesize that the expression of different CD44 isoforms affect in part the migration and in vitro invasion of the breast cancer cell lines under study. To test this hypothesis, we used cell culture inserts (uncoated for migration and Matrigel-coated for invasion), in which 10,000 cells were seeded in and incubated for 48 hours in 24 well plates. The cells that migrated from the upper side of the membrane to the lower side of the membrane were fixed, visualized by staining the lower chamber membrane with Diff-Quik stains and manually counted using an inverted microscope. The number of migrating cells was significantly higher for HCC1806 cells compared to HTB-132 cells. However, there was no significant difference in the in vitro invasion assay between these two cell lines. These results suggest that the difference in CD44 isoforms expression might affect the ability of the cells to migrate but not in vitro invade.

This project was supported in part by the DE INBRE program, with a grant from the NIH NIGMS (P20 GM103446), a DSU RCMI IHER Pilot Award (K.M.), a DE INBRE Pilot Award (K.M.) and the NSF HBCU-UP Research Initiation Award Grant No. 1700228 (K.M.)

01.01.44 – Poster Session 2 · Chesapeake Suites (MR)

MECHANISMS OF THE CD44-ICD-MEDIATED SIGNALING PATHWAY

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The expression of the MMP-9 gene can be in part transcriptionally promoted by CD44 via its intracytoplasmic domain (CD44-ICD). The CD44-ICD is a 74 residues peptide generated by the intramembranous proteolytic cleavage of CD44 by presenilin 1 within the gamma secretase complex. After cleavage this peptide can be translocated to the nucleus and/or kept in the cytoplasm physically interacting with the transcription factor Runx2. We have detected a nuclear and the cytoplasmic protein-protein interactions (PPI) using proximity ligation assays (PLA). The purpose of this study is to validate the CD44-ICD-Runx2 PPI using other experimental tools, and to determine whether these experimental techniques can be used to detect changes in the CD44-ICD-Runx2 PPI. The following techniques will be used: co-immunoprecipitations (co-IPs), CUT and RUN assays (conceptually similar to chromatin immunoprecipitations) and PLAs (as CD44-ICD-Runx2 PPI positive control). Initial Cut and Run experiments have shown it can detect the CD44-ICD-Runx2 PPI. If shown useful in detecting the CD44-ICD-Runx2 PPI, these techniques will be used to assess potential changes in these PPI caused by CD44-ICD deletion mutants designed to interfere with this signaling pathway that in most cases promotes a more aggressive cancer cell phenotype.

This project was supported in part by the DE INBRE program, with a grant from the NIH NIGMS (P20 GM103446), a DE INBRE Pilot Award (K.M.) and the NSF HBCU-UP Research Initiation Award Grant No. 1700228 (K.M.)

Cardiovascular and Cerebrovascular Diseases

01.02.02 – Poster Session 1 · Chesapeake Suites (MR)

SARCOMERIC PROTEIN PHOSPHORYLATION PROTECTS OLD HEARTS

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PURPOSE: Cardiovascular Disease is the leading cause of death worldwide and in the U.S. Among them, ischemic heart disease (IHD) affects most people, especially the aging populations. Minority populations also experience much higher risks, morbidity, and mortality of IHD. Post-translational modifications of cardiac troponin I (cTnI), an essential sarcomeric protein, are known to regulate heart function under physiological and pathological conditions. Discovered recently, the site-specific phosphorylation on cTnI Ser199 is upregulated in human IHD. Our previous study showed that cTnI Ser199 phosphorylation protected hearts against ischemia/reperfusion (I/R) injury in young male mice. The present study investigated whether such protective effect still existed in old mice of both sexes.

METHODS: We generated a transgenic mouse model (TgD) carrying Serine to Aspartic Acid mutation at cTnI Ser200 (equivalent to Ser199 in human) to mimic the site-specific hyperphosphorylation, which was a widely accepted method. Cardiac function was examined using Langendorff isolated hearts at baseline and after 30-minute global ischemia followed by 2-hour reperfusion. The hearts were paced at 330 beats/min.

RESULTS: At baseline, for both sexes, wildtype (WT) and TgD hearts (19-24 months) showed comparable heart function and life span, without detectable abnormalities. After I/R, TgD hearts recovered heart function over 40%, while WT hearts only recovered about 20% for both male and female mice. TgD hearts showed significantly better systolic and diastolic function after I/R, indicated by left ventricular developed pressure, peak rate of pressure increase, and peak rate of pressure decrease ($p<0.05$, $n=6$).

CONCLUSION: Human ischemic-heart-related cTnI Ser199 hyperphosphorylation protects heart function during global I/R in old mice of both genders. To our knowledge, it is the first time to reveal a cardiac protective effect against I/R delivered by cTnI phosphorylation in animal model, it may shed light to a new cardiac protective mechanism and potential new therapeutic strategy.

National Institute of General Medical Sciences (5SC2GM131969 to Y. L.), National Institute on Minority Health and Health Disparities (U54MD013376 to O.V. and H.Y.), and National Institute on Aging (R01 HL136918 to N.P.)

01.02.03 – Poster Session 2 · Chesapeake Suites (MR)

ML AS A WARFARIN SENSITIVITY PREDICTION TOOL IN PR COHORT.

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PURPOSE: Despite approval of novel direct oral anticoagulants, warfarin remains the most widely prescribed oral anticoagulant in the United States even though it has a narrow therapeutic index. An important cause of this narrow index is the genetic polymorphisms in the warfarin metabolizing enzymes. Implementation efforts for genetic data into the clinical setting has been performed in populations where Latino/Hispanic groups are underrepresented. Machine learning (ML) gained traction as a method to predict drug response using a patient's genetic data. We hypothesized that we could train a ML algorithm (MLA) to determine if a patient is sensitive to warfarin using clinical information from a small cohort of Puerto Rican patients on warfarin. METHODS: Clinical and genotyping data from 156 patients was analyzed using eight MLA to determine which better predicts warfarin sensitivity. To balance data, random over sampling was performed. Linear discriminant analysis (LDA), gradient boosting classifier (GDB), decision tree classifier (DTC), support vector machine (SVC), logistic regression (LR), random forest classifier (CLF), k-nearest neighbor (KNN), and gaussian naive bayes (GNB) were tested to predict warfarin sensitivity. The receiver operating characteristic curve (ROC) analysis was performed to determine sensitivity. RESULTS: GNB, CLF, SVC, LR, LDA, and GDB models had poor performance having low accuracy and low sensitivity values, while DTC and KNN had better performance. DISCUSSION: GNB, CLF, SVC, LR, LDA, GDB algorithms could not serve as ML models to predict warfarin sensitivity due to being inaccurate and inefficient. DTC had better outcomes, having an accuracy of 73% and being 77% efficient, while better than most models, it would still need improvement to be useful. KNN was the best model having an accuracy of 81% and efficiency of 82%. Results show that training of a MLA is possible for the Puerto Rican cohort.

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Diabetes / Obesity / Metabolic Syndromes

01.03.01 – Poster Session 1 · Chesapeake Suites (MR)

SMOKING MODIFIES THE EFFECT OF DIABETES ON SEVERE TOOTH LOSS

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Both smoking and diabetes have detrimental effects on tooth loss, however there are limited studies on how the two factors interact on tooth loss. This study utilized five waves of even year data from the Hawai'i Behavioral Risk Factor Surveillance System collected between 2012 and 2020. Weighted Poisson regression was used to estimate the unadjusted and adjusted prevalence of severe tooth loss. The 95% confidence intervals of difference in prevalence from interaction effect was computed by bootstrap method.

The prevalence of severe tooth loss in Hawaii was 9.7% among adults 18 or older. Native Hawaiians and Filipinos had higher prevalence relative to the other racial/ethnic groups. Among never smokers, diabetes was associated with a 10.3% difference in prevalence of severe tooth loss (15.7% diabetic vs. 5.4% non-diabetic). The difference by diabetes almost doubled among former smokers (19%) and current smokers (16.2%). Adjusting for sociodemographic factors, the effect sizes were smaller yet still statistically significant.

The effect of diabetes on severe tooth loss was stronger in former or current smokers than non-smokers. Awareness of the unequal distribution of smoking and diabetes is crucial for the development of policies aimed at health equity, such as smoking cessation and diabetes prevention measures.

This project is funded by the seed grant from College of Social Sciences at the University of Hawaii, Manoa.

01.03.02 – Poster Session 2 · Chesapeake Suites (MR)

POTENTIAL ROLES OF PLACENTAL PROGRAMMING IN THE VICIOUS CYCLE BETWEEN MATERNAL GESTATIONAL DIABETES AND OFFSPRING TYPE 2 DIABETES

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Epidemiological studies indicate a vicious cycle between maternal gestational diabetes (GDM) and offspring type 2 diabetes (T2D), but the underlying mechanisms remain unclear. Our recent study suggested that BNIP3 plays a critical role in maintaining mitochondria homeostasis in human trophoblast cells. Here we hypothesized that knockout of BNIP3 specifically in mouse trophoblast cells will recapitulate the typical symptoms of GDM in maternal pregnancy and T2D in offspring. First, we used Cyo19-Cre and Bnip3-LoxP mouse lines to generate trophoblast specific knockout mice (cKO group) and a control group (CT). Second, On Day 18 of pregnancy, glucose tolerance test (GTT) was conducted in pregnant cKO or CT mice. Placental tissues were collected and mRNA and protein levels of BNIP3 were measured. In 8-month old male offspring, GTT was conducted, and metabolic rate was measured. All numerical parameters between the cKO and CT pregnant mice, and between their male offspring were analyzed by ANOVA (n=5). The main findings include: 1) BNIP3 mRNA and protein levels in the placental tissue were reduced by 47% and by 40% in cKO ($P<0.05$), respectively ($P<0.05$); 2) Pregnant cKO mice demonstrated enhanced glucose intolerance; 3) The body weight of male offspring from cKO mothers was increased by 1.2-fold compared to those from CT mothers; 4) Male offspring from cKO mothers demonstrated enhanced glucose intolerance compared to those from CT mothers; 5) The metabolic rates was lower in male offspring from cKO mothers compared to those from CT mothers, with decreased oxygen consumption and carbon dioxide production by 1.18- and 1.19-fold, respectively ($P<0.05$). These results suggest that placental programming possibly via the disrupted functions of BNIP3 in trophoblast cells mediates the occurrence of maternal GDM and offspring T2D, and thus, being a potential target in treatment of GDM and prevention of T2D.

U54MD007597

ABSTRACTS

01.03.05 – Poster Session 1 · Chesapeake Suites (MR)

DISCRIMINATION, STRESS, AND LIPIDS IN AFRICAN AMERICAN WOMEN

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BACKGROUND: Prolonged stress factors play a role in inflammation, which is associated with metabolic syndrome (MS) and serum lipid panels in African Americans (AA). MS is considered a key risk factor for type 2 diabetes mellitus and hyperlipidemia. Forty-four percent of people diagnosed with T2DM in Georgia are AAs. The purpose of this analysis is to examine the correlation between perceived stress and discrimination, structural racism, current sociological environment, and metabolic output in AA women in metropolitan Atlanta. METHODS: Fifty-eight non-fasting women over the age of 18 were consented to participate. The participants completed demographics, perceived stress, perceived discrimination scale, and perceived ethnic discrimination surveys. The relationships between clinical metabolic parameters and demographics were assessed by Pearson's correlation coefficient (r). RESULTS: The mean age of female participants was 60 years old and mean BMI was 34.22 kg/m2. HgA1c levels less than 5.7% were inversely correlated with VLDL (p=0.005) and triglycerides (p=0.009). There were significant (p=<0.05) findings between age and perceived stress and discrimination factors in participants whose HgA1c was to 6.5%. BMI showed significant (p=<0.05) correlation with lipid panels and blood pressure in participants with HgA1c ≥5.7% - ≤6.4%. Triglycerides showed a correlation with life discrimination stressors (p=0.034) in participants with HgA1c <5.7%, and exclusion/rejection stressors (p=0.046) in HgA1c ≥5.7% - ≤6.4%. Lipid panels (Total Cholesterol, HDL, LDL, and VLDL) were significantly (p=0.05) correlated with perceived stress and discrimination factors in participants with HgA1c <5.7% and ≥6.5%. BMI and blood pressure showed greater significance (p=0.05) in participants with HgA1c ≥5.7% - ≤6.4%. CONCLUSIONS: Addressing racism as a stressor provides data that will advance our understanding of the relationship between the social and biological bases of health disparities.

Research reported in this poster is supported by the National Institutes of Health/National Institute on Minority Health and Health Disparities Research Centers in Minority Institutions (RCMI) (2U54MD007602) (SC, LWB, KSK), the Prostate Cancer Foundation (20YOUN04) (LWB), and the Georgia Clinical Translational Science Alliance KL2 Scholars Program (KL2TR002381) (LWB).

Gene-Environment Interactions

01.04.01 – Poster Session 2 · Chesapeake Suites (MR)

CLUSTERING OF IMMUNOSUPPRESSIVE CELLS AT THE BONE ENDOSTEAL NICHE

DM Grant; GJ Joseph; RW Johnson
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Breast cancer cells frequently metastasize to bone and home to the endosteal niche (bone surface), where they are thought to lay dormant until reactivated. Our knowledge of how tumor cells are impacted by the bone microenvironment is limited, as the spatial integrity of bone is often compromised. We hypothesize that myeloid populations infiltrate the bone endosteal surface and sustain tumor burden by creating an immunosuppressive environment. We performed Digital Spatial Profiling (DSP) of bone metastases from 6-wk-old female C57Bl/6 mice challenged with E0771 mouse mammary carcinoma cells by intracardiac injection (n=3/group) and evaluated immune cells residing in the marrow or endosteum. Mice were treated with α-PD-1 every 3-4 days to activate T cells and create a pro-inflammatory microenvironment. Antibodies for 70+ proteins (e.g., immune activation, cell death, proliferation, and cell stress), were hybridized to formalin-fixed paraffin-embedded tibial sections, released, and quantified within selected regions of interest (n=5-6/bone) on Nanostring GeoMx/nCounter instruments. We used DAPI, pan-cytokeratin, and α-CD45 to identify nuclei, tumor, and immune cells respectively. We observed increased CD45+CD163+ M2 macrophages ($p<0.0006$) and CD45+Ly6C+Ly6G+ myeloid cells ($p<0.0443$) at the bone endosteal surface. PD-1 ($p<0.0033$), and PD-L1 ($p<0.0025$) proteins were also enriched in CD45+ immune cells in the endosteum compared to immune cells in the marrow (n= 9 ROIs/group), suggesting the endosteum is an immunosuppressive environment. HER2 protein in CD45+ immune cells was also enriched in the endosteal niche ($p<0.0042$). In breast cancer patients, HER2 can be transferred from cancer cells to immune cells in the bone marrow through a process called trogocytosis, which improves tumor response to trastuzumab. Our data collectively suggest myeloid cells infiltrate the endosteal niche, creating an immunosuppressive environment that paradoxically supports HER2 trogocytosis.

This project was supported, in part, by 5T32GM144927 and W81XWH-22-1-0090.

01.04.02 – Poster Session 1 · Chesapeake Suites (MR)

POVERTY SHAPES THE TRANSCRIPTOME OF IMMUNE CELLS

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PURPOSE Psychosocial factors exert a powerful influence on health and contribute to health disparities. For example, overall life expectancy at birth throughout the United States tracks with poverty level, educational attainment, economic security and other social determinants of health. Socioeconomic status (SES) and psychosocial factors may affect gene expression in peripheral blood mononuclear cells, suggesting a molecular mechanism for some health disparities. Here we investigated the effects of poverty among Baltimore City residents participating in the Healthy Aging in Neighborhoods of Diversity across the Life Span (HANDLS).

METHODS We examined 204 participants whose reported household income was either above or below poverty. The population sample was balanced by self-reported race and sex. We performed RNA sequencing in peripheral blood mononuclear cells to assess differential gene expression patterns associated with poverty.

RESULTS We found 138 genes differentially expressed between individuals living in poverty compared to those living above poverty. These changes in gene expression are correlated with those reported in an independent study of 1,069 young adults from the National Longitudinal Study of Adolescent to Adult Health (Add Health). We found 104 differentially expressed genes in women, however, we did not observe any genes differential expressed in men living in poverty. Differentially expressed genes in individuals living in poverty are enriched in processes related to wound healing and coagulation. Of the genes differentially expressed in individuals living in poverty, VIL1 and EEF1DP7 are also associated with hypertension in transcriptome-wide association studies.

CONCLUSIONS Our results show that poverty affects peripheral blood immune gene expression and suggest that the impact of poverty on gene expression may be larger in women than in men.

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01.04.04 – Poster Session 2 · Chesapeake Suites (MR)

MAPPING SINGLE-CELL GENE CHANGES AND CELL FATE DECISIONS VIA OPTIMAL TRANSPORT & SINKHORN DIVERGENCE

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We introduce a multidimensional framework that integrates Optimal Transport (OT) and Sinkhorn divergence, leveraging Single-Cell RNA sequencing (scRNA-seq) to elucidate the intricate process of cellular reprogramming. Utilizing a dense scRNA-seq dataset, we meticulously trace individual cells' developmental pathways and molecular interactions, capturing dynamic transitions to induced pluripotent stem cells (iPSCs). Our methodology harnesses the high-resolution capabilities of scRNA-seq to analyze temporal expression profiles, embracing the variability inherent in gene expression and the technical nuances of single-cell transcriptomics. An entropic OT with Sinkhorn divergence, informed by scRNA-seq data, enables us to establish temporal connections and ancestral links between cell populations with unprecedented precision.

Specifically, the innovative approach combines the quantitative rigor of Waddington-OT with scRNA-seq data analysis and demonstrates Sinkhorn divergence-based debiasing outcomes, facilitating accurate predictions of cellular distributions and fates. Within this rigorous computational model, we further incorporated ligand-receptor interaction and signaling pathways to improve the emergence of pluripotent and lineage-specific cellular identities. Our findings, underpinned by scRNA-seq insights, illuminate the fundamental framework of transport in probability distribution driving cellular evolution and significantly enhance our understanding of the molecular complexities in developmental biology and regenerative medicine, opening new avenues for therapeutic strategies and clinical applications.

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HIV and AIDS

01.05.01 – Poster Session 1 · Chesapeake Suites (MR)

HIV TAT PROTEIN EFFECTS ON NEUROTRANSMISSION AND CB1 RECEPTOR-MEDIATED SIGNALING IN A MODEL OF ENDOGENOUSLY EXPRESSED CANNABINOID SIGNALING

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In the brain of HIV-infected individuals, microglia release neurotoxic agents which evoke excitotoxic synaptic injury. The HIV trans-activator of transcription (TAT) is one of the neurotoxins and a key player in HIV-associated neurocognitive disorders (HAND). Exogenous cannabinoids attenuate neurotoxicity in animal models of HAND. Targeting the cannabinoid system in HAND has therapeutic potential. However, it has not been determined if cannabinoid signaling in the brain is affected by HIV.

The hypothesis is that TAT protein will inhibit endocannabinoid mediated synaptic plasticity, likely by altering the membrane properties of neurons. We tested this in autaptic hippocampal neurons, a model that expresses an intact endogenous retrograde circuit with presynaptic cannabinoid (CB1) receptors that, when activated, inhibit neurotransmitter (glutamate) release, known as Depolarization-induced Suppression of Excitation (DSE). When neurons are stimulated with a series of successively longer depolarizations (50 ms to 10 sec) this results in progressively greater inhibition of neurotransmission and yields a "depolarization-response curve" which permits the calculation of an effective-dose (depolarization) 50 (ED50), i.e., the duration of depolarization that results in 50% of the maximal inhibition. Using an electrophysiological approach (whole-cell patch-clamp recording), we have tested the effect of a 5-min treatment with TAT protein at 100 ng/mL. At this concentration, the TAT protein did not alter baseline excitatory postsynaptic currents, indicating that TAT was not altering either pre- or postsynaptic components of neurotransmission. The DSE responses were not significantly different in terms of their ED50. Maximal responses were not altered. Other studies have reported robust effects of TAT in a cell line at 1ug/mL. Therefore, it will be important to test the effect of TAT at higher concentrations to determine its role at the cellular level.

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ABSTRACTS

01.05.02 – Poster Session 2 · Chesapeake Suites (MR)

CONTEXTUALIZING HIV PREVENTION ON HBCU CAMPUS: THE INTERPLAY BETWEEN HEALTH LITERACY, HOOKUP CULTURE AND INFORMATION SEEKING BEHAVIOR

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PURPOSE: The current study contextualizes HIV prevention strategies in an HBCU setting in North Carolina. We investigated participants' health information seeking habits, general knowledge about HIV prevention, testing, experience of campus sexual culture and exposure of misinformation.

METHODS The current study uses in-person focus groups and qualitative analysis using grounded theory approach. Participants are current or previous HBCU students.

RESULTS We conducted seven focus groups (N=20), age 18-27. All of them identify as cisgender. 17 of them are heterosexual, 2 are bisexual and 1 is pansexual. The following themes are identified

1.HIV knowledge are outdated and stigmatized. Majority of participants noted their knowledge about HIV, testing and prevention comes from sex education during middle school or earlier with no updates offered before college. They are required to take a Health class by the university which will cover STI, many do not take them until the first semester, missing the best window for update knowledge. More than half have reported having unprotected sex (in survey), common reasons including trust on a stable partner, uncomfortable and cost (in discussion).

2. Participants reported high sexual activity on campus. They are not often using apps to find sexual partners. Individual STI status were often gossiped around but open discussion between partners were difficult.

3. Active information seeking often happens more when they notice symptoms. On other times, many participants rely on running into health information on social media. Most participants trust information they have from social media.

4. Students do not pay much attention to health flyers in physical space or PSAs from the health department and are having a hard time recalling any (even non-HIV related). Some attributes this to distract

5. A barrier for testing is the medical staff's manner. Some participants raised the point: "So you walk into that testing center and they're already giving you a look for real"

6. Knowledge about PrEP and PEP is limited. We included this in the survey and discussion as a preventive measure and in every session participants would question researchers about what it is.

DISCUSSION The current study sheds light on the gap in knowledge and exposire in HIV prevention among HBCU students on HIV prevention. The finding implies that we should better align HIV prevention, STI education and create more safety feeling in testing.

NCCU Implementation Science Fellowship

01.05.03 – Poster Session 1 · Chesapeake Suites (MR)

IRON BALANCE IMPACTS HIV-1 RESTRICTION IN LUPUS

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PURPOSE: Intracellular iron levels and cytokines modulate host viral restriction factors. Systemic Lupus Erythematosus (SLE) is characterized by upregulation of interferon response, with co-occurrence of SLE and HIV infection being rare. Deregulation of proteins involved in iron homeostasis, including hepcidin, has been observed in lupus nephritis, suggesting a role in disease severity. HIF-1α, regulated by hypoxia and iron depletion, is upregulated in SLE, and reported to block HIV transcription. Additionally, SLE is associated with elevated levels of IL-10, IL-16, APOBECs, oxysterols, and Interferon Regulating Factors (IRFs), all known to impact HIV infection. The current study aims to investigate ex vivo HIV-1 infection in PBMCs from individuals with SLE and identify contributing factors.

METHODS: We used replication-competent HIV-IIIB to infect PBMCs from individuals with SLE. Real-time PCR to assess the upregulation of genes involved in HIV-1 replication and RNA-seq to identify HIV-1 restriction factors.

RESULTS: PBMCs from individuals with SLE demonstrated a significant reduction in HIV-1 infection compared to controls, indicated by lower mRNA levels of Gag and Nef. Increased levels of APOBEC3A, APOBEC3B, and CH25H restriction factors were observed in SLE-derived PBMCs. Additionally, elevated mRNA expression of HIF-1α, TFR1, IL-10, IFN-β, and IRF-7 was observed. IPA analysis of RNA seq of SLE PBMCs shows downregulation of Viral life cycle and upregulation of IRF-7 and IRF-3. These findings suggest lower susceptibility to HIV-1 infection in SLE-derived PBMCs driven by antiviral and iron regulatory factors. This intricate relationship between iron levels, HIF-1, and HIV-1 transcription regulation warrants further investigation.

CONCLUSION: PBMCs from individuals with SLE exhibit reduced susceptibility to HIV-1 infection, likely due to upregulated antiviral and iron regulatory factors. These findings highlight the complex interplay between host factors and viral replication, suggesting potential therapeutic interventions for both HIV-1 and SLE.

GRANT SUPPORT: RCMI Pilot Grant GRT001000E and NIH Research Grants 1R01HL125005.

01.05.05 – Poster Session 2 · Chesapeake Suites (MR)

A MODEL FOR THE ANALYSIS OF HIV ASSOCIATED VISUAL LOSS

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PURPOSE: Antiretroviral therapy (ART) has increased life span and improved the quality of life but there are over 38 million people living with human immunodeficiency virus (HIV). Among the infected, HIV noninfectious comorbidities (NICM), have emerged as a major medical problem. These non-infectious comorbidities can affect several systems. HIV associated retinopathy is a problematic NICM as it impacts quality of life. Moreover, there is a health disparity among African Americans and other minority groups, for increased frequency of HIV infection, and HIV associated vision loss. This research project aims to identify the mechanisms of HIV-1 associated vision loss by identifying pathologic changes throughout the visual system in a transgenic model of chronic HIV infection developed by us: The HIV-1 Transgenic rat.

METHODS: Alternate brain sections were immunohistochemically labeled for rat IgG, a marker for blood-brain barrier (BBB) permeability. A senescence marker, SA Beta-Galactosidase (SABG) was used to identify premature senescent cells. Nitrotyrosine staining was used to identify evidence of free radical production.

RESULTS/EXPECTED RESULTS: Areas if multifocal permeability of the blood brain barrier (BBB) in 6 brains were identified with localization to the visual cortex in 2 brains. SABG staining cells were observed throughout the brains including in the visual cortex. Free radical production was identified in areas of the visual system by Nitrotyrosine positive staining cells.

DISCUSSION: BBB permeability was observed in areas of the brain including the visual cortex. Premature senescent cells were also found in visual areas. Such cells have been found to be dysfunctional and die prematurely. In current experiments we are staining relevant structures such as blood-retinal barrier, retina, cornea, lateral geniculate, and optic nerve with these markers as well as CXCR4, and the HIV-1 proteins Gp-120 and TAT.

GRANT SUPPORT: Sigma Xi Grants in Aid to MD Worthington G03152021100991204MW, and Morgan Core facilities supported by the NIH 5U54MD013376 and National Institute of General Medical Sciences through grant 5UL1GM118973 and R29 NS31857.

01.05.06 – Poster Session 1 · Chesapeake Suites (MR)

USING NOMINAL GROUP TECHNIQUE TO IDENTIFY PREP PROGRAM ATTRIBUTES

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PURPOSE: Pre-exposure prophylaxis (PrEP) presents an opportunity to reduce the disproportionate HIV burden among Black women (BW). What BW want for PrEP programming remains grossly understudied. Understanding their preferences is vital for developing strategies to address inequities regarding PrEP. The present study aims to inform such strategies by describing and rank-ordering BW's considerations when deciding whether to start PrEP.

METHODS: The study used the nominal group technique (NGT), a consensus method that generates and ranks responses, to identify barriers and facilitators for a culturally tailored PrEP program designed for BW (N=6) living without HIV. The NGT process involved ranking 16 barriers and 16 facilitators, followed by a group discussion to review rankings, explain reasoning, and consolidate options. The group discussion generated themes for analysis; the ranks of the proposed barriers and facilitators are presented.

RESULTS: Participants' top 3 concerns about PrEP were: (1) Potential interactions with other medications; (2) Side effects; and (3) Being judged by their doctor. Regarding considerations for PrEP use, the top 3 choices were: (1) Using an app for medical consultations, tests, and home delivery of PrEP; (2) Obtaining PrEP from an OBGYN during routine visits, like Pap smears; and (3) Joining a supportive group of Black women using PrEP.

DISCUSSION/CONCLUSION: By employing NGT in this study as a qualitative exploratory method, we identified relevant and valued PrEP-related attributes; assessed their relative importance among study participants; and identified key barriers and facilitators influencing BW's PrEP use. Findings highlight the need to address BW's concerns about PrEP, as well as the importance of providing peer group support and offering diverse delivery methods for PrEP access (e.g., integration with existing healthcare services). These findings underscore the need for multifaceted approaches that prioritize accessibility, support, and integration to effectively address the PrEP needs of BW.

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ABSTRACTS

01.05.07 – Poster Session 2 · Chesapeake Suites (MR)

NANOTECHNOLOGY PLATFORM FOR HIV CURE

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PURPOSE: The World Health Organization indicated that about 38 million people are currently living with HIV. Antiretroviral therapy (ART) can control the virus but treatment requires life-long adherence. The search for an HIV/AIDS cure is of high priority and the HIV reservoirs remain the main target for an HIV cure. The curative intervention of our team is “poke and clear” (“shock and kill”) approach (using a nanotechnological platform for targeted delivery to HIV reservoirs) which involves drugs called latency-reversing agents (LRAs) to activate the dormant virus in HIV-infected cells followed by clearing (killing) the virus with existing ART. We report here our efforts in the development of ARVs (FDA approved)-loaded nanoparticles for clearing the virus.

METHODS: Cabotegravir and rilpivirine-loaded in biodegradable polymeric nanoparticles were fabricated by the dispersion polymerization method and characterized (particle size, zeta potential, morphology (SEM), structure (TEM), drug-loading and in-vitro availability (drug release)). To investigate the effect of nanoparticle-packaged antiviral drugs on ex vivo HIV-1 infection, we used VSVg-pseudotyped HIV-1 virus expressing luciferase for one round infection of CEM T cells.

RESULTS: Smooth spherical stealth nanoparticles (217.9 nm) were obtained with negative zeta potential. In vitro drug release was sustained for 148 hours for both drugs. Infection of pseudotyped HIV was efficiently inhibited (IC50=1.4 nM) in the presence of ARVs-loaded nanoparticles. No toxicity was detected with the automatic cell counter. Our future step is to test ex vivo and in vivo effects of the nanoparticles on the infection of mouse-adapted EcoHIV virus in the mouse spleen.

CONCLUSION: Cabotegravir and rilpivirine were successfully loaded in the nanoparticles. HIV-1 infection was effectively suppressed in T cells that were treated with the nanoparticles. These findings highlight the utility of the nanoparticles for developing future therapeutic curative interventions for HIV-1 infection with the capability for site-specific delivery and obviating off-target toxicity.

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01.05.08 – Poster Session 1 · Chesapeake Suites (MR)

ENCAPSIDATED APOBEC3G INCREASES HIV-1 CDNA G TO A HYPERMUTATION WITHOUT HINDERING VIRAL INFECTIVITY

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PURPOSE: Human apolipoprotein B mRNA-editing enzyme, catalytic polypeptide-like 3G (APOBEC3G, A3G), is a host restriction factor vital in antiviral innate immunity. It restricts human immunodeficiency virus type-1 (HIV-1) replication by inducing lethal G to A hypermutations in the viral genome. HIV-1 encodes virion infectivity factor (Vif) to counteract the effects of A3G by mediating its proteasomal degradation, which excludes A3G from encapsidation. Even though the degradation of A3G is efficient and robust, studies suggest that A3G is still detectable in the virion, and the impact of encapsidated A3G in the HIV life cycle has yet to be determined.

METHODS: The CRISPR transfection system was used to knockout (KO) A3G in A3G-expressing cells. The KO rate was estimated using Synthego ICE analysis and further confirmed via Western blot. Then the cells were challenged with wild-type HIV-1 to produce encapsidated A3G.

RESULTS: Using a Next-Generation Sequencing (NGS) based G to A hypermutation detecting assay, we found that HIV produced from A3G-expressing T cells induces a higher G to A hypermutation rate in viral cDNA than HIV from non-A3G-expressing or A3G knockout cells despite the presence of wild-type HIV-1 Vif. Interestingly, although the virus produced from A3G-expressing cells induced a higher G to A hypermutation rate in viral cDNA compared to the virus from A3G knockout cells, there was no significance in viral infectivity between them. We also measured the G to A hypermutation rate in the viral RNA genome. Surprisingly, there was no significant hypermutation rate increase in the viral genomic RNA of the virus released from the cells infected by the virus with encapsidated A3G despite the higher hypermutation rate observed in the viral cDNA during the viral infection.

CONCLUSION: This study revealed a new insight into the antiviral mechanism of A3G and might lay a foundation for new antiviral strategies.

2U54MD007586, T32GM144927 and R25GM059994

01.05.09 – Poster Session 2 · Chesapeake Suites (MR)

RESISTANCE OF FPN Q248H TO HEPCIDIN AND ITS EFFECTS ON HIV-1 INFECTION

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PURPOSE Increased iron stores correlate with rapid AIDS progression in HIV-1-infected patients, in some iron-loaded patients. Ferroportin (FPN) is the only known ferrous iron (Fe2+) transporter present mainly in enterocytes, macrophages, and hepatocytes. FPN exports Fe2+ from the cytoplasm, whereupon the iron is oxidized at the basolateral side of the cellular membrane and loaded in transferrin. FPN is negatively regulated by hepcidin, a short peptide secreted by the liver. The FPN Q248H mutation is linked to changes in iron load in African populations. Our study explored the effect of FPN Q248H mutation on HIV-1 infection.

METHODS HEK 293T cells were transfected with FPN-expressing vector, and sensitivity to physiologic hepcidin concentrations and ferritin concentrations were evaluated using immunoblotting and fluorescence analysis. A knock-in Slc40a1Q248H mouse model was developed to study the effect of FPN Q248H mutation on iron load. Mouse-adapted Eco-HIV-1 virus was used to infect mouse spleenocytes ex vivo.

RESULTS FPN Q248H mutant showed decreased sensitivity to hepcidin and lower ferritin concentrations in HEK 293T cells and human primary monocytes. Mice with the FPN Q248H mutation exhibited increased splenic and liver iron levels, and also demonstrated increased serum transferrin saturation. Ex vivo infection of splenocytes showed decreased HIV-1 replication in splenocytes from FPN Q248H mice compared to control WT mice.

CONCLUSION These findings suggest that FPN Q248H mutation may protect from HIV-1 infection and reduce the negative consequences of HIV-1 infection by moderately increasing the iron load. The Slc40a1Q248H mouse model may be useful for further exploring the effects of FPN Q248H mutation on HIV-1 infection.

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01.05.10 – Poster Session 1 · Chesapeake Suites (MR)

DISRUPTED TYPE 1 INTERFERON IN HIV AND ALZHEIMER'S PATIENTS

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PURPOSE: People with HIV (PWH) develop HIV-associated neurocognitive disorders marked by infiltrated monocytes, inflammation, and neuronal dysfunction. Despite effective antiretroviral therapy, there is no treatment for cognitive decline. Type 1 interferon (IFN-1) signaling is a potent antiviral immune response which is also important for synaptic plasticity and cognitive function. We hypothesized that disrupted IFN-1 response triggers monocyte infiltration, neurodegeneration, and cognitive decline. METHODS: Plasma and peripheral blood mononuclear cells (PBMCs) from HIV-negative participants, PWH stratified by cognitive status, and early Alzheimer's disease (AD) patients, were obtained from the UPR NeuroAIDS Cohort. Plasma IFN-alpha (IFN-a) and beta (IFN-b) levels were measured by ELISA. Surface IFN-a receptor 1 (IFNAR1) in PBMCs was measured by flow cytometry. Total IFNAR1 levels were measured in monocytes by western blot and ELISA. Brain IFNAR1 was measured by immunofluorescence. RESULTS: Cognitive impaired PWH showed slightly elevated plasma IFN-a1 levels, while AD patients had significantly higher levels (p=0.03) compared to HIV-negative. Plasma IFN-b significantly decreased in men and women with HIV (p=0.001). A lower percentage of IFNAR1+CD14+ monocytes was detected in PWH (p=0.02) and AD patients (p=0.01), which was significantly lower in men (p=0.03) but not in women. Preliminary ELISA and western blot analyses revealed a significant decrease in intracellular IFNAR1 in monocytes from PWH (p=0.037), and a slight decrease in monocytes from AD patients, compared with HIV-negative control participants. However, IFNAR1 levels were similar in brain tissues from PWH and controls. CONCLUSIONS: Disrupted IFN-1 signaling may alter monocyte phenotypes and functions, increase migration to the brain, and contribute to neurodegeneration. Differential IFN levels and biological sex differences warrant further investigation for future diagnostic and therapeutic approaches.

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01.05.12 – Poster Session 2 · Chesapeake Suites (MR)

HIV-1 INTEGRASE INHIBITOR-ASSOCIATED NEUROPSYCHIATRIC EFFECTS

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PURPOSE The preferred first line treatment regimen for people living with HIV (PLHIV) is a combination antiretroviral therapy (ART) based on dolutegravir (DTG)—an integrase strand transfer inhibitor (INSTI). Around 22 million PLHIV in over 110 countries are currently on DTG-based ART regimen. The INSTIs are generally considered to be safe and effective, but there is growing concern about higher reported rates of neuropsychiatric adverse events (NPAE) in PLHIV on DTG. Our hypothesis is that DTG disrupts neuronal communication in brain circuitry linked to neuropsychiatric disorders. Our goal is to decipher the molecular mechanism(s) underlying DTG-associated neuropsychiatric effects.

METHODS Human primary neurons or differentiated SH-SY5Y cells treated with DTG or raltegravir (RAL) or vehicle control were assessed for: alterations in morphology and neurite outgrowth by fluorescence and brightfield microscopy; changes in synaptic marker protein levels by western blot; and variations in extracellular glutamate and intracellular calcium levels by spectrophotometric and fluorometric methods, respectively. RNA-sequencing was used to identify differential gene expression patterns, and the data was analyzed to identify pathways functionally linked to neurological disorders. The alterations in the expression of genes-of-interest were further assessed and confirmed by quantitative polymerase chain reaction (qPCR) and western blot analysis.

RESULTS In contrast to the control and RAL-treated cells, DTG-treated cells exhibited a striking reduction in neurite outgrowth, decline in post-synaptic protein levels, and elevation in extracellular glutamate levels. Importantly, DTG-treated cells exhibited a distinct gene expression pattern signifying dysregulated glutamate neurotransmission and calcium signaling.

DISCUSSION / CONCLUSION These results have revealed the identity of key proteins and signaling pathways mediating DTG-induced dysfunction in neuronal communication.

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ABSTRACTS

Infectious and Immunological Diseases (non-HIV)

01.06.02 – Poster Session 1 · Chesapeake Suites (MR)

ALLEVIATING MYCOPHENOLIC ACID-INDUCED TOXICITY IN THE GI TRACT USING DIETARY SUPPLEMENTS

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Purpose: Gastrointestinal side effect is a serious concern of mycophenolic acid (MPA), an active metabolite of the prodrug mycophenolic mofetil (MMF) that is used as an immunosuppressive agent in clinical settings. This study is to develop safe and effective approaches to prevent/treat Mycophenolic acid-induced diarrhea (MID) in patients with organ transplantation. Method: MID model was established in rats by given seven consecutive doses of 70 mg/kg/day MMF from day 1 to day 7, pretreated with wogonin or chrysin at 100 mg/kg from day -3 to day 7. Bodyweight, stool consistency were monitored daily, conduct the PK study on day7, and collect the tissues to measure the tissue distribution of MAP and its metabolites. Histology study of intestinal to evaluate the intestinal damage caused by MMF, plasma and tissue expression of TNF-α was measured as markers of MID-induced inflammation using ELISA Kit. Conduct the vitro experiments using the Intestinal Epithelial Cells (IEC) in 24 well plate, grow for 10 Days, treat wogonin and chrysin with different ratio for 3 days. Incubated Genistein and MPA for 6 hours, collect the samples to measure the glucuronide concentration using LC/MS. Results: The body weights and the fecal condition results showed that wogonin significantly protected body weight loss and reduced diarrhea score. Chrysin's efficacy is mild. wogonin and chrysin didn't alter the exposure of MPA and MPAG in the plasma. However, wogonin significantly reduce the exposure of MPA in the ileum. wogonin and chrysin were mainly distributed in the ileum and the colon, suggesting that these two compounds are locally bioavailable. Inflammatory cytokine TNF-α was regulated by wogonin, suggesting that wogonin protect the tissue via anti-inflammatory pathway. Histology study show that in the treatment group, despite a remarkable thinning of the intestinal walls, epithelial morphologic of the ileum and colon did not display significant alternations. In the vitro study, wogonin and chrysin could induce UGT activity in the intestinal epithelial cells. Additionally, wogonin has a better induction when compared to that of chrysin. conclusion: MID model in rat was established successfully, and Wogonin could alleviate diarrhea induced by MPA without affecting the plasma exposure of MPA, probably due to the reduced MPA exposure in the ileum.

This work was supported by Center for Biomedical and Minority Health Research (CBMHR) grant number of 2 U54 MD007605-27A1. This work was also made possible, in part, by services provided by the National Institute of Health Grant number of R16 GM149425-01 for Song Gao and GCC Center for Comprehensive PK/PD and Formulation (CCPF) with CPRIT grant number of RP180748 and National Institute of Minority Health and Health Disparity (U54MD007605).

01.06.04 – Poster Session 2 · Chesapeake Suites (MR)

SARS-COV-2-SPECIFIC IMMUNE RESPONSES IN FILIPINOS RESIDING IN HAWAIʻI

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PURPOSE: Filipinos make up 16% of Hawaiʻi's population and during the COVID-19 pandemic experienced disproportionately high rates of severe disease and mortality. Clinical trials evaluating the COVID-19 mRNA vaccines did not disaggregate vaccine efficacy in Filipinos. Previous literature has indicated differences in immune response to vaccination between ethnic groups. The purpose of this project is to evaluate COVID-19 immunity, in COVID-19-vaccinated Filipinos as compared to non-Filipinos residing in Hawaiʻi. METHODS: Filipinos and non-Filipinos (ages 18 to 45 years) who received the primary mRNA COVID-19 vaccination series were recruited. Participants completed a survey about their age, sex, ethnicity, COVID-19 vaccination status, and history of SARS-CoV-2 infection. SARS-CoV-2-specific total and neutralizing antibody were measured in serum samples by ELISA and PRNT, respectively. SARS-CoV-2 specific memory B cells and plasma cells isolated from peripheral blood were analyzed by flow cytometry. RESULTS/EXPECTED RESULTS: The average age of study participants is 26 years, 81% are female, the average time after vaccination is 13.4 months, and the average time after the last infection is 16.4 months. Additional recruitment is ongoing. We are in the process of measuring antibody levels and memory B cell frequency are used as indicators of existing and long-term SARS-CoV-2 immunity, respectively. DISCUSSION: Results that reveal no difference in antibody levels or memory B cell frequency between Filipinos and non-Filipinos will support our null hypothesis that Filipinos are responding to COVID-19 vaccines as non-Filipinos. Results that reveal decreased antibody levels and/or memory B cell frequencies in Filipinos as compared to non-Filipinos will alert us a need to promote additional booster doses in the Filipino community.

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01.06.05 – Poster Session 1 · Chesapeake Suites (MR)

EXPRESSION OF A CHOLECYSTOKININ NEUROPEPTIDE IN BIOMPHALARIA GLABRATA, AN INTERMEDIATE HOST FOR SCHISTOSOMIASIS

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Schistosomiasis is a parasitic disease caused by blood flukes of the genus Schistosoma. It is considered a Neglected Tropical Disease (NTD) as it is prevalent in communities without access to potable water. One of the main species infecting humans, Schistosoma mansoni, requires snails of the genus Biomphalaria to support stages of its larval development and transformation into the cercarial form that can infect humans. This study aims to identify neuropeptide expression in the central nervous system (CNS) of Biomphalaria glabrata, a major intermediate host of S. mansoni. Increasing knowledge about host-parasite interactions, identifying physiological and behavioral changes in infected snails and leading to novel strategies for vector control. The neuropeptide cholecystokinin (CCK) has a recognized role as a gut-brain peptide in mammals but its localization in the gastropod nervous system is unknown. As part of a neural transcriptomics approach to identify neuropeptides that could act at the interface between Biomphalaria snails and their schistosome parasites, CCK expression was examined in the nervous system and peripheral tissues of B. glabrata. Double-labeling experiments combined whole-mount immunohistochemistry with the Hybridization Chain Reaction (HCR) in-situ hybridization technique (Molecular Instruments, LA, CA) were performed on dissected B. glabrata CNS and peripheral tissues. Expression of CCK in the male reproductive system and kidney was observed. In the central ganglia, CCK-like immunoreactive neurons were detected. The localization of CCK mRNA agreed with the immunohistochemical observations, confirming expression of the B. glabrata CCK-like neuropeptide in approximately 20 cells in the CNS. The association of the CCK peptide with male reproduction could suggest novel strategies for snail control.

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01.06.07 – Poster Session 2 · Chesapeake Suites (MR)

NOVEL ANTI-TUBULIN AGENTS WITH ANTI-PLASMODIAL ACTIVITY

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PURPOSE: Malaria, a mosquito-borne disease caused by Plasmodium parasites, is a public health problem worldwide, with 249 million cases and 608,000 deaths reported in 2023. Multidrug-resistant Plasmodium parasites are increasing alarmingly, highlighting the need for novel drugs. Plasmodium parasites possess alpha and beta tubulins, essential for the parasite cytoskeleton, making them a potential target for novel drugs. Using the tubulin destabilizing agent albendazole as a model, 183 novel targeted heterocyclic amides were designed and synthesized. Our goal is to determine the expression of tubulins throughout the parasite's life cycle and to determine the antiplasmodial activity of the synthesized compounds at multiple parasitic stages. METHODS: To assess tubulin expression (alpha1, alpha2, and beta) in P. falciparum, P. vivax and P. berghei, throughout the parasite life cycle, the PlasmoDB online resources and the Malaria Cell Atlas were used. The in vitro antiplasmodial activity of the heterocyclic amides was determined in Plasmodium falciparum (144) and P. berghei (183) blood stages using SYBR Green (drug-sensitive and drug-resistant strains) and drug luminescence assay, respectively. Analogs activity in P. berghei mosquito stages, ookinete (9), and male gametes (3) was assessed by in vitro drug luminescence assays and microgamete conversion experiments. RESULTS: Gene expression analysis reveals that tubulin is expressed throughout the parasite's life cycle, showing higher expression in P. berghei and P. falciparum gametocytes and other parasitic stages. Nine out of 183 anti-tubulin compounds exhibited activity in the P. berghei asexual stages (luminescence assay); two out of 9 were active in ookinetes, and three in male gametes mosquito stages. Initial results showed that 17 compounds analyzed displayed antiplasmodial activity in drug sensitive and resistant P. falciparum strains. CONCLUSION: Novel anti-tubulin compounds were identified with activity on multiple Plasmodium species and multiple parasitic stages, demonstrating promising potential for further development as anti-malarial agents.

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01.06.08 – Poster Session 1 · Chesapeake Suites (MR)

OJT010 DISPOSITION IN SARS-COV-2 INFECTED RATS AND CELLS

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PURPOSE Coronavirus disease continues to impact the world with transmission of new variants that pose challenges of poor response to drugs and vaccines. Repurposing existing drugs can reduce the health disparities of Covid-19 morbidity and mortality. Of recent OJT010 was shown to have potency against SARS-CoV-2 virus but the pharmacokinetic disposition in SARS-CoV-2 infection has not been evaluated. OJT010 is used to treat respiratory diseases and for improving motor function in Parkinson's disease but elicits its pharmacological responses at varying doses (0.025-1.2g/kg). We evaluated the pharmacokinetic disposition of high dose OJT010 in SARS-CoV-2 infected rats and in A549 and HEK293 cells.

METHODS Three rats infected with SARS-CoV-2 virus were administered single dose of 600mg/kg OJT010 orally, the animals were euthanized, and the lung tissues harvested. Lung (A549) and kidney (HEK293) cells were cultured for 24 hours and exposed to 10 µg/mL of OJT010 for 6 hours. Drug was extracted in acetonitrile and evaluated using the LC-MS/MS system. Drug levels were evaluated at 0, 5, 15, 30, 60, 45, 60, 90 mins, 2, 4, 6, 8, and 24 hours in lung tissues and in the cells. Pharmacokinetic parameters were derived using WinNolin® software.

RESULTS / EXPECTED RESULTS Concentration-time curve of OJT010 was generated, and from a standard curve the pharmacokinetic parameters were obtained using a linear trapezoid method. Mean ± standard deviation for AUC(0-Inf), Cmax, Tmax in lung tissues, A549 and HEK293 cells were compared which showed OJT010 accumulates substantially in the lung tissues and cells at levels high enough to elicit pharmacological response against SARS-CoV-2 virus.

DISCUSSION / CONCLUSION OJT010 showed high bioavailability and concentrates in the target cells of SARS-CoV-2 virus. Together with its demonstrated effects on SARS-CoV-2 proteins, OJT010 shows high potential for use to treat or augment Covid-19 drugs.

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ABSTRACTS

Nanotechnologies

01.08.01 – Poster Session 2 · Chesapeake Suites (MR)

ENGINEERING AFATINIB-LOADED PLGA-PEG NANOPARTICLES: A QUALITY BY DESIGN APPROACH FOR IMPROVED NON-SMALL CELL LUNG CANCER THERAPY

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Delivery of chemotherapeutic drugs via nanoparticles (NPs) enhances tumor targeting due to their small size and large surface area, which facilitate cellular entry and biomolecular interactions. However, rapid clearance by the mononuclear phagocyte system (MPS) often diminishes nanomedicine delivery efficacy. By engineering self-assembling NPs from a poly(lactide-co-glycolide) (PLGA) and polyethylene glycol (PEG) blend, we can reduce macrophage uptake and extend circulation time, circumventing the need for further synthesis, purification, and characterization. The anticancer effectiveness and physicochemical attributes of PLGA NPs—such as size, shape, and surface charge—are crucial for their behavior in vivo and can be precisely controlled by adjusting synthesis parameters. Traditional methods of single-parameter optimization are not only resource-intensive but also prone to failure. The Quality by Design (QbD) approach systematically controls these parameters to ensure the optimal quality and therapeutic effect of the product. Factorial two-level Screening and Central Composite Design have proven especially efficient in bioengineering for evaluating parameters, mathematical modeling, and optimization with fewer experiments, essential for scaling up. In this research, we utilized high pressure homogenization (HPH) and Design Expert software to optimize the formulation of PLGA-PEG nanoparticles loaded with afatinib, a hydrophobic drug for treating metastatic non-small cell lung cancer. We identified critical material attributes (CMAs) such as the drug-to-PLGA ratio, PLGA concentration, PEG-to-PLGA ratio, and organic solvent fraction to achieve nanoparticles with an ideal size and polydispersity index (PDI). The optimized nanoparticles, uniform in shape and ranging from 109 nm to 205 nm, highlight the efficacy of DoE-optimized afatinib-loaded nanoparticles as a promising anticancer therapy. Furthermore, this study investigates various PLGA/PEG blends to determine the optimal ratios and configurations, examining the impact of nanoparticle flexibility on cellular internalization.

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01.08.02 – Poster Session 1 · Chesapeake Suites (MR)

ELECTRODIFFUSION ACTIVE PUMP MODEL WITH THE IMMERSED BOUNDARY METHOD

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Electrodiffusion is essential in understanding the mechanisms of biological electrophysiology. Regarding volume homeostasis, in the presence of a non-uniform distribution of concentration between intracellular and extracellular domains and highly concentrated negatively charged macromolecules inside (e.g. proteins, nucleic acids), without elasticity of the plasma membrane and exchange pump mechanism working together, the cell inevitably swells; the volume swelling of a dead cell is a good example. Active exchange pumps involved in cellular volume regulation are also significant in the course of volume change through the mechanism of cell division, growth, and apoptosis.

In the sense of the immersed boundary (IB) method, we replace classical interface conditions across the membrane with regularized chemical potentials to control the permeation of each ionic species based on the Poisson-Nernst-Planck equation. Electroneutrality except for the space charge layers along the membrane is well satisfied. To regulate ion/solute transports, continuous chemical potential barriers are augmented with the energetic gradients represented by smoothed Heaviside kernels specifying the directionality of active pumping.

We obtain steady-state concentrations from electrodiffusion active pumps with extracellular and intracellular Na+, K+, Cl-, and H+ ionic species in a periodic boundary condition. The electrodiffusion active pump model for the exchange of sodium and potassium (NKE) shows a great fitting to the theoretical formula in a broad range of ionic concentrations. Currently, this model is further being developed for NKCC and NHE active pumps. This is thought to be one step forward for the IB electrodiffusion active pump model for cell migration.

RCMI U54MD013376, ASCEND UL1GM118973/ RL5GM118972

01.08.03 – Poster Session 2 · Chesapeake Suites (MR)

APTAMER-FUNCTIONALIZED HYBRID NANOPARTICLES TARGETING MRP-1 TO CIRCUMVENT MDR IN BREAST CANCER CELLS

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PURPOSE: Resistance to chemotherapeutic agents is a major reason for cancer treatment failure. When MRP-1 is highly expressed, it creates an extremely resistant cell environment for the breast cancer cells. We anticipate that knocking down MRP-1 by MRP-1 siRNA-encapsulated nanoparticles could enhance the delivery of doxorubicin (Dox) into the breast cancer cells. To minimize the non-targeted toxicity and unwanted side-effects, we plan to develop a targeted nanocarrier delivery system for siRNA into breast cancer cells. METHODS: For targeted delivery, Aptamer-A6 has been used which can bind to Her-2 receptors on breast cancer cells. The particles were prepared by high pressure homogenization (HPH) using different amount of DOTAP, cholesterol, PLGA or PLGA-PEG and Mal-PEG. After siRNA encapsulation, the particles were incubated with aptamer-A6 for surface labeling. The liposomal particles were characterized for their size, surface charge and cytotoxicity. The delivery of MRP-1 siRNA into 4T1-R cells has been assessed by immunofluorescence and FACS analysis. RESULTS: We have shown that aptamer labeled-nanoparticles having PLGA are smaller in size than those having PLGA-PEG. Surface charge was reduced when the particles were labeled with aptamer. When the cells were transfected with MRP-1 siRNA-encapsulated nanoparticles, the cytotoxicity was observed significantly lower in PLGA nanoparticles (F31) compared to PLGA-PEG nanoparticles. Similarly, the cell transfection increased significantly when the particles were labeled with aptamer. CONCLUSIONS: This preliminary study concludes that aptamer functionalization of the nanoparticles could enhance the knockdown of MRP-1 which might increase the delivery of doxorubicin into breast cancer cells.

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01.08.04 – Poster Session 1 · Chesapeake Suites (MR)

DEVELOPMENT OF THERMO-REVERSIBLE GEL CONTAINING TENOFOVIR-LOADED NANOPARTICLES

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Howard University

Background: Tenofovir, a nucleotide analogue reverse transcriptase inhibitor is commonly prescribed for pre-exposure prophylaxis. This study was designed to develop buffered thermo-reversible gel containing tenofovir loaded PLGA nanoparticles for prolonged protection from sexually transmitted HIV.

Method: TNF-loaded PLGA nanoparticles were prepared by modified emulsion/solvent evaporation technique employing ethyl acetate, pluronic®F68 and 2% w/v PVA solution. The solvent was later evaporated at room temperature. The nanoparticles were separated by ultracentrifugation, washed and lyophilized at -50oC for 24-48 hours. The thermo-reversible buffered gel was prepared from Poloxamer 407 (20% w/v), pH 4.2 citrate buffer and 2.5% w/v of Pluronic® F-108. The solution was verified for phase transition by gradually increasing the temperature in water bath and documented for gel formation by visual observation. Freeze dried TNF loaded PLGA nanoparticles of predetermined weights were added to this solution to obtain a thermo-reversible nano-gel formulation. The formulation was stored at 2-8oC for further use.

Results: Encapsulation and drug loading efficiencies were obtained in the ranges of 1.43-10.78 and 0.25-1.18% respectively. Particle sizes ranged from 265-413nm with polydispersity index ranging from 0.131 to 0.217. The thermo-reversible gel demonstrated gel matrix formation at temperatures 28-30oC and converted to a solution when refrigerated. Cytotoxicity study of formulation components (placebo gel, buffered gel, nanoparticles, and complete formulation) was conducted for 2 and 24 hrs. The formulation and components were found to be nontoxic to VK2/ E6E7 cells.

Conclusion: Thermo-reversible solution dispersed with tenofovir-loaded PLGA nanoparticles demonstrated the desired sol-gel transition for vaginal application. Further, the study demonstrates the development of a promising non-toxic vaginal gel formulation with an extended sustained drug release profile of tenofovir.

Neuroscience and Mental Health

01.09.01 – Poster Session 2 · Chesapeake Suites (MR)

RACIAL MINORITIES HAVE GREATER HEAT PAIN SENSITIVITY AND SELF-REPORT PAIN THAN WHITE PEOPLE

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Previous studies have demonstrated effects of racialized minority status on thermal pain sensitivity, sensibility, and tolerance. However, there is limited evidence demonstrating effects of minority status on painful punctate mechanical stimuli and self-report pain. We analyzed the effects of racialized minority status on heat pain sensitivity, sensibility to painful heat and punctate mechanical stimuli, and Pain Sensitivity Questionnaire (PSQ) scores. Our secondary purpose was to test face validity of the PSQ in a US population. Using quantitative sensory testing for painful heat and punctate mechanical stimuli (forces: 64, 128, 256 and 512 mN), and self-report PSQ, we evaluated pain sensitivity and sensibility in 134 healthy participants (34 Asian, 25 Black, and 75 White). We used linear mixed models to analyze outcomes allowing maximal inclusion of incomplete data sets. Racialized minority status was associated with greater heat pain sensitivity ($F=7.63$; $p=0.00074$) and PSQ scores ($F=15.45$; $p=9.84 \times 10\text{-}7$) but had no effect on painful suprathreshold heat (model improvement by addition of race: $X2=2.199$; $p=0.333$) or punctate mechanical stimuli ($F=1.50$; $p=0.229$). Face validity of the PSQ in racialized minorities was limited by differential experience of individual items ($F=19.87$; $p=3.28 \times 10\text{-}8$). Ratings of painful suprathreshold heat ($R=0.204$; $p=0.00020$) and punctate mechanical stimuli ($R=0.333$; $p=0.00062$) positively correlated with PSQ scores. Consistent with previous research, sensitivity to painful heat was affected by racialized minority status. In contrast, there was no significant effect of racialized minority status on suprathreshold painful heat or punctate mechanical stimuli. Certain items of the PSQ are inapplicable to healthy participants from racialized minority groups.

01.09.02 – Poster Session 1 · Chesapeake Suites (MR)

EFFECTS OF A DIFFERENTIAL OVEREXPRESSION OF THE VESICULAR ACETYLCHOLINE TRANSPORTER ON SYNAPTIC ACTIVITY AND BEHAVIOR IN DROSOPHILA MELANOGASTER

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Impairment in cholinergic neurotransmission is associated with normal and pathological aging, making cholinergic release a subject of sustained interest. However, the precise role of changes in central acetylcholine (ACh) release in mediating behaviors that range from locomotion to cognition has not been fully elucidated. The vesicular acetylcholine transporter (VAChT) is present in many species, including worms, flies, and humans, and is responsible for the packaging of ACh for exocytotic release. Although there is a plethora of knowledge about the molecular machinery that regulates ACh, the exact manner in which VAChT, an essential component of ACh regulation, alters ACh-linked neuronal function remains a subject of active investigation. Here, we use the overexpression of VAChT as a tool to increase the amount of ACh released into the synaptic cleft. And we are measuring the effect of that altered state on synaptic activity using two key behavioral circuits, locomotion and cognition. Previously, we showed that vast increases in VAChT expression cause severe behavioral deficits, including a sharp decline in lifespan. Our current study is focused on testing the hypothesis that more moderate increases in VAChT expression will not only lead to less severe effects but also beneficial ones. To test this idea, we used four VAChT overexpressing lines with varying levels of increased expression. We report the intriguing results that while strong increases in VAChT produced a corresponding decrease in lifespan, a less drastic overexpression of the protein led to a less steep decline in lifespan. Moreover, we show that in agreement with our previous published findings, our preliminary data show that VAChT overexpression caused an age-dependent decrease in locomotion ability in all lines tested. Further, immunohistochemical analysis showed that at least one VAChT overexpressor showed a strong increase in localization of the protein to punctate in the optic lobe, indicative of increased presence in synaptic vesicles. Taken together, these data indicate that morphological and behavioral effects of VAChT overexpression are driven by the levels of the protein's expression and inform further studies to be aimed at identifying precisely which dial in VAChT expression could lead to a beneficial effect on synaptic neurotransmission.

NIH/COBRE Program

ABSTRACTS

01.09.03 – Poster Session 2 · Chesapeake Suites (MR)

HIV-1 NEF DECREASES GLUTAMATE TRANSPORTER EXPRESSION ON ASTROCYTES OF THE NUCLEUS ACCUMBENS AND INCREASES COCAINE-SEEKING BEHAVIOR IN RATS.

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Cocaine use is elevated in HIV-infected individuals, contributing to increased vulnerability to and development of HAND. Both cocaine and HIV neurotoxins play roles in neuronal damage during HAND progression by disrupting glutamate homeostasis in the brain. Part of the dysregulation is due to the reduction of astrocytic proteins, including glutamate transporter (GLT-1) and cystine/glutamate antiporter (xCT). Even with the presence of cART, HIV-1 Nef protein, an early viral protein expressed in approximately 1% of infected astrocytes, remains a key neurotoxin and could contribute to ongoing neuronal degeneration. In this study, we explore the interplay between HIV-1 Nef and cocaine on glutamate homeostasis. We hypothesized that combined exposure to cocaine and Nef would exacerbate glutamate excitation, inducing neurophysiological changes that strengthen synaptic transmission and reinforce cocaine-seeking behavior. To test this, we infused a lentiviral vector expressing Nef in astrocytes under a GFAP promoter into the nucleus accumbens (NAc), a crucial structure in the reward circuit, or a control vector, into Sprague Dawley (SD) rats. After five weeks, we exposed the rats to a single dose of cocaine or saline and sacrificed 24 hours later for molecular analysis. Western blot and immunofluorescence (IF) analysis of GLT-1 demonstrated decreased expression by Nef and/or cocaine. Expression of xCT decreased only in the presence of cocaine. IF analysis additionally showed astrogliosis driven by astrocytic Nef expression in the NAc. Another group of SD rats was subjected to a behavioral paradigm of short-access cocaine self-administration and extinction. Data revealed that Nef increased cocaine-induced seeking behavior in the reinstatement phase compared to the cocaine group alone. Our findings suggest a convergence of HIV-1 Nef and cocaine in glutamate dysregulation which may explain the enhanced cocaine seeking. In conclusion, this study provides insights that may explain an increase in cocaine use among individuals infected with HIV.

MD007579, DA054814

01.09.04 – Poster Session 1 · Chesapeake Suites (MR)

A DOPAMINERGIC RELEASE AGONIST CONFERS NEUROPROTECTION AGAINST A DROSOPHILA MODEL OF SPORADIC PARKINSON'S DISEASE

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Parkinson's disease (PD) is the second most common neurodegenerative disease. Decades of research have established key environmental and genetic factors as contributors to its etiology although the precise cause of most PD cases remains unknown. Moreover, despite the advances in our understanding of the possible causes of PD, a viable treatment remains elusive. Rotenone, a potent laboratory model for sporadic PD has been used to uncover important insights into the etiology of the disease. We are interested in testing the neuroprotective capability of the small molecule dacarbazine (which we identified in a previous pharmacological screen) and its structural derivative, 5-Amino-4-imidazolecarboxamide (AICA) against Rotenone induced neuronal toxicity. Both compounds have been reported previously to increase synaptic activity in a manner that is dependent on vesicular monoamine release. In this project, we investigated whether both compounds are capable of conferring organismal and/or neuroprotection against rotenone toxicity. We report that dacarbazine confers a small but reproducible protection against organismal toxicity induced by rotenone exposure in both male and female Drosophila. These results are all the more remarkable given that dacarbazine is a chemotherapeutic drug with a toxic potential of its own. Crucially, we report for the first time, that consistent with its published role as a VMAT-dependent drug, AICA protects dopamine (DA) neurons against rotenone-induced neuronal toxicity in an assay in which we combined both a pesticide (rotenone) and age as risk factors for PD. Together, these findings identify an promising new anti-PD compound and highlight the feasibility of the physiological enhancement of DA release in vivo as a viable strategy for developing therapeutics against Parkinson's disease

NIH-COBRE

01.09.07 – Poster Session 2 · Chesapeake Suites (MR)

CHARACTERIZATION OF HEALTH DISPARITY VARIANTS IN ALZHEIMER'S DISEASE

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Alzheimer's disease (AD), the most common cause of dementia in older adults, disproportionally affects African Americans with an incidence rate as much as three times higher, compared to other racial/ethnic groups. Multiple factors contribute to this racial disparity however, an in-depth understanding of the biological or genetic contributions does not exist. Compelling evidence indicate that genetic variants of the lipid transport protein, ABCA7, is more strongly associated with AD in African Americans. To understand how ABCA7 contributes to AD on the molecular level, we used a combination of structural and cell biology techniques. We have found that the ABCA7 T319A variant is that confers risk in African Americans is expressed and localizes to the plasma membrane and has reduced ATPase activity when expressed in human cell lines. Proteomic studies indicate reduced levels of the phospholipase C eta (PLCH1) protein in cells that expressed ABCA7 T319A compared to wild-type. PLCH1 is involved in the metabolism of phosphoinositol bisphosphate PIP2. Our results suggest that this variant may contribute to AD by reducing the levels of PIP2, a phospholipid reported to be decreased in the AD brain. These results provide a framework for targeting mechanisms that can increase PIP2 levels as an effective strategy mitigating AD disparities.

Alzehimer's Association (ABA-23-975038)

01.09.08 – Poster Session 1 · Chesapeake Suites (MR)

METFORMIN ANTIINFLAMMATORY EFFECTS ON ACTIVATED BV-2 CELLS

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PURPOSE: Neuroinflammation is associated with several neurodegenerative diseases, such as Alzheimer's disease. Microglia are the brain's primary immune cells, and when excessively activated, they cause neuronal damage by releasing pro-inflammatory cytokines and reactive oxygen intermediates. Therefore, suppressing microglia-mediated inflammation and oxidative stress has been considered as an important strategy in neurodegenerative disease therapy. Metformin is used to treat Type 2 Diabetes and also have anti-inflammatory properties. The purpose of this study is to determine the potential role of metformin as an anti-inflammatory and antioxidant agent in lipopolysaccharide (LPS) activated BV-2 microglial cells. METHODS: In this study, BV-2 microglia cells were stimulated for 1 hr with 1µg/mL LPS and then incubated for 24 hr in the presence and absence of 1mM, 2mM, and 4mM metformin. This study used Alamar Blue (Resazurin) assay, PrimePCR array, and Western blotting technology to evaluate cell viability and inflammatory and oxidative stress signaling pathways. RESULTS: Our results indicated Metformin significantly downregulated the expression of mRNA of NF- κB1a, IL-1b, and CCL2(MCP-1), demonstrating that metformin can reduce inflammation. Metformin also significantly increased the expression of mRNA of Hmox1 and IL-10, suggesting its antioxidant and neuroprotective effects. The Western blot results also revealed that metformin significantly increased the protein expression of Nrf2, which participates in the transcription of many antioxidant genes. According to these results, metformin's anti-inflammatory and antioxidant effects may be mediated by inhibiting the NF- κB1a pathway and activating the Nrf2 signaling pathway. Modulating these pathways by metformin in the brain may protect neuronal cells against neuroinflammation, oxidative stress, and cell death. Conclusion: In conclusion, these findings suggest that metformin is not only beneficial for the treatment of Type 2 Diabetes but may also have therapeutic potential to prevent or slow the progression of neurodegenerative diseases, such as Alzheimer's disease, by reducing oxidative stress and neuroinflammation.

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01.09.11 – Poster Session 2 · Chesapeake Suites (MR)

CASEIN KINASE 1D/E INHIBITORS AS THERAPEUTICS FOR TAUOPATHY

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PURPOSE The objective is to identify and develop small molecule series that are casein kinase 1 d/e (CK1d/e) inhibitors. Tauopathy, the aggregation of tau into neurofibrillary tangles (NFTs), is the primary pathological feature of AD. CK1d and CK1e have been shown to phosphorylate tau at 36 and 7 sites, respectively, in in vitro studies. CK1d/e are highly overexpressed in AD-affected brains and co-localize with neuritic and granulovacuolar lesions. Blocking the phosphorylation of tau would not only decrease the propensity for NFT formation, but also decrease the negative cellular consequences of axonal microtubule depolymerization. We hypothesize that CK1d/e inhibitors can function as potential therapeutics for tauopathic neurodegenerative disorders including Alzheimer's disease.

METHODS Use of computational modeling software (MOE) and organic synthetic methods to create series of molecules as CK1d/e inhibitors. Aim 1 of the research is to enhance the inhibition potency and selectivity for CK1d/e by our inhibitor series by designing new derivatives based on docking studies of active compounds followed by synthesis and in-vitro kinase inhibition assays using FRET based technology. Aim 2 is the testing of inhibitors in biochemical and cell biological assays.

RESUTLS AND EXPECTED RESULTS Two series of the lead compounds 2-bromo-5,8-dihydroxynaphthoquinone and 4-acetamido-N-(7-amino-1,3-dioxoisoindolin-5-yl)benzamide are identified as CK1d/e inhibitors. Docking studies have revealed key structures features responsible for their binding to CK1d/e. New derivatives have been designed to enhance the potency and selectivity of the lead compounds. Synthesis and kinase inhibition analysis are ongoing. In reconstituted biochemical assays using purified components and in neuronal cell culture systems expressing constitutively active CK1d/e, we are testing our inhibitors' ability to decrease tau phosphorylation.

CONCLUSION New series of CK1d/e inhibitors have been identified. The efficacy of the compounds on the inhibition of tau hyperphosphorylation and tau isozyme levels are under investigation.

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ABSTRACTS

01.09.13 – Poster Session 1 · Chesapeake Suites (MR)

1H NMR-BASED METABOLOMIC CHANGES IN PRE-BÖTZINGER COMPLEX FOLLOWING ADMINISTRATION OF MORPHINE.

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Purpose: The most frequent cause of death associated with opioid overdose is respiratory depression. The respiratory depressant effects of opioids are mediated primarily through activation of μ-opioid receptors expressed by several brain regions involved in the regulation of breathing, including the respiratory rhythm generating neurons of the pre-Bötzinger complex (PBC). However, the biochemical and metabolic changes associated with opioid activation of μ-opioid receptors at the PBC remain unknown. In the present study in mice, we applied in-vivo 1H NMRS to measure morphine-induced metabolic changes in the brainstem regions overlapping PBC.

Methods: Localized in-vivo 1H spectra were acquired from PBC of the mouse brain using a 9.4T Bruker AVANCE 89mm bore NMR machine and quantified using LCModel software. 1H NMRS was acquired before and 5 days after subcutaneous implantation of morphine pellets.

Results: Morphine induced significant changes in the concentrations of several metabolites in PBC. Phosphocreatine, involved in energy metabolism, increased significantly whereas creatine + phosphocreatine decreased after morphine. This effect of morphine on energy balance is consistent with the known inhibitory influence of morphine on neuronal metabolism. In the absence of a change in glutamate, both the glutamine and the glutamine + glutamate (Gln+Glu) components of the Gln-Glu-GABA axis increased. This finding suggests a shift in the interconversions between Gln, Glu and GABA and in excitatory-inhibitory influences on PBC neurons. Levels of antioxidant neurometabolites, taurine and glutathione, as well as the levels of membrane integrity markers, glycerophosphocholine + phosphocholine (GPC+PCh), also increased after morphine.

Conclusion: This single-voxel 1H NMRS study is the first to measure morphine-induced neurometabolic changes in the vicinity of brainstem respiratory rhythm-generating sites using live animals.

RCMI

Oral Health

01.10.01 – Poster Session 2 · Chesapeake Suites (MR) 🏆

TITANIUM DIOXIDE EXHIBITS CYTOTOXICITY ON OECM-1 SQUAMOUS CARCINOMA CELLS

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PURPOSE Carcinoma of the oral tissues represents one of the major neoplasms that account for most cases of head and neck cancer globally. Epithelial to mesenchymal transition (EMT) plays a major role in the metastasis of oral cancer by progressing tumor cells to become more aggressive. Titanium dioxide (TiO_2) is one of the prominent metals utilized, but its role in oral carcinoma is yet to be investigated. Hence this study investigated the inhibitory effect of TiO_2 solution on human OECM-1 squamous carcinoma cell proliferation and cellular mechanisms through which it exerts its inhibitory effect.

METHODS Human OECM-1 squamous carcinoma cells were purchased from Millipore Sigma and cultured in RPMI media, supplemented with 10% FBS and 1% penicillin-streptomycin. Cells were passaged at 90% confluency, and then seeded in 96 well-plates. The cells were allowed to adhere for 24 hours, treated with TiO_2 at different doses between 1- 100μg/ml, and incubated at 37oC between 24 -72 hours. Cells without TiO_2 treatments and vehicle control (ethanol) were also included in the study. MTS-based cell viability assay was performed. The expression levels of EMT markers (HMGA2 & SNAIL) were determined using western blot analysis.

RESULTS The OECM-1 cell viability was significantly reduced following 72 hours of 100μg/ml TiO_2 treatment in relation to the vehicle control. Also, findings from the study revealed lower expression levels of HMGA2 and SNAIL proteins in the 100μg/ml TiO_2 treated cells as compared to ethanol vehicle and other doses tested at 24 hours.

CONCLUSION TiO_2 exhibits evidence of an inhibitory effect on OECM-1 Squamous Carcinoma cell proliferation via reduction of HMGA2 and SNAIL protein expression.

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Pulmonary Diseases

01.11.01 – Poster Session 1 · Chesapeake Suites (MR)

ESTABLISHING A PCD CENTER IN PUERTO RICO: IMPACT ANALYSIS

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PURPOSE: Primary ciliary dyskinesia (PCD) is a rare lung disease that can result in progressive lung damage and respiratory failure, often necessitating lung transplantation in adulthood. From 2008 to 2018 in Puerto Rico, PCD diagnosis relied solely on electron microscopy (EM). In 2021, an accredited PCD center was established, introducing PCD genetics, nasal Nitric Oxide (nNO) levels, and high-speed video microscopy analysis (HSVA) in 2023. This study aims to evaluate the impact of establishing a PCD center in Puerto Rico on diagnosing patients and contributing to local and global knowledge through publications.

METHODS: A retrospective analysis was conducted from 2008 to 2018, during which EM was the only diagnostic tool in Puerto Rico. After establishing the PCD center in 2021, medical records were analyzed to assess the number of patients diagnosed with PCD after implementing genetic, nNO measurement, and HSVA. A PubMed database search was conducted about PCD in Puerto Rico from 2008-2018 compared to 2018-2023.

RESULTS: From 2008 to 2018, no PCD cases were diagnosed using EM in Puerto Rico, as all EM results showed normal cilia. From 2018 to 2021, 28 new PCD cases were diagnosed using PCD genetics. A founder mutation in RSPH4A (c.921+3_921+6del (intronic)) was the primary genetic variant in 22 cases. In 2021, the implementation of nNO measurement and HSVA further validated PCD diagnosis. Decreased levels below 77nL/min and rotatory ciliary beat pattern were identified in those with the RSPH4A founder mutation. Scientific publications on PubMed increased by 6 after the center's establishment.

CONCLUSION: Establishing an accredited PCD center in Puerto Rico in 2021 significantly improved PCD diagnosis, highlighting the limitations of relying solely on EM. The addition of genetic testing, nNO measurement, and HSVA helped identify more cases. The center's expanding diagnostic tools have enhanced our understanding of PCD in the Puerto Rican population.

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01.11.02 – Poster Session 2 · Chesapeake Suites (MR)

IDENTIFICATION OF GENE SIGNATURES IN A MOUSE MODEL OF LUNG INJURY WITH PREDICTIVE POTENTIAL TO HUMANS

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Introduction. Identification of Gene expression signatures are evolving rapidly to be used in numerous applications of medicine including disease prognosis or guidance for clinical treatment decisions. The present study sought to identify gene signatures in a mouse-model of lung injury associated with lung histopathological responses.

Materials and Methods. Mice (C57BL/6J males) were instilled with multi-walled carbon nanotubes and after 7 and 56 d post instillation, the lungs were collected and used for microarrays analysis. Real-time qPCR was performed using TaqMan microfluidic low-density arrays (LDA) with custom designed gene primers on an ABI 7900HT Fast RT-PCR instrument (Applied Biosystems). Gene expression analysis was done using SDS2.3 software (Applied Biosystems) based on the number of cycles required to reach threshold fluorescence (Ct). 18S was used as an endogenous control gene. Results. We were able to identify two sets of gene signatures, one for the 7d post-exposure and one at 56d post-exposure in the mouse lungs exposed to multi-walled carbon nanotubes vs control. At 7d post-exposure, 7-genes signature was identified and at 56-d post-exposure a signature of 11-genes was identified. Among those identified gene sets, 4 genes including coiled-coil domain containing-99 (Ccdc99), muscle segment homeobox gene-2 (Msx2), nitric oxide synthase-2 (Nos2), and wingless-type inhibitory factor-1 (Wif1) showed a significant mRNA expression perturbations at both time points. Ingenuity Pathway Analysis (IPA) against whole mouse genome and human genome identified several carcinogenic-related and carcinogenesis signaling pathways that correlated with both identified gene signatures. In conclusion, we identified two gene-signatures from a mouse-model of lung injury which provides genes associated with human lung cancer development and prognosis and with predictive potential.

U54MD015929

ABSTRACTS

Behavioral and Social Determinants of Health

Behavioral and Mental Health

02.01.01 – Poster Session 1 · Chesapeake Suites (MR

VALIDATION OF THE ORGANIZATIONAL TRAUMA RESILIENCE - PATIENT REPORTED EXPERIENCE MEASURE

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Purpose: People with HIV (PWH) are 20 times more likely than the public to experience Post-Traumatic Stress Disorder. However, most HIV care providers do not routinely assess patients for PTSD or to ensure they feel psychologically safe in their care spaces. Innovative, evidence-based solutions are needed to attenuate HIV-related health disparities. At present, no instruments exist to measure patient experiences of organizational trauma resilience—or extent to which the care environment is perceived to be safe, stable, and nurturing.

Methods: To develop and test the Organizational Trauma Resilience – Patient Reported Experience Measure, we applied several methods to develop and test the psychometric properties, including iterative community engagement through community workgroups and cognitive interviews, application of Flesch-Kincaid to improve readability, and data collection in an HIV clinic and Community-Based Organization (CBO).

Results: Twenty cognitive interviews were conducted to refine items and resulted in a 48-item instrument with six dimensions. In total, 251 PWH completed the survey, including 193 in the CBO and the remaining 58 in the clinic. Cronbach's alpha Coefficient was .989, and the mean of the Corrected Item Total Correlation was .818. Scores for each dimension were assessed on a five-point scale and included the following: 1) Culture of Trust and Support: 3.47+.77; 2) Practices of Inclusivity, Safety, and Wellness: 3.38+.80; 3) Collaboration and Empowerment: 3.37+.79; 4) Training and Sustaining Trauma Responsiveness: 3.29+.84; 5) Impact of Provider Trauma Training: 3.12+.9; and 6) Cultural Responsiveness: 3.53+.77.

Conclusion: The 48-item OTR-PREM showed excellent reliability and validity. Dimensions assessed as being most aligned with OTR included Culture of Trust and Support and Cultural Responsiveness. Training and Sustaining Trauma Responsiveness scored the lowest. Next steps will include further data collection to refine instrument properties to make more parsimonious and confirm factor solution for items and unidimensional scoring and stanine scoring.

K01MH131471-01A1; P30AI110527; 1P50MD017347-01; U54MD007586-04;

02.01.02 – Poster Session 2 · Chesapeake Suites (MR)

RACIAL AND MENTAL HEALTH DISPARITIES IN SUBSTANCE USE DISORDER PATIENTS THROUGH NIH ALL OF US DATA

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Purpose Individuals suffering from substance use disorder (SUD) often face co-occurring mental health disorders, which can significantly influence their behavior and long-term health outcome. This study aims to explore the relationship between SUDs and other mental health disorders, and potential racial difference utilizing NIH All of Us data.

Methods We conducted multivariate analysis using electronic health records from the All of Us dataset between January 1, 2017 and December 1, 2023. Patients who had at least one SUD conditions (alcohol, opioid, cannabis, and cocaine) were identified via ICD10 codes. The most recent visits related to SUDs served as the index date for constructing risk variables, including demographics and clinical conditions. Logistic regression was used and adjusted odds ratio with 95% confidence interval were reported.

Results A total of 25,592 patients were identified, with a majority being male (53.4%) and a median age of 56 (IQR: 42, 70). The patients were White (48.6%), Black (30.3%), Hispanic (20%). Alcohol use disorder was the most prevalent (44.3%), followed by opioid (30.7%), cannabis (29%), and cocaine use disorders (16.4%). The most common co-occurring mental health disorders were depression (50.1%), anxiety (48.1%), and bipolar (17.2%). We built 13 variables and conducted logistic regression analysis for each SUD respectively. The adjusted odds ratio indicated patient were more likely to use SUDs ($p<0.0001$) when they experienced depression, anxiety, and bipolar. When compared with Whites, Black and Hispanic are more likely to use cannabis and cocaine, but less likely to use alcohol and opioid ($p<0.001$).

Conclusion The study indicated a strong association between mental health disorders and SUDs, with significant difference observed across patients from various racial backgrounds. To further explore these disparities, we plan to incorporate additional risk factors into our model, including healthcare utilizations, medication treatment, and social determinants of health.

This work is supported by NIH RCMI supplemental grant 3U54MD007586-37S1, and pilot grant from The Research Advisory Council and Office for Research & Innovation at Meharry Medical College. The authors would like to thank Dr. James Hildreth, Dr. Samuel Adunyah, and Dr. Anil Shanker for their continuous support.

02.01.03 – Poster Session 1 · Chesapeake Suites (MR)

ENGAGING PEERS TO ADDRESS TOBACCO USE AMONG BALTIMORE YOUTHS

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PURPOSE: Current use of any tobacco product is notably higher among high school students from families classified as having low affluence. The primary reason for our inability to assist those who are most vulnerable is primarily attributed to our lack of knowledge regarding their perspective on the world and the environments that surround them. Hence, peer-led interventions and support services developed with an understanding of the community based participatory research approach have shown great promise in helping communities and individuals become better informed about available resources and actively supported in benefiting from them, in this case, smoking cessation.

METHODS: Using a quasi-experimental design, a two-phase intervention was designed and implemented to leverage peer facilitators and peer support as a tool for tobacco cessation of diverse group of youths in Baltimore City. Phase 1 included implementation and Phase 2 included evaluation and measurement.

RESULTS: At Phase 1, the study partnered with American Lung Association (ALA), two colleges (Morgan State University and Coppin State University) and four high schools (Coppin Academy, Carver Vocational Technical High School, Vivien T. Thomas Medical Arts Academy and Mergenthaler Vocational Technical High School). ALA trained five peer facilitators recruited from the two colleges. The peer facilitators are responsible for supporting their peers quit tobacco utilizing the ALA developed curriculum. Two student ambassadors were recruited from each of the four high schools to support recruitment of their peers in the study. At phase 2, school survey will be issued to the interested high school students to understand their perception and knowledge of tobacco and tobacco use. After which individuals that have used any tobacco product in the last 30 days will be enrolled into either the peer facilitated tobacco intervention arm or the self navigated arm. The intervention is still an ongoing study.

DISCUSSION: Engaging the peers in a systematic way showed a lot of promises. They have the right messaging that resonates best with adolescent and young adults, they know the best channels to reach them, and they are the right messenger that motivates their peers.

This work was supported by the National Institute on Minority Health and Health Disparities. RCMI@Morgan #5U54MD013376-8281.

02.01.04 – Poster Session 2 · Chesapeake Suites (MR)

THE USE OF VIRTUAL FOCUS GRUPS TO EXPLORE COMMUNITY HEALTH CONCERNS IN THE SOUTHERN REGIONS OF PUERTO RICO

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Focus group discussions are a valuable tool for understanding the context of health concerns, especially in underrepresented communities with different health needs due to various social and health determinants, such as income and availability of services, among other factors. When combined with a CBPR approach in which community members become partners involved in all research phases, issues that would typically go unattended can be identified. However, due to the global COVID-19 pandemic, in-person focus group discussions were interrupted; due to this, many researchers had to adapt to the conditions so as not to risk participants' health. Our team designed and implemented a Virtual-Conference-Style Focus Group Protocol to collect the desired information. We created ten online focus groups (n=73) from 2020 to 2022 through this process. With this protocol, we obtained qualitative data analyzed using the Health Belief Model to create four main dimensions: Knowledge, Vulnerabilities, Barriers, and Identified Resources. The biggest concerns found were mental health, healthcare access, and the need for help from both the private and public sectors. Through this modality, we were able to conduct our studies and found added benefits to this method, which included the participation of individuals who usually would not be able to attend focus groups, such as geographically isolated participants, participants with conflicting work schedules, and most notably bedridden patients. Most importantly, we identified the concerns of these communities, which indicate the need for better interventions in terms of mental health and chronic health condition prevention.

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ABSTRACTS

02.01.05 – Poster Session 1 · Chesapeake Suites (MR)

IMPACT OF MENTAL HEALTH DISTRESS ON PRECONCEPTION HEALTH

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PURPOSE: Mental health distress (MHD) is broadly defined as an emotional state characterized by symptoms of stress, depression, and anxiety whereas preconception health embodies the physical and mental health prior to a pregnancy. MHD among women of reproductive age is associated with an increase in hypertension, diabetes, smoking, obesity, physical inactivity, and alcohol use. These risk factors have been identified as measurable indicators of preconception health. The study purpose is to examine the relationship between MHD and preconception health indicators after controlling for sociodemographic and healthcare access characteristics.

METHODS: Florida Behavioral Risk Factor Surveillance System was used. Analysis was limited to women of reproductive age. The main exposure variable involved MHD. Women who reported their mental health not well for ≥ 14 days during the past month were characterized as enduring frequent MHD. Multiple logistic regression analyses were used to assess associations between MHD and each preconception health indicator in separate models.

RESULTS: Among women of reproductive age, 15.8% reported frequent MHD. Our findings showed that nonpregnant women of reproductive age who experienced frequent MHD had worse preconception health indicator outcomes than those with lower levels of MHD, with the greatest disparities detected in fair or poor self-rated health, and smoking (AOR = 3.88; $p < 0.0001$ and AOR = 2.06; $p < 0.0008$, respectively). Older age, minority race, being uninsured, unemployed, divorced, having less than high school education, and financial barriers in healthcare access were associated with worse preconception health outcomes in most models.

CONCLUSION: Increased screening and treatment for mental distress, counseling women about unhealthy behaviors, and adapting behavior change interventions may help optimize the preconception health of women with MHD. Personalizing interventions that would target these preconception modifiable risk factors could lead to improved short-term, long-term, and favorable pregnancy health outcomes among women with MHD.

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02.01.06 – Poster Session 2 · Chesapeake Suites (MR)

ASSOCIATIONS BETWEEN PSYCHOLOGICAL DISTRESS AND NIGHTMARE DISTURBANCE ON SUICIDAL IDEATION

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INTRODUCTION: According to the World Health Organization (WHO) 703,00 individuals are suicide completer each year, while more report suicidal ideation (SI). SI is a strong predictor for suicide attempts. Research has shown that psychological disorders represent independent risk factors for SI. Sleep disturbances, such as nightmares, are also risk factors for SI. While research has primarily investigated relationships between depression and sleep disturbances and their impact on suicidal ideation, less is known about the contributions of mental health and nightmares' influence on suicidal ideation. This study explored relationships between PTSD and generalized anxiety symptoms, nightmare disturbance, and suicidal ideation.

METHODS: Participants (N=46; Age=34.59, SD=12.74; Female=63%) completed self-report measures as part of a larger study. The PTSD Checklist for DSM-5 assessed for PTSD symptoms, with higher scores indicating greater PTSD symptom severity. The Generalized Anxiety Disorder-7 scale evaluated the prevalence and severity of anxiety symptoms, with higher scores representing a greater degree of anxiety symptoms. Nightmare disturbances were determined by the Nightmare Distress Questionnaire (NDQ) and nightmare items from the SLEEP-50 questionnaire. Suicidal ideation was assessed using the Beck Depression Inventory-II, item 9.

RESULTS: Findings showed that PTSD ($r=.338$, $p=.022$), generalized anxiety ($r=.495$, $p<.001$), nightmare distress ($r=.509$, $p<.001$), and nightmare symptoms ($r=.345$, $p=.019$) were correlated with suicidal ideation, respectively. A linear regression model indicated that psychological distress and nightmare disturbances accounted for 37.8% of the variance. Beta coefficients indicated that generalized anxiety symptoms were the strongest predictor of suicidal ideation ($\beta=.418$, $p=.026$).

CONCLUSION: Data indicate that clinicians need to carefully assess for suicidal ideation among clients presenting with anxiety problems, and particularly with clients in suicidal crisis.

This study was funded by a Center Grant from the National Institute on General Medical Sciences (Grant #P20GM103653). JAB's time was supported by a Center Grant from the National Institute of Minority Health Disparities (Grant # U54MD015959).

02.01.07 – Poster Session 1 · Chesapeake Suites (MR)

SLEEP QUALITY AND PSYCHOLOGICAL DISTRESS ON NEUROCOGNITIVE AND ACADEMIC PERFORMANCE AMONG EMERGING ADULTS

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INTRODUCTION: Approximately 60% of college students report poor sleep quality. Research has shown that poor sleep quality has a profound impact on student's psychological health. Further, emerging adults experience both biopsychosocial and environmental changes that contribute to increased susceptibility to sleep disturbance and poor mental health outcomes during the college year. Few studies have investigated the collective toll of sleep and mental health problems and their influence on neurocognitive and academic performance. This study aimed to examine the impact of sleep quality and psychological distress on memory and attention.

METHODS: Data were obtained from college students who completed self-reported measures (N=107; Mean age= 20.3 (SD=1.9); 80.4% Females). The Pittsburgh Sleep Quality Index (PSQI) examined the overall quality of sleep, with higher scores indicating poor sleep. The Beck Depression Inventory-II assessed for depressive symptoms, the PCL-5 determined posttraumatic stress disorder (PTSD) symptoms, and the Generalized Anxiety Disorder-7 (GAD) scale assessed anxiety symptoms. The CANTAB neurocognitive battery was used to assess domains of memory (verbal recognition memory) and attention (rapid visual information processing). Academic performance was assessed using student's cumulative grade point average (GPA).

RESULTS: PTSD severity (r=.491, p<.001), generalized anxiety symptoms (r=.461, p<.001), and depressive symptoms (r=.566, p<.001) were significantly correlated with poor sleep quality. Generalized anxiety symptoms were negatively associated with verbal recognition immediate (r=-.220, p=.029) and delayed recall (r=-.231, p=.022), such that, as generalized anxiety symptoms increased, total number of correct responses decreased. GPA was correlated with verbal recognition distractors (i.e., inference) on immediate (r=.241, p=.019) and delayed recall (r=-.405, p<.001). None of the study measures were associated with attentional tasks (r= -.041-.084, p's>.05).

CONCLUSION: Data showed that psychological distress, specifically generalized anxiety symptoms, contributed to poor memory outcomes. These cognitive deficits may have clinical significance in college students and should be considered in treatment planning.

This study was funded by a Center Grant from the National Institute of General Medical Sciences (Grant #P20GM103653). JAB's time was supported by a Center Grant from the National Institute of Minority Health Disparities (Grant # U54MD015959).

02.01.08 – Poster Session 2 · Chesapeake Suites (MR)

NEUROBEHAVIORAL SYMPTOMS PREDICTS DEPRESSION AND ANXIETY AMONG EMERGING ADULTS

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INTRODUCTION: Approximately 33% of college students have been diagnosed with an anxiety disorder and about 44% with depression. Data indicates that neurobehavioral symptoms are likely to exacerbate psychological stress experienced by college students. Less is known about the impact of neurobehavioral symptoms on specific depressive and generalized anxiety symptoms. This study aimed to 1) explore relationships between neurobehavioral symptoms' impact on cognitive and somatic depressive symptoms and generalized anxiety symptoms, and 2) evaluate whether neurobehavioral symptoms contributed to depression and anxiety among emerging adults.

METHODS: The data were collected from 107 participants (Mean age= 20.29 (SD=1.86); 80.4% Females). The Neurobehavioral Symptom Inventory assessed for post-concussion symptoms, with higher scores indicated a greater degree of post-concussion symptoms. The Generalized Anxiety Disorder (GAD-7) scale assessed for the degree of worry and severity of GAD symptoms. Higher scores indicated greater anxiety severity. The Beck Depression Inventory-II evaluated overall depressive severity, including the cognitive and somatic subscales. Higher scores represented a greater degree of depressive symptoms.

RESULTS: Approximately 36.4% of the sample had probable depression and 36.4% had probable generalized anxiety disorder. Adjusting for depressive and anxiety symptoms, neurobehavioral symptoms were highly correlated with overall depressive (r=.780, p<.001), cognitive depressive (r=.725, p<.001) and somatic depressive (r=.739, p<.001) symptoms, and generalized anxiety symptoms (r=.613, p<.001), respectively. Logistic regressions showed that neurobehavioral symptoms increased the likelihood of probable depression (X2=24.55, OR=1.18, p<.001). The model explained 48.1% (Nagelkerke R2) of the variance in probable depression and correctly classified 79.4% of cases. Neurobehavioral symptoms also increased the likelihood of probable generalized anxiety disorder (X2=20.78, OR=1.13, p<.001). The model explained 34.8% (Nagelkerke R2) of the variance in probable generalized anxiety disorder and correctly classified 75.7% of the cases. CONCLUSION: A history of neurobehavioral symptoms may contribute to mental health outcomes among college students, necessitating interventions to improve optimal functioning.

This study was funded by a Center Grant from the National Institutes on General Medical Sciences (Grant #P20GM103653). JAB's time was supported by a Center Grant from the National Institute of Minority Health Disparities (Grant # U54MD015959).

ABSTRACTS

Social Determinants of Health

02.04.01 – Poster Session 1 · Chesapeake Suites (MR)

DELAYED HIV DIAGNOSIS AND CARE LINKAGE PRE VS COVID PANDEMIC

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PURPOSE The COVID-19 pandemic affected health care access and delivery including HIV testing and care. This study's aim was to identify disparity differences in timely HIV diagnosis and linkage to care between the pre-pandemic (2017-2019) and early COVID-19 pandemic (2020) periods among people with HIV (PWH) in Florida.

METHODS Florida enhanced HIV/AIDS Reporting System data merged with community data were used. Delayed HIV diagnosis was defined as AIDS diagnosis within three months of HIV diagnosis. Delayed linkage to HIV care was defined as no viral load or CD4 test within one month of HIV diagnosis. Adjusted odds ratios (aOR) and 95% confidence intervals (CI) were estimated using multilevel models.

RESULTS Of 12,733 Florida residents diagnosed with HIV 2017–2019, 21.2% were diagnosed late and 21.4% were linked late. For 2020 (N=3079), 21.7% were diagnosed late and 18.5% linked late. Black/White racial disparities appeared to decline during the pandemic for delayed diagnosis (aOR before 1.15, 95% CI 1.02-1.31; aOR during 1.01, 95% CI 0.77-1.29) and persist for delayed linkage (aOR before 1.44, 95% CI 1.27-1.63; aOR during 1.56, 95% CI 1.19-2.05). Older age was associated with lower odds of delayed linkage before (aOR 0.86, 95% CI 0.76-0.95), but higher odds during the pandemic (aOR 1.33, 95% CI 1.04-1.70). Residence in lower HIV prevalence rate areas was associated with delayed diagnosis before (aOR 1.27, 95% CI 1.01-1.59) and during the pandemic (aOR 1.74, 95% CI 1.24-2.42). Residence in high medical system avoider areas (aOR 1.15, 95% CI 1.01-1.30) was associated with higher odds of delayed linkage before the pandemic but not during.

CONCLUSIONS Although delayed diagnosis and delayed linkage did not increase during 2020, disparities increased in delayed linkage among older individuals. Enhanced efforts to expand linkage among older individuals may be needed to avoid further HIV disparities during public health emergencies.

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02.04.02 – Poster Session 2 · Chesapeake Suites (MR)

PILOT STUDY EXAMINING THE ROLE OF SEX HORMONES AND DISCRIMINATION IN ADDICTION-LIKE CRAVINGS

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INTRODUCTION Approximately 8 percent of adult women suffer from a substance use disorder. In prior studies, food cravings and substance use correlated with women's menstrual cycle state and stress. However, few research reports explicitly examine how actual discrimination stress interacts with sex hormones to predict drug cravings in Black women. The purpose of this study was to examine the relationship between estrogen fluctuation, discrimination stress, and cravings for addictive substances. It was hypothesized that higher estrogen levels would interact with discrimination experiences to predict an increased desire for psychoactive substances.

METHOD Self-identified Black female college students of at least 18 years of age were recruited after at Morgan State University (N= 30, M age= 20.83). Participants completed the Perceived Everyday Discrimination Scale (PED), Brief Cravings Scale (BCS) and Food Cravings Scale (FCS) then saliva was collected. They were then randomly assigned to play one of 3 Cyberball (CB) conditions, wherein participants were either excluded by a group of White virtual players (discrimination); Black virtual players (general social exclusion) or they were included in the game (inclusion), and salivary estrogen was measured using ELISA assays.

RESULTS Factorial ANOVA analyses revealed no significant interaction effect of CB and estrogen levels on mean BCS or FCS scores. There were no significant correlations between Brief Cravings Score and mean Perceived Everyday Discrimination (PED). However, a significant trend for a negative correlation between mean food craving score and mean perceived discrimination [r(30) = -.315, p=.090] was observed.

DISCUSSION The hypothesis was not supported. However, the near significant trend for a negative correlation between perceived discrimination and food cravings contrasts with findings from previous studies. The small sample size of this pilot study, limited the power to find significant predictors of addiction-like cravings. Follow-up studies will involve recruiting more participants and testing varying models of virtual discrimination.

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02.04.05 – Poster Session 1 · Chesapeake Suites (MR)

DISCRIMINATION AND INFLAMMATORY RESPONSES IN BLACK WOMEN

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PURPOSE Black Women (BW) suffer increased morbidity and mortality from health conditions involving dysregulated inflammation, but few if any studies use experimental designs to study this phenomenon. This study addresses the knowledge gap regarding the effects of discrimination on inflammation in Black women (BW). It also aims to experimentally examine how racial discrimination during a virtual social exclusion game affects BW's inflammatory response. We hypothesized that racial discrimination experiences in a virtual game will increase salivary inflammatory cytokines in BW.

METHODS Forty BW (M = 20.3, SD = 3.96) provided pre-experiment saliva and were assigned to one of three conditions: exclusion by White avatars (discrimination condition), exclusion by Black avatars, or inclusion by racially diverse avatars in Cyberball™. Participants completed surveys and provided post-game saliva. Inflammatory cytokine levels were measured using ELISA assays to determine pre-post differences.

RESULTS Thirty percent of participants experienced discrimination compared with 40% and 30% in the exclusion and inclusion conditions. ANOVA showed no significant changes in interleukin-six or interleukin one-beta. However, a near-significant decrease in tumor necrosis factor-alpha ($F(2,37) = 2.93$, $p = 0.07$) was observed in the discrimination condition.

DISCUSSION/CONCLUSION Although no statistical support for the hypothesis was found, possibly due to small sample size, the trend in tumor necrosis factor-alpha (TNF-α) decrease suggests a potential blunted or abnormal immune response in BW post-discrimination. Should the TNF-α decreases persist to significant levels in subsequent studies, it would explain, in part, disparities in the outcome of inflammation-mediated diseases in Black women compared to White women.

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02.04.08 – Poster Session 2 · Chesapeake Suites (MR)

DIGITAL CEASE ADULT SMOKING CESSATION PROGRAM USING CBPR

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PURPOSE: Communities Engaged and Advocating for a Smoke-Free Environment (CEASE) is a long-standing partnership between Morgan State University and communities of Baltimore City. Leveraging the power of community-based participatory research (CBPR), CEASE has provided underserved communities with a peer-led smoking cessation program for over a decade, undergoing constant improvement through collaborative efforts. Recently, CEASE conducted a community needs assessment to understand tobacco-related needs and implemented a digitized version of the program to assess its effectiveness.

METHODS: The development of a digitized smoking cessation curriculum was informed by the CBPR approach and by partnerships with several community residents and organizations. First, a community survey was conducted in three underserved Baltimore City communities. For the intervention, a mixed-methods experimental research design was used. Current smokers aged ≥ 21 years participated in virtual/hybrid, in-person, or self-help smoking cessation classes led by peers in community settings.

RESULTS: Over 20 partners collaborated with CEASE, including service providers, residents, faith institutions, and community organizations. Among 633 community survey participants, the majority were current smokers (71.4%), reported secondhand smoke exposure (84%), had internet access (88.9%), and preferred in-person classes (55.7%). Three hundred ninety participants were recruited in the classes (virtual/hybrid: 130, in-person: 116, and self-help: 146). To date, 212 follow-up surveys (virtual/hybrid: 90, in-person: 68, and self-help: 54), 12 focus group discussions, and six key informants interviews were conducted. Three main themes emerged through combined constant comparison and thematic coding of qualitative data: health impact on participants, experiences with cessation class modes (online, virtual/hybrid), and the quitting process.

CONCLUSION: The application of CBPR principles allowed CEASE to deepen community connections and incorporate community and peer knowledge throughout various project stages. Digitizing CEASE interventions can provide invaluable insights to guide the development of culturally relevant smoking cessation services.

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ABSTRACTS

02.04.09 – Poster Session 1 · Chesapeake Suites (MR)

INVESTIGATING SARS-COV-2 VACCINE HESITANCY IN HOUSTON: A QUANTITATIVE STUDY

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PURPOSE: Vaccine uptake is crucial in mitigating the impact of COVID-19 in the U.S.; however, structural inequalities pose a threat to progress. COVID-19 has disproportionally affected Black and Latinx communities. Herein, we evaluate the quantitative results from a mixed methods study of factors affecting attitudes and perceptions towards COVID-19 vaccine from participants serving/living in minoritized communities from Houston metropolitan areas.

METHODS: During the pandemic, 17 focus groups were conducted with 79 participants comprising 22 community partners from public and community health organizations, faith-based organizations, and 57 Black/Latinx community residents domiciling in six high-risk, underserved communities in metropolitan Houston. Of the 79 participants, 55 complete online surveys were received (34.55% community partners, 65.45% community residents). Comparisons between participants' characteristics (i.e., COVID-19 vaccination status vaccine willingness, community partners vs. community members) on measures were examined using Fisher's exact tests and ANOVAs from online survey data.

RESULTS: COVID-19 vaccinated participants were more likely to believe the effectiveness of COVID-19 prevention actions (p=.002), hold a positive attitude toward child vaccines (p=.017), and were less likely to view having COVID-19 as a sign of personal weakness (p=.003). COVID-19 vaccinated participants also self-reported more years of education (p=.028) and higher food security (p=.014). Participants and/or their parents who were non-U.S. born were more willing to receive a COVID-19 vaccine (p=.002). Relative to community members, community partners self-reported higher SES (p=.017), were more likely to believe in the effectiveness of COVID-19 prevention actions (p=.003), and held positive attitudes toward child vaccines (p=.002).

CONCLUSIONS: Acceptance and attitudes towards COVID-19 vaccines were influenced by SES and education, highlighting areas where greater effort is needed to boost vaccine uptake rate. Findings indicate the critical need to identify barriers, establish trust-building relationships, and develop culturally-tailored public health messages to disseminate accurate information in underresourced and historically minoritized communities.

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02.04.11 – Poster Session 2 · Chesapeake Suites (MR) 🏆

ASSESSING STAKEHOLDER PERSPECTIVES ON SOCIAL SCREENING AMONG MARGINALIZED POPULATIONS IN CLINICAL SETTINGS

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PURPOSE: Screening for adverse social determinants is increasingly being implemented in community health centers (CHCs) as part of comprehensive strategies to improve health equity. The implicit assumption is that by addressing social and economic adversity it will disproportionately improve care for marginalized populations. But little is known about how social care is experienced by patients from different backgrounds, including people with different language preferences, experiences of migration, and lived experiences of racism and discrimination.The purpose of this study is conduct an in-depth exploration how clinical staff and providers perceive the experience of social screening among these populations.

Methods: To learn more about how staff in CHCs adapt care or perceive the need to adapt social care for marginalized populations, our research team conducted interviews from December 2020- October 2021 with CHC staff and providers (n=62) in Oregon and Texas on social screening implementation. All participants provided informed consent and interviews were recorded and transcribed verbatim. Data related to the implementation of social screening among marginalized populations were extracted and analyzed using an inductive thematic approach.

RESULTS: Four themes were identified: cultural competency is needed to appropriately screen patients for social risks; additional resources are necessary to identify and address the complex social needs of marginalized racial and ethnic groups; language barriers stifle social screening; structural racism influences access to social care.

CONCLUSION: These four themes identified barriers to social screening implementation among racialized and non-English preference populations and calls for specific pragmatic measures needed to screen marginalized populations. Future research efforts should focus on specific approaches and strategies to screening racial, ethnically, and linguistically diverse populations in order to more accurately collect social determinants of health data.

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02.04.12 – Poster Session 1 · Chesapeake Suites (MR)

REINFORCING THE BEHAVIORAL CHANGES ABOUT PROSTATE CANCER SCREENING TEST

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Purpose: African American men are known to be at a high risk of prostate cancer. Although the educational interventions could increase prostate cancer literacy among African American males, a sizable proportion of African American men could not take a PSA test because of various reasons. Some African American men may stop taking a PSA test after the educational intervention was ended. To sustain the effects of the prior prostate educational interventions and encourage them to take a PSA test annually, the study revisited African American men who have attended the educational seminars in 2018 and 2019.

Methods: This study employed a mixed-methods approach. Initially, quantitative data was collected through phone interviews using a survey questionnaire. Rigorous data analyses was conducted to systematically examine the key mechanisms influencing African American men's decision-making regarding PSA testing, as well as factors that significantly impact their cancer screening beliefs and behaviors. Subsequently, to provide contextual understanding and ensure accurate interpretation of the quantitative findings, qualitative data collection was conducted through semi-structured individual interviews with African American men.

Results: To date, attempts have been made to contact a total of 151 individuals via phone who had previously attended educational seminars. Among these attempts, 35 survey questionnaires were completed through phone interviews. Additionally, 11 in-depth interviews were conducted and completed. Preliminary data analysis revealed that various barriers, such as affordability issues, continue to impede individuals from undergoing prostate cancer screening tests.

Discussion: Awareness of prostate cancer among African American men has increased, with many recognizing the importance of screening tests. However, factors such as health insurance limitations and work schedules have prevented some from undergoing screening. Future community interventions should adopt a more comprehensive approach, potentially incorporating self-administered prostate cancer screening test kits to address these barriers.

2U54MD007590-33

02.04.13 – Poster Session 2 · Chesapeake Suites (MR)

NARRATIVES FROM EASTERN CUBA: A STUDY ON THE EXPERIENCES OF MICROAGGRESSIONS AND HEALTH

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Background information: The model of microaggressions is young. It has been linked to the following effects: anxiety, depression, difficulty sleeping, self-esteem problems, hopelessness, loss of mood, intrusive cognitions, and cognitive decline. Because Cuba has a socialized and egalitarian society, we proposed to study the narratives of people from the Eastern side of Cuba while living in Havana and their experiences with microaggressions while navigating in the capital.

Methods: This project utilized a qualitative methodology. Data was collected between July 2021 through May 2022. Six in-depth interviews were conducted with Cubans from the Eastern provinces living in Florida. The interview process was prematurely ended due to the COVID-19 travel restrictions. Data was analyzed using thematic and interrater reliability analysis.

Results: The interviewees' ages ranged between 24 and 63 (M=41). Five identified themselves as female, and one as male. Our participants knew how people from Havana perceived them as second-class citizens. Regarding health access, people living in Havana have more comprehensive services, which hurts the quality of care that people from other provinces have. Due to the high poverty rates, traveling for medical procedures is not a possibility. Due to geographic and racial discrimination, people from the Eastern provinces have difficulty accessing high-paying jobs and good living conditions, which has a direct impact on their quality of life.

Conclusions: Our findings suggest that structural barriers exist in a setting that touts itself as an egalitarian society. Our participants were exposed to interpersonal discrimination due to their place of birth and their skin color. Due to the restrictions from the Cuban government, conducting this type of research is complex, and proposing ways to address health disparities is almost impossible. However, bringing attention to this issue is a first step towards change. More extensive research is needed to measure the effects of microaggressions in this population segment.

Suicide

02.05.01 – Poster Session 1 · Chesapeake Suites (MR)

FORCED SEXUAL INTERCOURSE AND SUICIDALITY AMONG FEMALE HIGH SCHOOL STUDENTS

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PURPOSE: Suicide is one of the leading causes of death in the United States. Unlike many other leading causes of death, suicide continues to claim more lives each year. In 2021, 30% of female high school students seriously considered attempting suicide during the past year. In 2021, 18% of female high school students had ever been physically forced to have sexual intercourse when they did not want to during the past year. Beyond the trauma of the immediate event, research suggests victims of forced sexual intercourse often experience depression and post-traumatic stress disorder. This study examined the link between forced sexual intercourse and suicidality among female high school students using data that are nationally representative which include other critical youth suicide risk factors. METHODS: The data for this research has been taken from the 2021 Youth Risk Behavior Surveillance System (YRBSS) conducted among a representative sample of students in grades 9-12. The YRBSS is the largest public health surveillance system in the United States, monitoring a broad range of health-related behaviors among high school students. In addition to descriptive and bivariate analysis, several weighted unadjusted and adjusted logistic regression models were estimated for estimating the odds of suicidal attempts because of forced sexual intercourse among female high school students. RESULTS: The odds of suicidal attempts in the past 12 months are more than four times significantly ($p<0.001$) higher among those female youths who reported having forced sexual intercourse compared to those female students who didn't have forced sexual intercourse in the past 12 months. DISCUSSION/CONCLUSION: Adolescent female sexual assault is a major public health problem that takes an enormous toll on families, friends, and classmates. A vigorous policy followed by intervention needs to be developed to prevent female high school students from forced sexual intercourse.

ABSTRACTS

Violence and Crime

02.06.01 – Poster Session 2 · Chesapeake Suites (MR)

DEPRESSION AND RACISM CORRELATED WITH EXPOSURE TO VIOLENCE AMONG AMERICAN AFRICAN YOUNG ADULTS

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Background: There are several environmental determinants associated with health disparities in the USA including exposure to violence (ETV). ETV an directly influence health through biological mechanisms and can be measured as indicator of stressors.

Objective: This research examines gender differences among African American (AA) young adults in their ETV, and its relationship to depression and perceived racism. We detail these experiences in 531 self-identified AAs, ages 18 to 25, from socio-economically disadvantaged wards in Washington, DC.

Method: Correlations were calculated between perceived racism, depression, and ETV measures (exposure to interpersonal/community violence; witness/victim).

Results: Both males and females had significant positive correlations between individual ETV and childhood ETV (RM=0.61 and RF=0.59), having witnessed violence (RM=0.55 and RF=0.58), and being a victim of violent theft (RM=0.49 and RF=0.49). This suggests that the experience of violence victimization both as an adult and as a child predominantly reflects the experience of being in communities with both high personal property violence and secondary exposure to violence. Depression was significantly correlated with community ETV for both males and females (RM=0.44 and RF=0.48). Finally, racism was correlated with community ETV (RM=0.44 versus RF=0.33). Males had a correlation between community ETV and childhood ETV (RM=-0.48, $p<0.05$).

Conclusion: In this research, we find that community violence was most strongly correlated with depression, while childhood ETV was most strongly correlated with racism and with being a victim of violent theft.

This project was funded in whole or in part with U.S. Government funds from the following National Institutes of Health (NIH): National Institute of Minority Health & Health Disparities (NIMHD) (Grant # 4RO1MD005851

02.06.02 – Poster Session 1 · Chesapeake Suites (MR)

BIPOC SEXUAL VIOLENCE SURVIVORS BARRIERS TO HELP-SEEKING

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Florida International University (FDM, SLM, MH, SF, EFW, MECP); Northern Arizona University (MA)

PURPOSE: This qualitative research study explored the challenges faced by survivors of sexual violence from BIPOC (Black, Indigenous, and other people of color) backgrounds when engaging in help-seeking behaviors to informal (e.g., family or friends) or formal support systems (e.g., therapists, medical professionals, or law enforcement).

METHODS: BIPOC participants were recruited on a university campus through the distribution of flyers. Flyers were placed in individual bathroom stalls to minimize risk of self-disclosure. Participants who expressed interest were screened for eligibility. Participants were included in this study if they: were 18 or older, identified as cisgender female, and identified as Hispanic/ Latine, Middle Eastern, Asian, or Black. Eligible participants signed an informed consent and were scheduled to complete a 90-minute zoom interview. The interview audio recordings were transcribed verbatim eliminating identifiers to maintain participants privacy. Transcripts were analyzed using an inductive thematic analysis approach influenced by Grounded Theory.

RESULTS: Participants (11 total) were 18 to 33 years old and identified as Hispanic/Latine (8), Asian (2), or Haitian (1). Most of the participants (10) had multiple sexual violence experiences. Nine participants experienced sexual violence under the age of 18. Thematic analysis is currently ongoing; however, the following overarching themes are emerging from the data: adverse help-seeking experiences, disclosure to informal support systems, and reinforcement of rape myths.

DISCUSSION/ CONCLUSION: The results analyzed will inform clinical practice and policy making by considering the perspective of BIPOC sexual violence survivors. The Intersectionality Theoretical Model will also be utilized to acknowledge subsets of BIPOC survivors' identities that elucidate experiences of health inequities within informal and formal support systems.

This research was supported in part by the National Institute on Minority Health and Health Disparities of the National Institutes of Health under award number NIMHD (U54MD012393), Florida International University Research Center in Minority Institutions.

02.06.03 – Poster Session 2 · Chesapeake Suites (MR)

LIFETIME INTERPERSONAL VIOLENCE OR ABUSE AMONG FEMALES

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Meharry Medical College (MS, LLB, MC, VM); University of Kentucky (ALC)

PURPOSE: Few studies investigate lifetime interpersonal violence or abuse (IVA) rates in a lower income, primarily minority population or in the Southeastern United States (U.S.). Using data from the Southern Community Cohort Study (SCCS) , we explored forms of lifetime IVA among females by race.

METHODS: Data on lifetime IVA were collected between 2012-2015 with 22,570 females residing in 12 states in the southeastern U.S. Relative to White females included in the SCCS, Black females were hypothesized to be more likely to have experienced lifetime violence or abuse.

RESULTS: After adjusting for differences in age, income and enrollment source, Black females were 60% less likely to have experienced either adult intimate partner violence or childhood abuse or neglect (adjusted rate ratio (aRR)=0.40; 95% confidence interval (CI): 0.37-0.43) than White females.

CONCLUSION: Explanations for finding lower IVA rates among Black compared with White females include racial differences in violence or abuse experienced, a difference in understanding of what constitutes violence or abuse, and/or willingness to disclose these experiences. Findings underscore the importance of creating a clear and shared understanding of what constitutes violence or abuse. Our regional data agreed with national data in terms of IVA against women of all races - a staggering 41% - indicating a need to create an environment where females of all races feel comfortable disclosing lifetime IVA.

Research reported in this abstract was supported by the National Cancer Institute of the National Institutes of Health under award number U01CA202979 and by the National Institute on Minority Health and Health Disparities of the National Institutes of Health under award number U54MD007586. SCCS data collection was performed by the Survey and Biospecimen Shared Resource which is supported in part by the Vanderbilt-Ingram Cancer Center (P30CA068485).

Capacity Building

Education and Training

03.01.02 – Poster Session 1 · Chesapeake Suites (MR)

THE IMPORTANCE OF A COMMUNITY ADVISORY BOARD FOR COMMUNITY ENGAGEMENT IN HEALTH DISPARITIES RESEARCH

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Center for Collaborative Research in Health Disparities, UPR-Medical Sciences Campus (ILP,CMVV, AGV, EFR)

PURPOSE: We invited individuals from community and health organizations to participate as Community Coalition Team (CCT) members of our Community Engagement Core (CEC). The intention was to coordinate a CCT to advise investigators on research areas, strategies to improve participant recruitment, and methods to disseminate research findings. METHODS: The objectives of our CCT are: 1) Advise investigators who conduct basic and clinical/health projects in research areas of high interest to communities; 2) Increase investigators' ability to incorporate community perspectives in research projects addressing health disparities; 3) Define strategies to improve the recruitment and retention of participants in studies; and 4) Disseminate research findings to a variety of audiences. CEC follows up on recommendations provided by the CCT members during bi-monthly meetings. The CCT meetings are evaluated using a short survey. RESULTS: The CCT has contributed to our CEC in the following initiatives, considering each of our aims: 1) We invited investigators from our research center to prepare presentations for CCT meetings and receive feedback. 2) We coordinated educational activities, including Retreats, Mini-Symposium, and Facebook Lives. 3) CCT members provided contact information to enhance recruitment materials like brochures. 4) We have encouraged investigators to participate in community activities and develop educational materials to be disseminated. The survey results consistently show that the CCT members are satisfied with how the CEC values their feedback and the sense of community and cohesion of the CCT. DISCUSSION: The CCT has been an integral part of our CEC initiatives, helped review our work plan, and come up with new ideas to further community outreach related to health disparities research in Puerto Rico. CCT members bring diverse perspectives to initiatives, allowing us to reach a range of communities in Puerto Rico and collaborate with researchers in community engagement initiatives.

This project is supported by the Center for Collaborative Research in Health Disparities (CCRHD), which is funded by an RCMI-Grant from the National Institute on Minority Health and Health Disparities (U54 MD007600) at the University of Puerto Rico, Medical Sciences Campus.

03.01.03 – Poster Session 2 · Chesapeake Suites (MR)

DEVELOPMENT OF HISPANIC CLINICAL-TRANSLATIONAL RESEARCHERS

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University of Puerto Rico (UPR), Medical Sciences Campus (MSC) (RGG, MIR, EFR, LDJO, JCSS, ELRS)

PURPOSE: Responding to the needs and interests of students (S)/faculty (F) from undergraduate (Ug) academic programs in Puerto Rico (PR), the Title V UPR-MSC Project (TV) developed an Interdisciplinary course (INTD 5998), organized a Center for Research Education-Entrepreneurship and Science Communication Opportunities (CRESCO) and designed a Pilot Project Program (PiP) to support their development in Clinical-Translational Research (CTR). METHODS: Each semester, a group of collaborators offers the INTD 5998 – Introduction/Principles of CTR, to S at any accredited university in PR. In addition, CRESCO provides online resources/services to S/ F to strengthen their research and scientific writing skills: bibliographic databases/managers, writing assistants, anti-plagiarism software, and e-books. It also has a scientific editor and a statistical consultant who assist participants with their research projects. Through the PiP, TV has provided a primary strategy for hands-on experiences in CTR, in which UgS and UgF, under the mentoring of a principal researcher and as a team, work on a research problem, make scientific presentations, and publish their results. RESULTS: Since the academic year 2020-2021, TV collaborators have taught the course INTD 5998 six times, 46 UgS approved, and 6 UgS are currently taking it, for a total of 52 UgS from 7 UPR-campuses; 479 S/F have attended one or more of the CRESCO's online workshops on statistics, writing assistant platforms, anti-plagiarism software, and databases, 355 F have received licenses, 5,789 S/F have consulted the databases, and 79 S/F have received advice in scientific editing and/or statistics, providing support for PiP that has engaged 17 UgS, 14 UgF, 4 medical S, 9 graduate S and 15 primary researchers in 8 different post-secondary institutions participating in 15 research teams. CONCLUSION: A vigorous support program in CTR with an interdisciplinary approach has brought diversity and a pathway for creating a new cadre of Hispanic clinical-translational researchers.

Supported by the US Department of Education: Title V Grant Award # P031S200104

ABSTRACTS

03.01.05 – Poster Session 1 · Chesapeake Suites (MR)

BUILDING CAPACITY FOR HEALTH EQUITY: OUTCOMES FROM A COMMUNITY HEALTH PROMOTION PROGRAM IN SOUTHERN PUERTO RICO.

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PUBLIC HEALTH PROGRAM, PONCE HEALTH SCIENCES UNIVERSITY (LM, DAV, FJR, JMA, JLM, MM), SCHOOL OF BEHAVIORAL AND BRAIN SCIENCES, PONCE HEALTH SCIENCES UNIVERSITY (JJ, EC, AR), PONCE RESEARCH INSTITUTE (LM, DAV, FJR, JMA, JLM, DR, EC, AR, ER, JJ, MM)

PURPOSE: Promoting community health offers a promising approach to addressing enduring healthcare obstacles, with community health workers assuming a crucial role. METHODS: The Community Training Institute for Health Disparities (CTIHD) has implemented a problem-solving curriculum focused on Community Health Promotion, which integrates a competency-based learning model across two courses: "Introduction to Community Health Promotion" and "Designing an Action Plan for Community Health Promotion." Each course consists of 10 three-hour sessions, including pre/post-tests, evaluations, and cognitive debriefings. The evaluation of knowledge change involved assessing pre- and post-test scores from 27 community leaders in southern Puerto Rico. RESULTS: Cohort 1 and Cohort 2 exhibited overall retention rates of 62.6% and 96.7%, respectively. While there were no statistically significant differences in knowledge acquisition between cohorts and courses, there was a noticeable trend towards increased knowledge. Cohort 1 saw a 22% knowledge gain in Course 1 and a 24% gain in Course 2, while Cohort 2 experienced a 41% increase in Course 1 and a 25% increase in Course 2. CONCLUSION: The CTIHD's Community Health Promotion Program has made substantial progress in raising awareness and knowledge, representing a positive stride towards reducing health disparities and fostering healthier, empowered communities in southern Puerto Rico.

This work received support from the Research Centers for Minority Institutions (RCMI-U54MD007579).

03.01.06 – Poster Session 2 · Chesapeake Suites (MR)

EVALUATION OF THE OLA HAWAII MENTORING BOOTCAMP

EVALUATION OF THE OLA HAWAII MENTORING BOOTCAMP
University of Hawai'i at Mānoa

PURPOSE: The Ola HAWAII Mentoring Bootcamp provides a structured introduction to the fundamental principles governing grant writing, responsible research conduct, and professional integrity. Based on the outcomes of the 2022 Mentoring Bootcamp, we tailored new sessions for basic biomedical, clinical, and community/behavioral researchers in 2023, and evaluated the effectiveness of the revamped program.

METHODS: The 2023 Mentoring Bootcamp was held on Tuesdays, Wednesdays and Thursdays over a two-week period in May. The first week featured general sessions covering five topics: grant structure, NIH biosketch, budgets and subcontracts, community engagement, and specific aims. The second week offered 5–6 sessions each for specific tracks in basic biomedical, clinical, and community/behavioral research. Promotional materials with registration links were disseminated across the University of Hawai'i and the RCMI Consortium. At the end of each week, participants received an evaluation link via email, comprising seven questions gauging the usefulness of content, applicability to career development, and duration of sessions.

RESULTS: Of 169 registrants, 106 participated, including post-docs (20%), assistant professors (24%), and graduate students (21%). Although attendance decreased to 58% by the last day, this was markedly improved compared to 2022 (12%). Participants represented all 22 RCMI grantee institutions, but the majority were from Hawai'i (55%). Survey responses indicated high satisfaction levels, with an average usefulness rating of 1.1 (where 1=very useful, 2=somewhat useful, 3=not useful) and the content was deemed very informative and applicable (mean=1.1). Ratings showed slight improvement from 2022 (mean=1.2 for usefulness and topic content). Respondents also expressed a desire for longer sessions in the future (mean=1.5, where 1=more time, 2=same amount of time, 3=less time).

CONCLUSION: The redesigned Ola HAWAII Mentoring Bootcamp effectively met the needs of participants engaged in health disparities research and served as an useful platform for mentoring across the RCMI U54 Centers.

U54MD007601, U54GM138062

03.01.07 – Poster Session 1 · Chesapeake Suites (MR)

INTRODUCTION OF THE HOWARD UNIVERSITY IMAGING CORE FACILITY

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Howard University (SL, TWT, PCW)

PURPOSE The Howard University Molecular Imaging Laboratory (MIL) is a university core facility that promotes and supports sustainable long-term research using imaging technology to study the mechanisms of disease processes and their response to therapy from the molecular to whole animal levels. The objectives of the MIL are (1) to provide state-of-the-art instrumentation, technical expertise and essential services for in vivo imaging, (2) to provide a broad training in biomedical imaging, and (3) to foster new multidisciplinary research collaborations using imaging techniques.

METHODS The MIL has Bruker 7T and 9.4T MRIs, a PerkinElmer IVIS Spectrum optical imaging machine, and a Bruker Albira PET/SPECT/CT for small animal studies. The MIL provides expertise in designing imaging studies, development of organ and intracellular targeting, as well as identifying suitable biomarkers, or imaginable gene products.

RESULTS The MIL supported 21 research projects proposed by 16 Howard faculty members from the Colleges of Arts & Sciences, Engineering, Pharmacy, Dentistry and Medicine, and 11 external researchers from neighboring universities and biotech companies. 7 postdocs, 6 graduate, 2 undergraduate, and 5 high school students received training performing research in the MIL with their mentors. MIL users generated 6 publications and submitted two patent applications in the past year. MIL staff submitted 10 grant applications, 3 of which were funded.

DISCUSSION The MIL has been a synergetic center, fostering multidisciplinary research collaborations among researchers from Howard and neighboring institutions, allowing faculty and students to be involved in cutting edge biomedical research. The MIL provided training in imaging science through seminars, hands-on workshops, and internships. The MIL will continue to provide scientific expertise and state-of-the-art imaging equipment in support of its mission to support and expand biomedical research and training at Howard.

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03.01.08 – Poster Session 2 · Chesapeake Suites (MR)

INTEGRATING SOCIAL JUSTICE AND HEALTH DISPARITY IN DATA ANALYTICS COURSES

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Jackson State University

PURPOSE: This project aims to integrate social justice with health disparity in light of COVID-19 and highlights such relationships through data analysis, particularly in Mississippi. Such relationships are emphasized by incorporating various datasets and prediction modeling in undergraduate and graduate-level courses to train Jackson State University (JSU) students.

METHODS: Mississippi COVID-19-related data (82 counties) were collected from various sources, including the COVID-19 Data tracker of the CDC and the Mississippi Department of Health, along with Alabama, Florida, Georgia, Louisiana, and Tennessee. The food safety data were collected from The Foodborne Diseases Active Surveillance Network (FoodNet) for 2015-2020. The cumulative Mississippi COVID-19 and socio-demographic data variables were grouped into feature and target variables. Statistical and exploratory data analysis was conducted using Excel, SPSS, and Python software.

RESULTS: Significant geographical variations in COVID-19 cases and death rates were observed among various races and ethnic groups. Most cases were observed among the Hispanic and Black populations, and the highest death rates were found among non-Hispanic Blacks and Whites. Asians had the highest vaccination coverage, 77%, compared to 52%, 46%, 42%, and 25% for African Americans, Whites, Hispanics, and American Indians/Alaska Natives, respectively. COVID-19 cases and deaths in Mississippi were positively correlated with per capita income and negatively correlated with the percentage of persons without a high school diploma (age 25+). Using this initial analysis, a comprehensive dataset was developed along with simple-to-use correlation and prediction models for students to explore in the classroom and through critical thinking projects and subsequent reports compilation and presentations.

CONCLUSION: To understand health disparity and its relationships to social justice, training students using real-time data and various modeling procedures can better highlight the issues. This project has developed easy-to-use models and incorporated them into undergraduate and graduate-level courses.

This research was supported by the National Institutes of Health/National Institute on Minority Health and Health Disparities Grant # 1U54MD015929-01 through the RCMI Center for Health Disparities Research at JSU and through the Institute of Justice and Race Relations at JSU.

Institutional Readiness

03.02.02 – Poster Session 1 · Chesapeake Suites (MR)

THE NEW GENE EDITING CORE SERVICE AT MEHARRY AND ITS APPLICATIONS IN BIOMEDICAL RESEARCH

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PURPOSE: CRISPR-Cas9 gene editing technology has revolutionized medicine with the potential to cure many genetic diseases, including neurodegenerative diseases, blood disorders, cancer, and ocular disorders. It also quickly became a widely used tool to knock-out gene expression and knock-in mutations. To accommodate the growing demands for gene editing services, Meharry RCMI Research Capacity Core (MRRCC) started to offer gene editing services in 2022.

METHODS: The CRISPR-Cas9 gene editing service was built on years of experience in gene editing in our lab. We have established various CRISPR systems, including plasmid, lentiviral vector, AAV vector, primary-editing system, and the RNP transfection system. We make the above CRISPR systems available to investigators on and outside campus. The core service helps users design CRISPR experiments, perform transfection/infection, determine CRISPR efficiency, clone positive cells, and evaluate on/off-target effects.

RESULTS: The Core has successfully edited many genes for users at Meharry. We successfully knocked out the human SMARCA1 gene for Dr. Zhenbang Chen's Lab for his DoD-supported research project on novel mechanisms and targeting of neuroendocrine prostate cancer. We also knocked in a point mutation into the human APBOEC3G gene in CD34+ Hematopoietic Stem Cells (HSC) to develop a highly efficient gene-editing tool for improving HIV-1 treatment. In this project, we successfully knocked in an APOBEC3G point mutation into a human T-cell line (92% recombination rate), human HSC (up to 65% recombination rate), and knocked out the APOBEC3G gene in a T-cell line (near 100% KO rate).

CONCLUSION: With the gene-editing service added to the MRRCC, we offer our expertise and CRISPR systems to the other investigators on campus and outside Meharry. The new core service has provided highly efficient gene-editing tools to our users and eliminated the need for labs to establish their own CRISPR systems.

NIH grants: 2U54MD007586 and P30AI110527

ABSTRACTS

03.02.03 – Poster Session 2 · Chesapeake Suites (MR)

OPPORTUNITY FOR INCREASING USE OF CONTINUOUS GLUCOSE MONITORING AMONG PATIENTS WITH TYPE 2 DIABETES

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School of Nursing, San Diego State University - Imperial Valley; School of Social Welfare, University of California Berkeley; Imperial County Clinical Research Network, San Diego State University; School of Public Health, San Diego State University; Inner

PURPOSE Continuous glucose monitors (CGM) can improve diabetes management and reduce healthcare costs for patients with diabetes requiring multiple daily doses of insulin. However, inequities in CGM use persist, particularly in historically marginalized and under-resourced regions where patients rely on primary care providers rather than endocrinologists to help with diabetes management. This study assesses multilevel factors influencing CGM prescribing practices in a large, federally-qualified health center (FQHC) serving predominantly Hispanic/Latino adults in a rural, US-Mexico border region.

METHODS We conducted semi-structured interviews with a purposeful sample of individuals responsible for providing or coordinating care for patients with type 2 diabetes (N=12). Interviews were tailored to respondent role within the FQHC and assessed multilevel factors affecting CGM uptake. Interview transcripts were analyzed using applied thematic analysis.

RESULTS We interviewed primary care providers, medical assistants, and clinical administrators. While nearly all respondents were familiar with the benefits of using CGM, few providers reported prescribing the devices to their patients. Primary barriers to CGM prescription included perceived challenges with insurance coverage, patients' technological literacy, and limited clinic resources to assist patients with CGM use. Diabetes management practices varied considerably across providers and clinics; however, all respondents expressed a need for more robust patient diabetes education and viewed improving diabetes management as a high priority Most were also supportive of efforts to increase CGM prescriptions and ultimately, patient CGM use.

DISCUSSION Study findings highlighted multiple opportunities to better support CGM uptake via a system-level intervention. Potential intervention strategies included clarifying CGM eligibility criteria and documentation practices, improving patient diabetes education, reviewing clinical practice guidelines for diabetes management, and organizational training on coding and billing strategies related to CGM.

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Investigator Development

03.03.01 – Poster Session 1 · Chesapeake Suites (MR)

WRITING SUPPORT AT MORGAN STATE UNIVERSITY: SUCCESSES AND LESSONS LEARNED

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Morgan State University (SM, BE, CH), University of Maryland, College Park (SM)

PURPOSE To assess the effectiveness of the Investigator Development Core (IDC) writing support and training initiatives.

METHODS Since 2019, two grant writing workshops (GWW) have been offered annually. The first workshop, "Research Question & Study Design", is a 6-week hands-on summer workshop that guides novice grant writers to compose a concise and testable research question, support it by an in-depth literature review, and construct a rigorous study design. The second workshop, "Proposal Development", is a semester-long workshop guiding investigators through the development of an NIH-style proposal ready for submission. These workshops are complemented by science writing accountability groups (SWAGs) to enhance persistence and support the completion of writing tasks. Effectiveness was evaluated using surveys to assess satisfaction and gains in self-efficacy using constructs with 5-point Likert scales, as well as tracking scientific networking and productivity.

RESULTS To date, 56 trainees have successfully completed workshops, and 38 have actively participated in SWAGs. Surveys indicate high levels of satisfaction and significant increases in writing self-efficacy. Among participants, 16 have received IDC Pilot Project Program awards, 7 have pilot proposals under review, and 19 have been awarded 36 external grants for a total amount of $15,370,000.

CONCLUSION Our outcomes support the importance of providing investigators with structured training and peer support in the writing process. The GWW have drawn new investigators into biomedical and health disparities research which is an important aspect of extending the RCMI footprint. We have found that peer review in addition to instructor review/mentorship are valuable in building participant self-efficacy. They also lead to cross-disciplinary post-workshop collaborations, an important goal of RCMI@MSU. We have also learned some valuable lessons about optimizing workshop structure, timing, and incentivizing participation.

NIMHD/NIH U54MD013376; NIGMS/NIH UL1GM118973

03.03.03 – Poster Session 2 · Chesapeake Suites (MR)

NAVIGATING UNFORESEEN CHALLENGES: LESSONS FOR TOMORROW

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University of Puerto Rico Medical Sciences Campus (KMJ, NAR, EFR)

PURPOSE: A retreat activity was conducted with investigators and staff of the RCMI Center for Collaborative Research in Health Disparities (RCMI-CCRHD) at the UPR Medical Sciences Campus to identify the unforeseen challenges experienced and actions taken during and after the COVID-19 pandemic. METHODS: A retreat activity was organized including oral presentations from COVID-19 supplemental projects and discussion groups. Participants were requested to identify the main challenges faced during and after the pandemic, the actions taken to minimize them, and new opportunities emerging from this experience. Twenty participants, actively involved in research and health-related activities, attended the retreat. RESULTS: The top challenges identified by the participants included the sudden need to conduct remote work, difficulties in the recruitment and incentive distribution to study participants, diminished social interactions affecting mental health, limited access to online platforms, and revision of protocols to include remote modalities. Actions taken comprised: modifying protocols taking into consideration remote planning strategies, identifying recruitment strategies for difficult times, implementing secure strategies to distribute participant incentives, increasing usage of feasible digital platforms and technologies to connect with research staff and participants, and knowing your community needs. Opportunities that emerged from the pandemic experience: take advantage of remote modality to work on publications, new protocols, and supplement applications; identify and adopt mental health tools to support personnel, be alert to new funding opportunities, and be knowledgeable of technology tools and social media platforms. The oral presentations and group discussions were both rated as excellent. Over 80% of the responders completely agreed that this activity contributed to their professional development and 90% will participate in similar activities. CONCLUSION: Research challenges during a healthcare emergency can heavily impact health disparities research. The lessons learned on methodological and practical responses will assist in successfully addressing these challenges.

Supported by NIH Grant U54MD007600

03.03.04 – Poster Session 1 · Chesapeake Suites (MR)

EXPANDING THE APPLICATION OF COMMUNITY ENGAGED STUDIOS

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SOUTHWEST HEALTH EQUITY RESEARCH COLLABORATIVE, NORTHERN ARIZONA UNIVERSITY (CC, MR, CM, NIT, KAL, SJS)

PURPOSE Through cross-core collaboration, the Southwest Health Equity Research Collaborative (SHERC) Community Engagement Core (CEC) and the Investigator Development Core (IDC) with guidance from the Community Expert Board (CEB) adapted the Community Engagement Studio (CE Studio) model to increase community input in SHERC-related research. The CE Studio, originally developed at Meharry-Vanderbilt, engages community members' perspectives through a one-time consultative session with researchers to increase its relevance and promote translation of discoveries into improved health outcomes.

METHODS The SHERC CEC and IDC identified potential research teams to participate in a CE Studio and consulted SHERC's CEB about community panel recruitment. The CEC assisted research teams with presentation development, including project overview, value of community input, and 3 discussion questions for the community member panel. The CEC facilitated the 90-minute CE studio via Zoom. Community panelists received a $50 gift card and completed an evaluation survey. Researchers received a written summary report of community panel feedback.

RESULTS To date, the SHERC has implemented 2 CE Studios and engaged a total of 13 community experts. CE Studio #1 convened 7 community members who oversee youth sports management and provided feedback on preventative training programs in youth sports. CE Studio #2 convened 6 Indigenous community members who provided input on the design considerations of a mobile health game to improve high blood pressure.

DISCUSSION/CONCLUSION The adapted CE Studio is an effective strategy for increasing cross-core collaboration and engaging community members' input to enhance research project feasibility, appropriateness, and community benefits. Research teams and community member panelists both reported their CE Studio participation as being worthwhile. While CE Studios were used to inform initial design aspects of research, the SHERC CEC is now considering the expansion of this practice to inform research dissemination efforts.

The Southwest Health Equity Research Collaborative at Northern Arizona University is supported by the National Institute on Minority Health and Health Disparities grant U54MD012388.

Mentoring and Professional Development

03.04.01 – Poster Session 2 · Chesapeake Suites (MR)

INCREASING BLACK MEN IN THE HEALTHCARE WORKFORCE: THE EDGE-PA PROGRAM

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Charles R. Drew University of Medicine and Science

Workforce diversity has been identified as a crucial factor in addressing health disparities. The United States faces a longstanding challenge of racial underrepresentation in the healthcare sector, particularly among Black men, who are significantly marginalized, especially in professions like medicine. The Physician Assistant/Associate (PA) field reflects this disparity, with Black men constituting less than 2% of the PA workforce. Amidst the rapid growth of the PA profession, training programs have become exceedingly competitive.

In response to this inequity, the Charles R. Drew University of Medicine and Science initiated the EDGE-PA (Empowerment, Diversity, Growth, and Excellence) program in 2022. This pioneering endeavor aims to provide mentorship and support to Black men aspiring to pursue careers as PAs. Remarkably, since its inception, 19 out of 21 Black men have successfully matriculated into PA programs through mentorship from this program.

This poster presentation will delve into the comprehensive activities and impactful outcomes of the EDGE-PA program, showcasing firsthand testimonials from participating students. It will underscore the urgent need for similar initiatives across various medical professions to address workforce diversity gaps. By amplifying the representation of underrepresented groups, such programs hold the promise of mitigating health disparities and fostering a more equitable healthcare landscape.

Clinical Research Education and Career Development (CRECD) NIMHD/NIH Award number R25 MD007610.

ABSTRACTS

03.04.02 – Poster Session 1 · Chesapeake Suites (MR)

DEVELOPING HU-MÉTIS APP TO IMPROVE FACULTY ADVISING AND STUDENT ACADEMIC EXPERIENCE

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Howard University, College of Pharmacy

Introduction: Progression criteria of the ACPE standard 17 requires the colleges of pharmacy to render supportive and proactive student services, including mentoring/advising by faculty members, preceptors, and professional staff. Current faculty advising of the student primarily involves in-person meetings coordinated via email communications. The process is often inefficient and time-consuming, as it requires multiple communications between a faculty member and student groups.

Research Question: We hypothesize that developing a novel smartphone-based application that sync's faculty member's availability from outlook calendar will enable the students to request advising / non-advising appointments with faculty members in real-time.

Study Design: The primary aim of the project is to develop an IOS and Android-compatible application (HUCOP-METIS) to enable the students to schedule advising and related academic appointments with the faculty of the college of pharmacy. The secondary aim would be to create and employ constant connectivity via smartphone-enabled app to ensure seamless communication between advisee (mentee) and advisor (mentor).

Methods: HUCOP-METIS app, that's compatible with both Apple (iOS), and Microsoft (android) platforms are developed. The app is made available for free download on their smartphones by the HU-COP faculty members and students. The app requires a password enabled login and enables the students to request real-time appointments with faculty members.

Results: The app was downloaded and utilized by ~35 faculty members and administrators combined. Further, the app was downloaded by ~350 students at HU-COP. The app-enabled a successful scheduling of over ~1200 advising appointments between Spring 2018 and Fall 2021.

Conclusions: The HU-COP-METIS app was designed and successfully implemented at HU-COP. The app significantly reduced the time lags imparted by communication delays and enabled a real-time, seamless two-way interaction between the faculty members and students. Further, the app contributed to the diversity mission by promoting social equity and inclusivity in faculty student communications.

Programmatic Efforts

03.05.01 – Poster Session 2 · Chesapeake Suites (MR)

CONVERGENT AIMS TO BUILD RESEARCH CAPACITY AT NAU

CR PROPPER; MR Lininger; C Kirby; A Gelatt; M. Coder; K. Laurila; RT Trotter II; JA Baldwin
Northern Arizona University

PURPOSE: Our Research Capacity Core's (RCC) goal within the structure of the Southwest Health Equity Research Collaborative (SHERC) at Northern Arizona University is to facilitate high quality research that leads to a reduction of health disparities throughout the Southwest.

METHODS: We have renovated our computational core facility, continued expansion of our Technical Assistance Group-Service Center (TAG-SC), developed and implemented our Methodological Dissemination Program, and supported a Capacity Enhancement Program for providing for technological needs associated with equipment repair, computational facilities, and data resources such as access to the All of Us data set.

RESULTS: Our program has facilitated enhancement of our computing core through improved heating and cooling in support of the addition of server capacity. Since 2021, the TAG-SC has grown to support more than 200 requests for secure server access and for faculty/staff assistance with study design and data analysis. In 6.5 years SHERC's RCC has offered 88 workshops/seminars/networking events reaching over 915 attendees, and in 6 years SHERC's Research Capacity Core (RCC) sent 40 team members and investigators to 81 external workshops. We are developing digital badges for programs in GIS and Science Communication, and we have further built our research capacity by providing equipment repair and maintenance along with field equipment to conduct community-engaged research.

DISCUSSION/CONCLUSION: NAU's SHERC RCC is serving as a facilitator for high quality research leading to the reduction of health disparities throughout the Southwest.

This work was supported in part by an NIMHD center grant to the Southwest Health Equity Research Collaborative at Northern Arizona University (U54MD012388).

03.05.02 – Poster Session 1 · Chesapeake Suites (MR)

RCMI SUPPORT OF UNDERREPRESENTED AND EARLY-STAGE INVESTIGATORS: SOCIAL NETWORK ANALYSIS OF RESEARCH PRODUCTIVITY OVER A FIVE-YEAR PERIOD

HA Wayment; KA Laurila; JA Baldwin
Northern Arizona University (HAW, KAL, JAB)

PURPOSE: The Southwest Health Equity Research Collaborative (SHERC) recently completed its first 5-year funding cycle supported by the National Institute on Minority Health and Health Disparities Research Center in Minority Institution program. This study examines progress on two of SHERC's principal goals: to support the expansion of health equity research produced by SHERC-affiliated faculty at Northern Arizona University and to advance early-stage investigators (ESI) and underrepresented (UR) faculty research productivity.

METHODS: A database of all SHERC-affiliated faculty publications between 2017-2022 was created using SHERC participation records cross-checked with public access compliant publication records linked to the RCMI grant in PubMed. For each faculty author in the database, SHERC records also allowed for the identification of ESI and UR status. In addition to descriptive analyses over time, a series of social network analyses (SNA) were conducted on adjacency matrices reflecting co-authorship networks (per publication) across each year of funding.

RESULTS: SHERC-affiliated faculty had access to opportunities including methodological support, research start-up, pilot projects, grant and manuscript writing workshops, and community partnership development. The number of supported faculty (across five colleges) increased from 32 to 100 with a growing percentage of ESI and UR faculty. The number of health-equity publications increased steadily over time. The number of UR and ESI faculty authors increased most rapidly over time. ESI and UR SHERC-affiliated faculty were co-authors in 72% and 45%, respectively, of the 139 total publications in the 5-year publication record. SNA centrality metrics revealed the importance influence of ESI and UR faculty in the demonstrated increases in health-equity related research publications over time.

DISCUSSION/CONCLUSION: The demonstrated increase health-equity related research publication and concomitant expansion of ESI and UR faculty participation in these efforts can be facilitated by coordinated types of support offered by federally funded faculty development programs such as SHERC.

The Southwest Health Equity Research Collaborative at Northern Arizona University is supported by the National Institute on Minority Health and Health Disparities grant U54MD012388 (PI: Baldwin)

Clinical, Community, or Translational Minority Health and Health Disparities Research

Clinical and Translational Science Research

04.01.01 – Poster Session 2 · Chesapeake Suites (MR)

DIVERSITY AND CHARACTERISTICS OF THE ORAL MICROBIOME INFLUENCED BY RACES AND ETHNICITIES.

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Diversity of the human oral microbial communities is known to be associated with states of oral health, age, race and ethnicity. We previously investigated microbiologic risk factors associated with periodontal health disparities using qPCR and determined several key members of oral bacteria that play distinct roles in periodontal health in African Americans (AAs), Caucasian Americans (CAs), and Hispanic Americans (HAs). To further identify population-associated differential microbial profiles, we selected a total of 161 dental plaque samples from AAs, CAs and HAs with intact periodontium for whole metagenome shotgun sequencing. A total of 2,221,643 genes were predicted using MetaGeneMark. Numbers of non-redundant genes in AA group were significantly higher than those found in their counterpart CA and HA groups ($p < 0.001$). In addition, unique bacterial species were found in each racial/ethnic group. Several bacterial species were detected in 5 or more samples of each racial/ethnic group. One bacterium, Pedobacter petrophilus, is particularly interesting, which is unique in the AA group and also in samples of the group with high level of P. gingivalis. These data provide evidence that race/ethnicity-associated oral microbiome variation may contribute to periodontal health disparities. Our findings underscore the need for comprehensive studies to identify differential core microbiota associated with race and ethnicity and their roles in initiation and development of periodontitis.

U54MD007586 from the National Institute on Minority Health and Health Disparities, USA; grant 2117282 from the National Science Foundation, USA; and grant R16GM149359 from National Institute of General Medical Sciences, USA.

ABSTRACTS

04.01.02 – Poster Session 1 · Chesapeake Suites (MR)

SUBSTANCE USE DISORDER HOSPITALIZATION PROFILES AND READMISSIONS: AN ANALYSIS FROM 2015 TO 2017 HAWAII INPATIENT DATA

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Introduction: Hawaii consistently ranks in the top 3 states for houselessness rates, linked to socioeconomic inequities like substance use disorder (SUD). SUD increases risks of various pathologies. Despite political and communal efforts, there's a lack of epidemiologic data. This study aims to provide and compare SUD trends across demographics to assess social efforts against houselessness.

Methods: Patients admitted to major Hawaii hospitals from 2015–2017 for SUD were analyzed. Data included age, race, gender, BMI, hospital location, insurance, housing status, and readmission. Statistical tests (Pearson's Chi-squared, Kruskal-Wallis, Fisher's Exact) were used for analysis. Odds ratios assessed readmission rates across demographics and clinical characteristics.

Results: From 2015–2017, 25,478 cases were recorded. Highest SUD readmission rates were in Native American (35%), African American (28%), Caucasian (28%), and Hawaiian (26%) populations. Japanese, Chinese, and other Asians had lower BMIs (24-25) than Native Hawaiians and Pacific Islanders (26–33). African Americans, Filipinos, Japanese, and Chinese had fewer female admissions (29-34%) than Caucasians (38%) and Native Hawaiians (46%). Hawaiians had the lowest rates of private insurance (<22%). African Americans were most commonly houseless (20%), followed by Native Americans (15%), Caucasians (12%), and Hispanics (12%).

Discussion: Underserved demographics, like Hawaiians, African Americans, Hispanics, and Native Americans, experience SUD and co-morbidities at higher rates. Asian demographics typically fare better socioeconomically, contributing to this complex issue. Future research should explore trends in SUD across demographics to assess social improvements in Hawaii.

2U54MD007601-36 and U54GM138062

04.01.03 – Poster Session 2 · Chesapeake Suites (MR)

POOR SLEEP QUALITY IS ASSOCIATED WITH ATTENUATED CORTISOL AWAKENING RESPONSES AND HIGH DEPRESSION LEVELS IN PREGNANT WOMEN

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PURPOSE: Identifying pregnant women at heightened risk for adverse perinatal outcomes, particularly depression, remains challenging with current risk factors. This study tested the hypothesis that poor sleep quality dysregulates the cortisol stress (coping) response and predisposes women to depression.

METHODS: We studied 18 healthy pregnant women (aged 18–40, BMI 18.5–40) at gestation weeks (GW) 12-14 and 24-26, alongside 28 non-pregnant controls. Sleep quality and quantity were evaluated using the Pittsburgh Sleep Quality Index and continuous 7-day actigraph monitoring. In addition, participants were given kits designed for home use to collect saliva samples for cortisol quantification at specified times (i.e., 0, 30, 45, and 60 minutes) after waking up from bedtime sleep. Depression levels were measured with the Center for Epidemiological Studies Depression Revised questionnaire.

RESULTS: Pregnant women exhibited higher rates of poor sleep quality (GW 12-14: 71%, GW 24-26: 67%) than non-pregnant controls (29%). Actual sleep hours did not significantly differ (pregnant: GW 12-14: 5.9 ± 1.1 hours, GW 24-26: 6.2 ± 1.3 hours; non-pregnant: 6.2 ± 1.3 hours), but pregnant women experienced significantly more wake after sleep onset, indicating fragmented sleep ($F(2,50)=3.53$, $p=0.037$, ANOVA). Cortisol awakening response (CAR) was attenuated with deteriorating sleep quality in both groups ($F(2, 50)=3.76$, $p=0.03$, ANOVA). Poor CAR was associated with higher depression levels in both pregnant and non-pregnant women ($F(2, 50)=8.37$, $p=0.0007$, ANOVA).

CONCLUSION: The findings support the notion that poor sleep quality and fragmentation diminish the stress response, potentially predisposing women to depression. These results underscore the importance of considering sleep parameters in identifying pregnant women at risk for mental health issues, providing valuable insights for developing targeted interventions to improve both sleep and mental well-being during pregnancy.

NIH grant U54 MD007586

04.01.04 – Poster Session 1 · Chesapeake Suites (MR)

PHARMACOGENOMIC PROFILES OF PATIENTS WITH SICKLE CELL DISEASE

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PURPOSE Opioids are the primary treatment modality for managing pain during a sickle cell crisis. Implementing pharmacogenomics may facilitate enhanced medication adherence due to increased tolerance to these therapies. The objective of the study was to detect the frequencies of polymorphisms occurring in the cytochrome P450 (CYP) 2D6, catechol-O-methyl transferase (COMT) and the mu-opioid receptor 1 (OPRM1) genes.

METHODS This prospective cohort study was conducted in 2023 and included sickle cell patients who were at least 18 years old. The genes of focus were CYP2D6, OPRM1, and enzyme COMT. The primary outcome was the frequency of gene-drug polymorphisms. Descriptive statistics were conducted to characterize the patient's baseline and clinical characteristics. The statistics were conducted to obtain mean (SD) for continuous variables and proportions for categorical variables.

RESULTS There were 50 participants in the study, about (56%) were female, and the mean age was 46 + 13.21. All participants self-identified as Black or African American, and the majority (74%) had public insurance. Nine participants (18%) were homozygous (A/A) for COMT, 17 participants (34%) were heterozygous (A/G), and 24 participants (48%) had normal COMT function (G/G). There were 47 participants (94%) with normal OPRM1 function (A/A) and three participants (6%) had altered OPRM1 function (A/G). Twenty-six (52%), 20 (40%) and four (8%) patients were extensive metabolizers, intermediate metabolizers, and ultrarapid metabolizers of CYP2D6, respectively.

CONCLUSION Pain management is a priority when it comes to treating patients with SCD. Detection of polymorphisms in CYP2D6, COMT, and OPRM1 can help improve the landscape of pharmacogenomic testing in sickle cell patients by providing real-world data from ethnically-diverse populations to enhance existing testing algorithms.

This project was supported in part by the National Institutes of Health (NIH) Research Centers in Minority Institutions (RCMI) IDC grant under the award number GRT010000D

04.01.05 – Poster Session 2 · Chesapeake Suites (MR) 🏆

THE ROLE OF ANNEXIN A6 IN THE INVASIVENESS OF BASAL-LIKE TNBC PROGRESSION

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PURPOSE: Triple-negative breast cancer (TNBC) is characterized by aggressive tumor growth, resistance to treatment, higher likelihood of relapse, and overall worse prognosis when compared to other breast cancer subtypes. The TNBC tumor microenvironment is not only molecularly heterogeneous, but also contains varying numbers of rapidly growing basal-like (BSL) and invasive mesenchymal-like (MSL) stromal and TNBC cells. Annexin A6 (AnxA6) is a multifunctional calcium (Ca2+)-dependent scaffolding protein that is highly expressed in MSL TNBC cells but expressed at low levels in BSL TNBC, and is implicated in cell proliferation, motility, and drug resistance. It is currently unclear how altered AnxA6 levels influence the invasiveness of MSL and BSL TNBC cells. We hypothesize that altered expression of AnxA6 differentially contributes to the invasiveness and drug resistance of BSL and MSL TNBC phenotypes. METHODS: Short hairpin RNAs were used to downregulate ANXA6 in model MSL (BT-549) cells and BSL (MDA-468) TNBC cell lines. The invasive fractions of these cell lines with or without AnxA6 downregulation were isolated from parental control and AnxA6 downregulated cells by sequential invasion assays in Boyden chambers. The parental and their respective invasive fractions were then assessed for markers of invasiveness and drug sensitivity. RESULTS: Invasive fractions of the MSL BT-549 cells expressed higher levels of VIM and Ki-67 in an AnxA6-dependent manner. The invasive fractions of the BSL MDA-468 cells also AnxA6-dependently expressed decreasing levels of E-Cadherin and increasing levels of EpCAM compared to their parental controls. Interestingly, the invasive fractions from both MSL and BSL TNBC cells were less migratory but were more resistant to chemotherapy agents than their respective parental controls, and that AnxA6 downregulation sensitized the invasive fractions to chemotherapy. CONCLUSION: Our data suggest that altered ANXA6 expression is associated with differential sensitivity to chemotherapy and proliferation of MSL versus TNBC cells.

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04.01.06 – Poster Session 1 · Chesapeake Suites (MR)

CHANGES IN IN VESICULAR ACETYLCHOLINE TRANSPORTER EXPRESSION ALTER ACETYLCHOLINE HOMEOSTASIS IN THE CENTRAL NERVOUS SYSTEM

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Acetylcholine neurotransmission is necessary for the regulation of essential life functions such as locomotion and cognition. As a result, increases or decreases in neuronal cholinergic signaling lead to an impairment in learning and memory, and normal locomotive functions. Although much about how acetylcholine is regulated is known, the mechanism through which changes in cholinergic signaling effects changes in ACh-linked behavior is not fully understood.. The vesicular acetylcholine transporter (VAChT) mediates the packaging and transport of acetylcholine (ACh) for exocytotic release. However, the manner through which this process occurs and is regulated is not fully understood. Here we use both an overexpression of VAChT (using a construct that we have reported on previously) and mutants in Vacht that cause varying decreases in the gene's expression, as tool to increase or decrease (respectively) the amount of ACh released into the synaptic cleft. And we are measuring the effect of that altered state on synaptic activity using a biochemical approach. We have optimized an assay that allows us to reliably measure cholinergic pathway components ACh and choline from as little as ten Drosophila heads. Using this assay, we report the surprising data that while VAChT overexpression does not increase total head ACh levels, there is an increase in choline levels, suggesting that there are homeostatic consequences for changes in VAChT expression. We also present preliminary findings from similar experiments with Vacht mutants that have reduced transporter expression. Importantly, we reports the effects of increase or decreases in Vacht expression of the distribution of VAChT to synaptic vesicles relative to other subcellular compartments using super resolution microscopy. Taken together, these data provide important insight into the consequences that follow a disruption in VAChT expression and advance our understanding of how the vesicular acetylcholine transporter mediate the exocytotic release of ACh in Drosophila.

ABSTRACTS

04.01.08 – Poster Session 2 · Chesapeake Suites (MR)

EARLY MARKERS IN ASSESSING THE RISK OF ALZHEIMER'S DISEASE

TK SUR; T Mondal; Z Noreen; J Johnson; CA Loffredo; B Korba; ST Cotin; G Nunlee-Bland; S Sarkar; S Ghosh*
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PURPOSE: Early diagnosis of Alzheimer's disease (AD) is challenging since it can only be detected in advanced stages that require complex and invasive investigations. Recent advancements in targeted gene expression profiles from a blood sample can identify potential biomarkers for AD. Our previous study observed key genes and pathways that were associated with AD in the Pakistani population (PAK) with diabetes. In the present study, we compare those results with those of African Americans (AA) from the Washington DC, USA and the PAK population, who have diabetes, with the aim of exploring the possibilities of developing gene-based biomarkers.

METHODS: The AD gene panel (96 transcripts, Applied Biosystem, our genes of interest) was validated among PAK and AA participants compared to healthy people (control) (n=12 in each group) by using TaqMan Low-Density Arrays coupled with IPA analysis to identify the pathways and was used for analysis with our studied populations (PAK and AA Diabetic) for the commonality with the AD disease process and the pathways.

RESULTS: The top Canonical Pathways (CP) that includes Amyloid Processing, Neuroinflammation Signaling, eNOS Signaling in Neurons, and Mitochondrial Dysfunction, which were common in both populations, among which APP. IL18, PSENEN, and MAPK are the signature genes in APP pathways, in particular with PHLPP2, IL33, APP, CRP, and TAC1 as common upstream regulators. The top common disease and biofunctions included Metabolic Disease, Neurological disease, Organismal Injury and Abnormalities, Psychological Disorders, & Cardiovascular Disease in both the groups.

DISCUSSION: The specific genes and pathways that were common to both diseases may suggest common underlying processes and causes in both the population. This pilot study resulted in the development of potential molecular classifiers from the transcriptome for the early detection of AD. Future large-scale population validation is needed to establish a reliable non-invasive liquid biomarker applicable to AD diagnostics.

U54 (MD007597-31-5959) from NIMHD, USA

04.01.09 – Poster Session 1 · Chesapeake Suites (MR)

TRANSCRIPTOMES OF PAKISTANI CHILDREN WITH DYSLEXIA AND ADHD

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PURPOSE: Developmental Dyslexia (DD) and Attention-Deficit/Hyperactivity Disorder (ADHD) are complex neurodevelopmental disorders affecting learning abilities in children worldwide. In Pakistan, the prevalence of these learning disabilities among school-age children ranges from 6-10%. Our pilot study aims to assess differential gene expression to identify the altered genetic signature of DD comorbid ADHD and their pathways for the first time among children of Pakistan.

METHODS: Participants were recruited from different cities of Pakistan, who have DD comorbid ADHD (control, n=3 and DD comorbid ADHD, n=3). Background information was obtained from parents (through a questionnaire) and child psychiatrists. Clinical evaluation included the Slosson Intelligence Test, Woodcock-Johnson IV test, The Conners Comprehensive Behavior Rating Scale, and the Bangor Dyslexia test assessment. A complete blood panel was completed for each participant, and total RNAseq analyses coupled with Ingenuity Pathway Analysis were performed, comparing cases and controls

RESULTS: The mean age was 10.0(±3.0) years. The demographic factors i.e., age, gender, literacy, and residence area, including biological conditions were non-significant in cases compared to control group. The transcriptome analysis of differentially expressed genes (n=35,324) revealed that 78 and 189 were significantly (p-value <0.05 at 2-fold change) up- and downregulated, respectively. Top upregulated genes were SOAT2, IFI27, IGFBP2, and SNX7. Top downregulated genes were SFR1P1, PCDHB15, CPLX2, and FAM238B. Top upstream regulators were GATA4, LMNA, TBX5, HAND2, and MYOCD with Neurological Disease, Cancer, and Organismal Injury and Abnormalities as top diseases and disorders.

DISCUSSION: This pilot study opens up an opportunity to gain insights into molecular correlates of DD comorbid ADHD in Pakistani school-age children. The study may help identify a group of altered gene expressions and pathways, which may contribute to a better understanding of the genetic mechanism of the disease. However, further validation using a large sample size is necessary to strengthen our findings.

5G12MD007597-25 (NIMHD, USA), 1-8/HEC/HRD/2022/12637 (HEC, PAK)

04.01.10 – Poster Session 2 · Chesapeake Suites (MR)

SIGNALING PATHWAY DIFFERENCES IN MASLD AFRICAN AMERICANS

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PURPOSE: Metabolic Dysfunction-Associated Steatotic Liver Disease (MASLD, formerly termed Non-alcoholic Fatty Liver Disease (NAFLD)) is becoming the predominant chronic liver disease worldwide. The prevalence of MASLD has increased from ~20% in 2009 to 25–30% in 2023 in the US population. The incidence of MASLD among African Americans (AAs) is lower than for other groups, but AAs are understudied overall in such. Our previous molecular transcriptomic study identified a significant TGFB1 and E2F1 upregulated and downregulated respectively as one of the key genes in MASLD patients. In this pilot study, we aimed to characterize associated altered signaling pathways in AA with MASLD and compare them with other ethnic population data sets.

METHODS: A total of 47 AA individuals (NAFLD=23, healthy control=24) were recruited from the Georgetown University Liver Transplantation Unit, Washington DC. Their sociodemographic and lifestyle exposures and medical background information were documented. Global gene expression array data (MASLD=4 and control=4) and TaqMan qRT-PCR data (NAFLD=19, healthy control=12) were used for pathway analysis with the help of Ingenuity Pathway Analysis (IPA®). Comparison analysis was performed using GEO data set curated from different ethnic groups.

RESULTS: IPA-based analysis of cellular processes and pathways revealed that Hepatic Fibrosis Signaling Pathway, Hepatic Fibrosis, and Hepatic Cholestasis were the top canonical pathways (p-value <0.0001), that correspond to top bio-functions, viz., Proliferation of hepatic satellite cells, Progressive hepatic fibrosis, and Acute-Chronic Liver failure. We observed that TGFB1 (upregulated) and E2F1 (downregulation) were the central molecules of the top gene network. Ethnicity-based comparison analysis yielded three major pathways (molecular mechanisms of cancer, hepatic fibrosis signaling, and estrogen receptor signaling), similar to our expression results.

CONCLUSION: This pilot study opens an opportunity to understand the molecular correlates of MASLD in an AA population, potentially paving the way to develop molecular classifiers to identify future disease risks and progression.

This study was supported by a P20 grant (CA262617-01) (PI: Ghosh) from the NCI of Health (NIH), and by U54 (MD007597-31-5959; PI/PD: Southerland, Lead PI: Ghosh) from the National Institutes of Health (NIH). During this period, this project has been supported in part with Federal funds (Grant # UL1TR000101 previously UL1RR031975) from the National Center for Advancing Translational Sciences (NCATS), National Institutes of Health (NIH), through the Clinical and Translational Science Awards Program (CTSA), a trademark of DHHS, part of the Roadmap Initiative, “Re-Engineering the Clinical Research Enterprise”, towards receiving the GHUCCTS-CRU support.

04.01.11 – Poster Session 1 · Chesapeake Suites (MR)

FEARFUL-BONDS IN PARENTING: IMPACT OF ADVERSE EXPOSURES

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PURPOSE: Exposure to maternal and child adversity (environmental/emotional) may affect developmental processes within the dyad (mother and child). These experiences may increase stress, anxiety, and fear within the dyad. We hypothesize that mothers with history of adversity, who have been repeatedly exposed to environmental stressors perinatally (stressed during pregnancy/postpartum), will demonstrate higher levels of stress, fear, and atypical bonding patterns that affect child neurodevelopment.

METHODS: This cross-sectional study aims to develop a translational model of repetitive adversity on bonding and offspring development in a pilot sample of rodent mother-pup models and human mother-child dyads. Specific Aim 1: Test an animal-model of early-adversity and inhibitory avoidance (maternal fear that leads to offspring behavioral inhibition). Specific Aim 2: In a sample of 30 dyads characterized for adversity (early life and perinatal), assess if maternal fear responses relate to atypical maternal attachment and bonding, affecting child neurodevelopment. Specific Aim 3: Assess if behavioral assessments, in animal and human model, correlate with biomarkers of stress and inflammation. Statistical analysis will be performed for individual aims and a general interaction model to combine data from different aims using STATA or R- software.

RESULTS: It is expected that the animal models will provide a foundation of areas that need to be furthered studied in dyads at risk of psychopathology. The assessment of fear, stress and neurodevelopment will provide preliminary data on the impact of repeated adversity on atypical mother-child bonding. Biomarkers of stress and inflammation will evidence the presence of altered physiological patterns when exposed to repeated adversity. CONCLUSIONS: Our findings aim to generate behavioral assessment paradigms to study long-term attachment security amid adversity and its impact on child neurodevelopment. This study will open doors for pinpointing causal relationships to identify risk factors for future psychopathologies and transference mechanisms (behavioral and physiological) in mother-child dyads.

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ABSTRACTS

04.01.12 – Poster Session 2 · Chesapeake Suites (MR)

ADVANCING HPS-1 TRANSLATIONAL RESEARCH IN PUERTO RICO

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PURPOSE: In Hermansky-Pudlak Syndrome type 1 (HPS-1), pulmonary fibrosis (PF) develops in 100% of patients, eventually necessitating lung transplantation. While recent evidence indicates that Neutrophil Extracellular Traps (NETs) may advance PF progression, their specific role in HPS-1-related PF remains unexplored. This study aims to investigate the involvement of NETs in PF progression among HPS-1 patients to uncover new therapeutic approaches to delay PF advancement.

METHODS: HPS-1 is globally rare, with a prevalence of approximately 1 in 1,000,000 individuals. However, in Puerto Rico, the prevalence is estimated at 1 in 1,800 people. To ensure specialized care for patients, the HPS Network established quarterly community clinics. We initiated a collaboration with the HPS Network to integrate research into these clinics. Patients participated voluntarily, providing blood samples and undergoing spirometry. To date, we have evaluated levels of NETs and interleukin-8 (IL-8), comparing HPS-1 patients to healthy individuals. Additionally, we investigated the relationship between these biomarkers and pulmonary function to assess their potential association with pulmonary health in HPS-1.

RESULTS: Preliminary findings demonstrated a significant increase in circulating NETs levels among HPS-1 patients compared to healthy controls (P= 0.0018). Moreover, a subgroup of these patients had detectable levels of IL-8, a crucial factor in recruiting and activating neutrophils, displaying a tendency to be inversely correlated with pulmonary function.

DISCUSSION/CONCLUSION: These findings support the hypothesis that NETs and associated inflammatory pathways may contribute to PF development in individuals with HPS-1. The identified correlation between IL-8 and declining pulmonary function has been observed in other types of PF, indicating the importance of further investigation into its role as an indicator of severity or a target for therapeutic intervention. This research represents progress in our understanding of PF in HPS-1. Additionally, it highlights the significance of community clinics in driving HPS-1 translational research in Puerto Rico.

Research Centers in Minority Institutions (RCMI) Program #U54MD007579, Hispanic Clinical and Translational Research Education and Career Development (HCTRECD) program #5R25MD007607-22 and The Hispanic Alliance for Clinical and Translational Research - Mentor Mentee Program #5U54GM133807-03

04.01.13 – Poster Session 1 · Chesapeake Suites (MR)

AFRICAN AMERICAN COLORECTAL CANCER SCREENING STUDY

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PURPOSE: African Americans in the US South experience colorectal cancer (CRC) health disparities in screening, incidence, and mortality. Test Up Now Education Program (TUNE-UP) is a pragmatic behavioral clinical trial in partnership with two community health centers (CHC). The study is focused on increasing stool-based testing and adherence to annual screening among low-income African American patients.

METHODS: The TUNE-UP study baseline survey includes demographic characteristics, communication with health professionals, and CRC-related questions using validated measures. A 3-month and 9-month follow-up survey collect CRC screening outcome data for study participants. Intervention participants received a Community Health Advisor educational intervention. Bivariate and multivariate analyses were used to compare intervention outcomes at follow-up.

RESULTS: From April 2021 to March 2023, 115 participants were recruited using CHC messaging, and 95 participants completed the 3-month follow-up survey. For the 3-month follow-up survey results, 41 participants out of 95 (43%) completed their stool tests following being enrolled in the study according to self-report. In the intervention group, 26 out of 47 (55%) had completed the stool test compared to 15 out of 48 (31%) in the control group. The 3-month outcome favored the intervention group according to the result of the chi-square test ($p<0.05$). For preliminary 9-month findings, significant differences by study arm were not observed, with 29 out of 41 (71%) participants in the intervention group compared to 31 out of 42 (74%) participants in the control group completing stool tests. Additional participants are still completing their exit surveys and clinical outcome data from the CHCs is in progress.

CONCLUSION: This behavioral clinical trial aims to improve accessible stool-based screening in this CHC patient population. In partnership with the CHCs, the study team has observed system improvements in both CHCs to track their patients and notify them when they are due for annual screening.

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04.01.14 – Poster Session 2 · Chesapeake Suites (MR)

DYSREGULATION OF NEUTROPHIL PHENOTYPES IN INDIVIDUALS WITH PULMONARY POST-ACUTE SEQUELAE OF SARS-COV-2

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PURPOSE: Coronavirus disease 2019 (COVID-19) is a major health concern with nearly one-third of patients showing long-term Post-Acute Sequelae of SARS-CoV-2 infection (PASC). While studies have shown that neutrophil dysregulation plays a role in the immunopathology and severity of COVID-19 disease, little is known about the involvement of neutrophils in PASC. Neutrophils are known to produce neutrophil extracellular traps (NETs), which may play a role in the development and persistence of pulmonary symptoms. However, understanding neutrophil dysregulation beyond the acute phase of infection and its involvement in pulmonary PASC (PPASC) is less well understood. Here, we demonstrate long-term neutrophil alterations in PPASC individuals.

METHODS: Neutrophil phenotypes and plasma levels of NET markers were assessed in blood samples (Control [n=12], Recovered [n=10], PPASC [n=35]) collected from the entry time point of the factors responsible for the development of pulmonary PASC in Hawaii longitudinal study.

RESULTS: Within the PPASC group, all participants (n=35) had additional PASC symptoms. Leukocyte and neutrophil counts were comparable between the three groups, but platelet counts tended to be lower in PPASC. Neutrophils from PPASC individuals exhibited increased MPO levels and granularity (p=0.001,0.002) compared to controls. Neutrophils from PPASC had a significantly higher percentage of PD-L1+ cells compared to Recovered (p=0.008), and PD-L1 expression on neutrophils was higher in PPASC than in Recovered and Control groups (p=0.008, 0.014). In PPASC samples, there was an increasing trend in NET forming cells and CitH3 levels compared to the Recovered and Control groups, although there were no statistically significant differences.

DISCUSSION: Neutrophils from PPASC individuals display an activated phenotype but a less profound effect of NET formation. Our study indicates that neutrophil dysregulation may play pathogenic roles in PPASC. Further research is needed to determine if altered neutrophil phenotypes are associated with prolonged pulmonary dysfunction among PPASC individuals.

This work was supported by the NIH/NIMHD (U54MD007601) and the NIH/NIMHD Minority Health Research Training (MHRT) program (T37MD008636).

04.01.16 – Poster Session 1 · Chesapeake Suites (MR)

INNER-CITY OBESITY GROUP VISITS IMPROVED HEALTH MARKERS

MAGDA SHAHEEN; Ramirez FE; Duran P; Nemeth M, Morales K, Friedman TC
Charles R Drew University

PURPOSE: Obesity is highly prevalent in U.S., particularly among minority groups. Medical group visits have been used to treat chronic diseases, but their efficacy in obesity have not been well studied, especially compared to individualized dietitian-led visits (standard of care) in safety-net settings. The purpose of this study is to compare the two approaches in a randomized trial of 12-months duration to evaluate if weight will decline more and diet quality will improve in the medical group arm compared to the dietitian-led arm.

METHODS: Adult patients were recruited from LAC-DHS and randomized to medical group (n=333) and dietitian-led visits (n=112). Obesity was assessed using change of weight (lb) after 12 months compared to baseline. Diet quality was assessed using DHQ instrument as difference at 12 months relative to baseline. We analyzed data using Mann Whitney test and p-value of <0.05 was statistically significant.

RESULTS: There was no significant difference between the groups in the demographic characteristics. The dietitian group had higher number of visits compared to the medical group (mean=14.6 ± 9.0 versus 10.5 ± 6.9 visits respectively) (p=0.001). There was no significant difference between the median change in weight in the medical group and the dietitian group, however, the weight change per visit was higher in the medical group compared to the dietitian group (p=0.02). Significant improvement was found for hemoglobin A1c (HbA1c), cholesterol, LDL, non-HDL, and triglyceride in the medical group (p<0.05) both compared to baseline and compared to the dietitian group. Diet quality improved in both groups with no differences between the groups.

CONCLUSIONS: In summary, the improvement in weight and health makers and the fact that more weight loss per visit occurred in the medical group suggest that group visits may be an effective and cost-efficient way of improving overall health in a cost-restrained system.

NIH Accelerating Excellence in Translational Science (AXIS) Award # U54MD007598

ABSTRACTS

04.01.17 – Poster Session 2 · Chesapeake Suites (MR)

RACIAL/ETHNIC TRENDS IN MASLD: DATA FROM NHANES 1988 TO 2018

MAGDA SHAHEEN; K Schrode; D Pan; S Najjar; TC. Friedman
Charles R Drew University, Los Angeles, CA; Ohio University-Heritage College of Medicine, Athens, OH

PURPOSE: In 2023, multiple liver societies recommended replacing the term non-alcoholic fatty liver disease (NAFLD) with metabolic dysfunction-associated steatotic liver disease (MASLD). The purpose of this study was to examine the trends in the racial/ethnic disparity of MASLD prevalence among the U.S. adult population overtime.

METHODS: Data from 32,726 adults from the National Health and Nutrition Examination Survey (NHANES) 1988-2018 were analyzed. Hepatic steatosis (HS) was diagnosed using the U.S. Fatty Liver Index (US-FLI). MASLD was diagnosed among those with both HS and at least one of the following: overweight/obesity, diabetes mellitus, hypertension, high triglyceride or HDL-Cholesterol or in treatment. Data were analyzed using logistic regression to test for trends over time for the overall sample and for each racial/ethnic group considering the design and sample weights. Prevalence was age-adjusted using the direct method and the census data. We also estimated the percent change in the adjusted prevalence.

RESULTS: Overall, the age-adjusted prevalence of MASLD increased significantly over time from 16% in 1988 to 38% in 2018 for 138% percent increase, while the age-adjusted prevalence of obesity increased from 23% in 1988 to 40% in 2018 for a 74% increase ($p<0.05$). Among Mexican Americans, the age-adjusted prevalence of MASLD was higher than the overall population and other racial/ethnic groups across time.

There was a significant increase in the percent change of the age-adjusted prevalence of MASLD in all racial/ethnic groups (Mexican Americans=69%; Blacks=117%; Whites=140%) except Other Hispanics (no change). The age adjusted prevalence of obesity also increased significantly in all racial/ethnic groups (% change: Mexican Americans=58%; Other Hispanics=18%; Blacks=59%; Whites=77%) ($p<0.05$).

CONCLUSIONS: Our study showed an increase in the age-adjusted prevalence of MASLD over time that was greater than the increase in obesity. The racial/ethnic disparity in MASLD persisted over time with Mexican Americans consistently having the highest prevalence.

R01MD012579, R24DA017298, U54MD007598, S21MD000103, UL1TR001881

04.01.18 – Poster Session 1 · Chesapeake Suites (MR)

STIGMA, EMOTION, STRESS, AND COGNITIVE PERFORMANCE IN PWH

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NeuroHIV Program, University of Puerto Rico Medical Sciences Campus (VW, LJRR, DT, YCR, MM, ER), University of Puerto Rico Rio Piedras Campus (BD, NG)

PURPOSE: HIV-associated cognitive impairment (HIV-CI) prevails in 20-50% of people living with HIV (PWH). Chronic brain inflammation has been implicated as a possible mechanism to explain why HIV-CI prevails in PWH treated with antiretrovirals (ART). Stress may also contribute to the development of chronic inflammation. Perceived stigma has a high prevalence in PWH and may contribute to the persistence of chronic inflammation and brain injury. The study's goal is to determine the associations between perceived stigma, emotional dysfunction, stress, and cognitive impairment in a Hispanic cohort of PWH. METHODS: Hispanic cohort was recruited in Puerto Rico. A total of 46 participants (59% men) were evaluated with physical exam, questionnaires for perceived stigma, emotional dysfunction, and depression symptoms. Laboratories included viral immune profile, toxicology, and cortisol levels. Neuropsychological (NP) tests were administered to determine HIV-CI (n=25). Correlations and nonparametric associations were performed using SPSS (v. 23). RESULTS: Median age was 55 years old, mostly men (59%) and had 14 years of education. There were no sex differences between the viral immune profile, depression symptoms, co-infections, toxicology, or HIV-CI stages. Women presented with significant higher BMI and lower cortisol levels while men presented significant higher perceived stigma scores ($p<.05$). A positive correlation was observed between stigma and emotional dysfunction, and cortisol levels. Women showed a positive correlation between stigma and higher stages of HIV-CI. CONCLUSIONS: PWH continue to present with HIV-CI even when using ART. Perceived stigma and emotional dysfunction may contribute to the presence and severity of HIV-CI by increasing stress and promoting chronic inflammation. Identifying and addressing biological sex differences of stress factors such as perceived stigma and emotional dysfunction may aid in the prevention of HIV-CI.

UPR-MSC RCMI TPC U54MD007600, NINDS R01NS099036, NIMH R21MH095524, The Alliance U54GM133807

Community-Based Participatory Research Addressing Minority Health and Health Disparities

04.02.02 – Poster Session 2 · Chesapeake Suites (MR)

THE IMPACT OF BREASTFEEDING PATTERNS ON PHYSICAL GROWTH OF AFRICAN AMERICAN INFANTS

Michelle Kaimenyi, M.H.S., Flora AM Ukoli, M.D., MPH.
Meharry Medical College

Background: The American Academy of Pediatrics and World Health Organization established standardized guidelines for infant physical growth. Breastfeeding influences infant physical growth, and breastfeeding rates have declined worldwide. This study aims to compare infant physical growth across breastfeeding practices.

Methods: An education intervention conducted in Nashville, Tennessee involved 254 pregnant African American women. Participants were recruited from prenatal clinics and health fairs by flyers. After signing informed consent, participants completed a 5-page pre-intervention survey providing demographics, and breastfeeding knowledge, attitude and practice. They attended four 30-minute education sessions monthly. A 4-page survey was completed 1 month postpartum, and 2-page surveys at 3- and 6-months postpartum. Infant weight and length were obtained from well-baby clinic measurements. Breastfeeding was self-reported as EBF (exclusive breastfeeding), BF (breastmilk and formula) or NBF (formula only). Infant BMI was computed using an online Baby BMI calculator. T-tests were performed to compare infant weight across infant feeding patterns for each gender. Obesity status was compared across demographic and breastfeeding pattern subgroups by Chi-Square tests.

Results: Mothers were more likely to BF at 3 months and NBF at 6 months. Infant BMI was statistically associated with breastfeeding pattern at 3 months ($p<0.01$) and 6 months ($p<0.05$). EBF or BF infants maintained normal BMI (5th-85th percentile). Male infants of single mothers were more overweight by 3 months compared to infants of married mothers. Female infants maintained normal BMI status at 3- and 6-months regardless of marital status.

Conclusion: Mothers were unlikely to continue EBF up to 3 months. High rate of infant overweight by 3 months might therefore be a consequence of a greater proportion of formula fed infants. Increasing breastfeeding education and providing substantial breastfeeding support initiatives can contribute to maintaining EBF up top 6 months, thus subsequently decreasing the prevalence of infant overweight among Africa American infants.

04.02.03 – Poster Session 1 · Chesapeake Suites (MR)

COMMUNITY ENGAGEMENT STUDIOS: A TOOL TO PROMOTE ACADEMIC-COMMUNITY INTERACTIONS

AC GUZZI VASQUES ; CM Vélez Vega ; I Lafarga Previdi; E Fernández Repollet
Center for Collaborative Research in Health Disparities, UPR-Medical Sciences Campus (AGV, CMVV, ILP, EFR)

PURPOSE: The Community Engagement Studio (CE Studio) is a model developed by Meharry-Vanderbilt Community Engaged Research Core that provides a way for investigators to get community perspectives on the development, implementation, or dissemination of research projects. This is a simple and effective strategy for researchers to participate in community engagement efforts and provides a bi-directional approach to foster collaborative relationships. METHODS: For the coordination of CE Studios for three research projects, we: 1) Organized meetings with the researchers to assess the objective of each Studio, 2) Prepared questions to facilitate discussion, 3) Made a list of community experts related to each research topic, 4) Implemented a survey instrument to evaluate each activity. RESULTS: The CE Studio #1 focused on dissemination efforts related to vaginal microbiome and reproductive health. The participants (n=6) indicated that the digital app was an innovative idea for dissemination. The CE Studio #2 focused on finding new collaborations among PreP providers. Several participants (n=5) have been recruited for qualitative interviews. The CE Studio #3 focused on recruitment and retention efforts related to a project about HIV and structural racism. Participants (n=7) gave advice on how to contact and engage potential participants and indicated that they wanted updates from the study. All CE Studio participants expressed that they totally agreed that their input would improve the project. Follow-up meetings with researchers were coordinated to present CE Studio notes and prepare individualized plans to ensure the incorporation of community feedback. DISCUSSION: The recommendations investigators received from community partners were invaluable and could have saved them a lot of time and effort in planning their research, building community partnerships, and recruiting participants for their study. CE can increase the quality and relevance of research while enhancing public participation in clinical research activities and developing community experts for future research initiatives.

This project is supported by the Center for Collaborative Research in Health Disparities (CCRHD), which is funded by an RCMI-Grant from the National Institute on Minority Health and Health Disparities (U54 MD007600) at the University of Puerto Rico, Medical Sciences Campus.

04.02.04 – Poster Session 2 · Chesapeake Suites (MR)

ETHNIC DISPARITIES IN OPIOID USE FOR JOINT PAIN MANAGEMENT

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Howard University College of Pharmacy (BKS, SBW, LTW)

PURPOSE: Prescribed opioids have been used to treat both chronic and acute joint pain in the United States. However, there is a lack of consistency in prescribing opioids for joint pain treatment. Our objective is to determine if there are any disparities in prescribed opioids among adults of different ethnicities and age groups receiving pharmacotherapy for joint pain management.

METHODS: This cross-sectional study uses data from the Medical Expenditure Panel Survey (MEPS). MEPS is a set of large-scale surveys containing data on the cost/use of health care and health insurance coverage. The outcome is receipt of an opioid prescription. We carried out descriptive and logistic regressions analysis to ascertain predictors of prescribed opioids among adults with joint pain. All estimates were adjusted for the probability survey design using sampling weights, stratification, and clustering to provide nationally representative estimates.

RESULTS: The sample contained 9,797 respondents among which 4,193 had joint pain. The weighted sample corresponded to 142,534,387 people with joint pains that last 12 months. Of those, 54% were female, 53.5% were 50 years old or older, and 56.4% were White. The proportion of adults with joint pain who received at least one opioid prescription was 74.3%. For one year increase in age, the odds of receiving opioids significantly increased by a factor of 1.01(OR = 1.01, 95% CI: 1-1.02; P-value 0.048), after controlling for other covariates. Compared to Whites, Blacks (OR = 0.58, 95% CI: 0.35–0.95; P-value 0.034) had significantly lower odds of being prescribed opioids after accounting for other variables.

CONCLUSIONS: The results seem to indicate that disparities in prescribed opioids exist between age groups and race/ethnic.

ABSTRACTS

04.02.05 – Poster Session 1 · Chesapeake Suites (MR)

UNRAVELING THE COMPLEXITIES OF FOOD INACCESSIBILITY: AN IN-DEPTH ANALYSIS OF BALTIMORE'S PREDOMINANTLY BLACK NEIGHBORHOODS

M HAGAN; T Fungwe; GS Brown
Howard University (MH, TF, GSB)

PURPOSE After migrating to Baltimore, African Americans faced industrial job opportunities, often under substandard conditions compared to whites. Racial divisions led to isolated Black neighborhoods, restricting urban access. Discriminatory practices like redlining fueled social unrest, urban abandonment, and resource depletion. The lack of accessible grocery stores within a half-mile radius hindered fair and sustainable food systems. Motivated by the author's residency in this community, an investigation into factors contributing to food inaccessibility was initiated. The purpose of this study is to explore the challenges of food accessibility in Baltimore's predominantly Black neighborhoods.

METHODS This research employed critical textual analysis, historical investigation, and ethnographic approaches. A comprehensive examination of 126 Tweets spanning the years 2015 to 2021, encompassing retweets, language nuances, and overall tone, provided valuable insights into the sentiments of Black Baltimoreans regarding food accessibility. The ProQuest database facilitated an exploration of how African Americans leveraged media agency in 1950, involving the analysis of 53 editorials from The Afro News. Additionally, a 4-hour critical ethnographic study was conducted at Lexington Market to evaluate the availability and quality of produce.

RESULTS Within the market, observations revealed the presence of one fresh fruit and vegetable stand, six stands offering Asian-originated meals, eight fried food stands, and 29 empty stands, among others. The study brought to light three key issues prevalent in predominantly Black-dominated areas of Baltimore City: food inaccessibility, racial discrimination, and redlining, with Lexington Market serving as a tangible illustration of these challenges. Black individuals visiting the market, as representatives of the Black community, faced hurdles linked to limited availability and subpar quality of produce.

CONCLUSION Limited access to diverse, high-quality produce may affect the food choices and health outcomes of Black Baltimoreans. This study reveals the complex interplay of socioeconomic factors, systemic racism, and geographic location in food accessibility. Its findings play a vital role in shaping policies and community programs addressing the root causes of food inaccessibility. Emphasis is on developing tailored solutions for diverse communities, fostering equitable and sustainable food systems.

04.02.06 – Poster Session 2 · Chesapeake Suites (MR)

IMPLEMENTATION OF CLINICAL RESEARCH AND ENGAGEMENT CONFERENCE THROUGH NIH-FUNDED COMMUNITY ENGAGEMENT CORE OF CENTER FOR BIOMEDICAL AND MINORITY HEALTH RESEARCH AT TSU

VB Ajewole; IO Poon; VL Elkins
Texas Southern University

Abstract Background: While chronic disease rates are higher among ethnic minorities, representation of ethnic minorities in clinical trials remains low. The shared barriers to health research participation reported by ethnic minorities includes mistrust, lack of access to information, competing demands, stigma, health insurance status, and legal status in the U.S.

Objective: The objective of the Clinical Research and Engagement Conference is to educate and address barriers to ethnic minority participation in clinical research.

Methods: The Community Engagement Core (CEC) of the NIH-funded Center for Biomedical and Minority Health Research (CBMHR) at TSU implemented the 1st Annual Clinical Research and Engagement Conference in April 2021 and has held this conference annually successfully. Conference speaker sessions included "Should I Participate in Clinical Trials?"; "Ethics & Clinical Trials"; Clinical trial panel session included previous ethnic minority clinical research participants, clinical trial principal investigators, research coordinators, and clinical research support staff.

Results: Between 2021 and 2023, 505 individuals attended the Clinical Research and Engagement Conference both virtually and in person (2021: 97, 2022: 105, 2023: 303). Attendees consisted of diverse individuals from the greater Houston community. Between 2021 and 2023, 209 individuals completed the post-conference survey (2021: 45, 2022: 64, 2023: 100), among which 128 (61.2%) were African Americans. 175 (83.7%) of the attendees stated openness to participating or learning more about specific clinical trials and a very good understanding of clinical trial enrollment while 141 (67.5%) shared their contact information so they can be contacted for future clinical trials.

Conclusion: Our annual Clinical Research and Engagement Conference has been successful with feedback from attendees indicating a positive impact in addressing the gap in clinical trial participation among ethnic minority populations.

NIMHD U54 RCMI 2U54MD007605-27A1

04.02.07 – Poster Session 1 · Chesapeake Suites (MR)

TOOLS FOR THE "LONG GAME" – CULTIVATING COMMUNITIES IN THE RESEARCH PIPELINE BY INTENTIONAL DESIGN

MR Dela Cruz; K Corpuz; J Tsark; and K Braun
University of Hawai'i at Mānoa (MRDC, JT, KB); Hawai'i Public Health Institute (KC)

PURPOSE: The Ola HAWAII Community Engagement Core (CEC) aims to address the underrepresentation of minority communities in academic research. The leaders of the CEC program collectively bring seven decades of experience in community-based participatory research in Native Hawaiian, Pacific Islander (NHPI) and Filipino communities. The CEC members bring lived experience, academic expertise and represent the communities we serve. Our partnership recognizes the significance of the development, strengthening, and sustainability of a research pipeline for emerging leaders from NHPI and Filipino communities.

METHODS: CEC strategies include: (1) advising and mentoring individuals from Native Hawaiian, Pacific Islander, and Filipino communities to advance their academic and community research skills and credentials, (2) increasing diversity at the University of Hawai'i and leadership in community-based organizations, and (3) facilitating minority researchers' progression to leadership positions on research proposals focused on their communities.

RESULTS: This partnership strategically convenes a CEC Hui (Advisory Group) representative of minority communities in research, establishes a network for community members seeking academic credentials and supports research proposals that are culturally informed and respectful. Noteworthy policy changes include fostering bidirectional research engagement with communities through "report back" events, active involvement of CEC in research studios, CEC member participation in all pilot project reviews, and the establishment of a network of experts to engage and mentor new researchers (175 total).

DISCUSSION/CONCLUSION: Addressing the disparity–lack of community participation in the research enterprise–requires the active involvement of NHPI and Filipino communities. Experienced staff members bring established relationships and networks in the community and advocate alignment with the academic system, alongside policy changes to overcome systemic barriers such as input on grant reviews, and access community capacity building opportunities. RCMI-supported research has benefited greatly from the input, partnerships, and participation of people who were, are, aspire and deserve to be in this pipeline.

U54MD007601 NIMHD-NIH

04.02.09 – Poster Session 2 · Chesapeake Suites (MR)

COMMUNITY-BASED PROSTATE CANCER SCREENING FOR BLACK MEN

P COOPER; K Carter-Wicker; ER Stanley; IA Boyd; N Mavingire; S Young; B Rivers; KS Kimbro; RA Kittles; L Woods-Burnham
Morehouse School of Medicine (PC, KCW, ERS, IAB, NM, SY, BR, KSK, RAK, LWB)

PURPOSE: The 5-year relative survival rate for men with PCa is greater than 99% when diagnosed at an early stage. The prognosis is much worse for men diagnosed with advanced disease as there is no cure for metastatic PCa. With the establishment of prostate-specific antigen (PSA) blood testing as an effective tool for early screening for PCa, the prevention of morbidity and mortality from this disease proves possible. However, Black men are more likely to develop aggressive prostate cancer (PCa) and die, yet less likely to be screened despite population-specific guidelines recommending shared decision-making for high-risk groups to begin at age 40. For these reasons, increasing the rate and reach of PSA screening within the community is an innovative approach to raise awareness and reduce mortality from PCa for Black men. METHODS: Morehouse School of Medicine's (MSM) Prostate Cancer Precision Prevention Program (PCP3) leverages community partnerships to provide point-of-care PSA testing at no cost to Black men in the greater Atlanta area and rural Georgia. Community-based screening events were initiated in June 2023 and have been conducted in collaboration churches, municipalities, and non-profit organizations. Participants were recruited at these events and consented to provide one tube of blood drawn by MSM phlebotomists and registered nurses for quantification of PSA levels. Results were processed through Morehouse Healthcare and participants were contacted with individual results and provided with options for follow-up. RESULTS: To date, PCP3 has conducted more than two dozen community-based screening events. Nearly 1000 Black men have received PSA testing with variable results. CONCLUSION: PCP3 has provided awareness and PSA testing to nearly 1000 Black men in Atlanta and rural Georgia at higher risk for aggressive and lethal PCa. PCP3 aims to assess whether community-based screening reduces mortality from PCa for Black men in Georgia over the next few years.

Research reported in this poster is supported by the National Institutes of Health/National Institute on Minority Health and Health Disparities Research Centers in Minority Institutions (RCMI) (2U54MD007602) (PC, ERS, IAB, NM, KSK, LWB), the Prostate Cancer Foundation (20YOUN04) (LWB), and the Georgia Clinical Translational Science Alliance KL2 Scholars Program (KL2TR002381) (LWB).

ABSTRACTS

04.02.10 – Poster Session 1 · Chesapeake Suites (MR)

MALAMA AQUAPONICS STUDY: A QUALITATIVE ANALYSIS OF FAMILY INTERVIEWS

Ilima Ho-Lastimosa, Jena Funakoshi, Sai Kamakani Furukawa, Naomi Manuel, Jane Pascual, John Clark, Samantha Keaulana Scott, Kahau Vegas, LeShay Keliʻiholokai, Jane J. Chung-Do
Ke Kula Nui O Waimānalo (IHL, LK, JJCD) University of Hawaiʻi at Mānoa Office of Public Health Studies (NM, JF, SKF, JP, JCC, SKS, KV, JJCD) University of Hawaiʻi at Mānoa College of Tropical Agriculture and Human Resources (IHL)

PURPOSE Native Hawaiians face pervasive cardiovascular health disparities in their own ancestral land. In response, a culturally-grounded family-based intervention called MALAMA was developed, which consists of 9 hands-on workshops. These workshops focus on teaching families to build and use a backyard aquaponics system as a home food production method. The purpose of this study was to qualitatively analyze in-depth interviews conducted with MALAMA participants to understand changes in their health perceptions, attitudes, and behaviors.

METHODS In-depth interviews were completed with 24 participants from nine families who completed the MALAMA intervention in 2023. Interviews were conducted in-person, via Zoom, or by phone. Interviews lasted 30-60 minutes, were transcribed verbatim, and analyzed using inductive coding.

RESULTS Six themes were found: 1) Ma ka hana ka ʻike 2) Abundance 3) Lōkahi 4) Aloha 5) Mindfulness and Pride and 6) Ahupuaʻa. These themes centered on the importance of integrating hands-on learning and the cultural relevance of aquaponics technology, which mirrors the Native Hawaiian traditional food system These elements of MALAMA helped foster a sense of lōkahi (harmony and balance) and aloha (love, compassion, and care) where their aquaponics systems led to healthier eating habits and strengthened their connections to their family, community, and ʻāina (land). The integration of aquaponics into participants' lives brought a heightened sense of mindfulness in food waste and water usage as well as embracing the ideas of caretaking, protection, and a sense of responsibility. In addition, they appreciated the abundance of plants from their backyard aquaponics systems, which allowed them to feed their families and neighbors.

DISCUSSION/CONCLUSION Current research is underway to test MALAMA with 60 Native Hawaiian families on three Hawaiian islands. Findings will inform the implications of MALAMA as a prevention strategy in other minority, Indigenous, and Pacific communities who face similar health disparities.

NIMHD

04.02.11 – Poster Session 2 · Chesapeake Suites (MR)

BREASTFEEDING PATTERN IMPACT ON INFANT PHYSICAL GROWTH

Michelle Kaimenyi, M.H.S., Flora A. M. Ukoli, M.D., MPH.
Meharry Medical College, Nashville, Tennessee

Background: The American Academy of Pediatrics and World Health Organization established standardized guidelines for infant physical growth. Breastfeeding influences infant physical growth, and breastfeeding rates have declined worldwide. This study aims to compare infant physical growth across breastfeeding practices.

Methods: An education intervention conducted in Nashville, Tennessee involved 254 pregnant African American women. Participants were recruited from prenatal clinics and health fairs by flyers. After signing informed consent, participants completed a 5-page pre-intervention survey providing demographics, and breastfeeding knowledge, attitude and practice. They attended four 30-minute education sessions monthly. A 4-page survey was completed 1 month postpartum, and 2-page surveys at 3- and 6-months postpartum. Infant weight and length were obtained from well-baby clinic measurements. Breastfeeding was self-reported as EBF (exclusive breastfeeding), BF (breastmilk and formula) or NBF (formula only). Infant BMI was computed using an online Baby BMI calculator. T-tests were performed to compare infant weight across infant feeding patterns for each gender. Obesity status was compared across demographic and breastfeeding pattern subgroups by Chi-Square tests.

Results: Mothers were more likely to BF at 3 months and NBF at 6 months. Infant BMI was statistically associated with breastfeeding pattern at 3 months ($p<0.01$) and 6 months ($p<0.05$). EBF or BF infants maintained normal BMI (5th-85th percentile). Male infants of single mothers were more overweight by 3 months compared to infants of married mothers. Female infants maintained normal BMI status at 3- and 6-months regardless of marital status.

Conclusion: Mothers were unlikely to continue EBF up to 3 months. High rate of infant overweight by 3 months might therefore be a consequence of a greater proportion of formula fed infants. Increasing breastfeeding education and providing substantial breastfeeding support initiatives can contribute to maintaining EBF up top 6 months, thus subsequently decreasing the prevalence of infant overweight among Africa American infants.

04.02.12 – Poster Session 1 · Chesapeake Suites (MR)

BUILDING CAPACITY FOR COMMUNITY-BASED PARTICIPATORY RESEARCH: MORGAN CARES COMMUNITY AWARDS PROGRAM

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The Center for Urban Health Disparities Research and Innovation, Morgan State University (MSU)

PURPOSE: The Morgan CARES Community Engagement Core has launched and assessed a community awards program to foster research partnerships between partnering academic and community researchers at Morgan State University. This presentation will highlight the results, insights, and challenges of these funded initiatives, along with their impact and the experiences of the participants involved.

METHODS: The program issued 29 small community awards across four cohorts, focusing on health disparities. These awards, totaling $2,000 for new partnerships and $5,000 for ongoing ones, supported projects to discern community needs and assets, provide education, promote health, or evaluate current programs. Evaluation was conducted through interim and final project reports, as well as comprehensive surveys with qualitative and quantitative elements completed by Morgan CARES community award recipients. These surveys examined various success indicators, such as trust, equity, partnership dynamics, project results, and encountered challenges.

RESULTS: A significant portion (62%) of the community awards was allocated to health education and promotion, with needs assessment and program evaluation comprising 24% and 14%, respectively. High levels of community involvement and progress toward program objectives were reported, with scores of 71% and 67%. Both academic and community researchers provided these positive evaluations. Preliminary results show a favorable perception of trust and equity within partnerships, with 91% of researchers acknowledging the relationships as beneficial and equitable. However, issues like limited resources and communication hurdles were noted.

CONCLUSION: The partnership evaluation survey pinpointed key areas needing enhancement, while the project impact evaluation underscored the concrete advantages of the funded projects, including better health service access, increased community participation, and improved health outcomes.

The integration of data from partnership and project impact assessments into our analysis sheds light on the efficacy of the partnerships and the influence of the funded initiatives.

This work was supported by the National Institute on Minority Health and Health Disparities RCMI@Morgan #5U54MD013376-8281.

04.02.13 – Poster Session 2 · Chesapeake Suites (MR)

RANDOMIZED BEHAVIORAL TRIAL TO PROMOTE COVID-19 BOOSTER VACCINATION: THE PUERTO RICO VACCINE UPTAKE STUDY (PR-COVACUPS)

K MATOS-JIMÉNEZ; A García-Seguí; CM Pérez; C Rivera-Cátala; GD Torres-Irizarry; A López-Cepero; V Colón-López
University of Puerto Rico Medical Sciences Campus (AGS, CMP, KMJ, CRC, GDTI, VCL); University of Puerto Rico Comprehensive Cancer Center (VCL); Rollins School of Public Health at Emory University (ALC)

PURPOSE: As of February 2024, 2,450,180 eligible individuals in Puerto Rico had not received a booster shot for COVID-19. Vaccine uptake has been lagged among adults, highlighting the urgent need to target booster uptake. The Puerto Rico COVID-19 Vaccine Uptake Study (PR-COVACUPS) evaluated the efficacy of an educational intervention to reduce vaccine booster hesitancy and assessed barriers to booster completion in a vulnerable and socioeconomically disadvantaged population in Puerto Rico. METHODS: A two-group randomized-controlled trial recruited 386 adults aged 21 years or older who had not received the booster vaccine. Participants were recruited from the health clinics at the University of Puerto Rico Medical Sciences Campus and the University District Hospital. The intervention group received an educational toolkit delivered by a health promoter, which addressed the most common misconceptions regarding the COVID-19 vaccine, complemented with access to a website containing educational videos created by local physicians and scientists. The control group received standard care. Log-binomial regression models were used to compute relative risks (RR) and 95% confidence intervals (95% CI) of booster completion at 2 and 4 months of follow-up, adjusting for marital status and history of flu vaccination. RESULTS: The participants were mostly middle-aged, female, college-educated, low-income, employed, and public health insurance beneficiaries. Participants in the intervention group were 40% more likely to have their booster vaccine 2- or 4 months after baseline assessment (RR=1.40, 95% CI=0.65-3.00). However, this association was not statistically significant. The main barriers to booster uptake at the 2- or 4-month follow-up for both groups included concerns regarding the vaccine's side effects (52.1%), vaccine development (28.0%), and personal and religious beliefs (13.5%). CONCLUSION: The direction and magnitude of our findings highlight the relevance of implementing health promoters as a public health social promotion strategy for targeting vaccination urgency among hesitant groups. Simultaneous population-based massive campaigns might also impact the significance of our findings. Health concerns in both groups continue to be the main barrier to vaccine hesitancy.

GRANT SUPPORT: Supported by NIH RCMI Grant U54MD007600

ABSTRACTS

04.02.14 – Poster Session 1 · Chesapeake Suites (MR)

PILI PONO LIFESTYLE: AQUAPONICS FOOD PRODUCTION FOR WHOLISTIC HEALTH

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PURPOSE Native Hawaiians are the Indigenous people of Hawai'i who developed sophisticated food cultivation systems that sustained a thriving and robust population for centuries. These sustainable systems were disrupted by colonization, contributing to the health disparities that Native Hawaiians face today, including cardiometabolic diseases. Building on these efforts, the MALAMA study tests a culturally-grounded backyard aquaponics program developed to curb these disparities and promote Indigenous food sovereignty. This purpose of this presentation is to report on the findings of interviews and focus groups conducted with the pilot cohort of family participants to identify how participating in the MALAMA program wholistically impacted their health.

METHODS Focus groups and interviews were conducted with ten Native Hawaiian families who participated in the MALAMA program as a part of a pilot feasibility study. The focus group and interviews were transcribed verbatim and were uploaded into NVivo version 20. In total, there were five coders from our research team. Initially, three coders reviewed the transcripts individually and used a grounded theory approach to find codes that emerged from the data.

RESULTS The major theme that emerged from the data was the concept of pilina, which loosely translates to connection, relationship, joining. Participants spoke mainly about how MALAMA fostered their wholistic health through 1) pili ʻāina (land) 2) pili kānaka (people) and 3) pili kaiāulu (community). From these findings, the Pili Pono Practice framework was developed to conceptualize the connections and relationships that are vital to Native Hawaiian health.

CONCLUSIONS The MALAMA program fostered the participants' connection to traditional foods, land, cultural identity, family, and community, all contributing to the program's quick adoption into Native Hawaiian communities. To address food insecurity, utilization of Indigenous-developed, community-based, and culturally-grounded programs and solutions like the MALAMA program is imperative.

NIMHD

04.02.15 – Poster Session 2 · Chesapeake Suites (MR)

RELATIONSHIPS BETWEEN PAIN AND SLEEP ON PHYSICAL AND MENTAL HEALTH AMONG ADULTS LIVING WITH SICKLE CELL DISEASE

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INTRODUCTION: Sickle cell disease (SCD) is an inherited genetic disorder that results in abnormal hemoglobin. In the United States, approximately 100,000 individuals are affected by this condition. SCD complications may lead to adverse health outcomes including acute and chronic pain, difficulty sleeping, and overall quality of life and well-being. Limited data exist regarding the contribution of pain and sleep on mental and physical health outcomes. This study aimed to investigate the impact of pain severity, insomnia symptoms, and sleep quality on physical and mental health among individuals living with SCD/sickle cell trait (SCT).

METHODS: Data were obtained from participants who completed self-report measures (N=20, Mean age= 33.45 (SD=10.48); 55% Female). The Insomnia Severity Index assessed for the nature, severity, and impact of insomnia symptoms and the Pittsburgh Sleep Quality Index evaluated an individual's quality of sleep and disturbance. The Pain, Frequency, Intensity, and Burden Scale evaluated the degree to which pain, its frequency, and distress interfered with daily life. The SF-12 Health Survey assessed for quality of life to include mental and physical health, with lower scores indicating poor health.

RESULTS: Data showed negative associations between insomnia symptoms ($r=-.645$, $p=.002$) and sleep quality ($r=-.586$, $p=.007$) on quality of life. Insomnia symptoms ($r=-.509$, $p=.022$), pain severity ($r=-.739$, $p<.001$) and sleep quality ($r=-.484$, $p=.031$) were correlated with physical health, while only insomnia symptoms ($r=-.498$, $p=.025$) were associated with mental health. Linear regression analyses indicated that pain severity, sleep quality, and insomnia symptoms accounted for 58.3% of the variance in physical health. Beta coefficient showed that pain severity ($\beta=-.630$, $p=.004$) was the strongest predictor of physical health.

CONCLUSION: Data indicated that sleep disturbances and pain severity should be monitored and assessed among those with sickle cell disease/trait to improve overall quality of physical health, with a primary focus on pain.

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04.02.16 – Poster Session 1 · Chesapeake Suites (MR)

COMMUNITY NAVIGATION FOR NATIVE HAWAIIAN DIABETIC PATIENTS

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PURPOSE: Native Hawaiians (NH) face disproportionate burden of chronic diseases. The Kilolani Project is piloting the use of NH community navigators to foster trust and reduce barriers to care among vulnerable NH diabetic patients within an urban, academic, safety-net clinic. To investigate the impact of the Kilolani Project, we performed a qualitative study to examine patient perspectives, with the broader goal of ensuring that their recommendations form the basis of future project expansion.

METHODS: Fifteen adult NH diabetic patients enrolled in the Kilolani Project were recruited through convenience sampling to participate in one of three focus group sessions. Focus group interviews followed a semi-structured format with open-ended questions. Transcripts were analyzed thematically through iterative readings and coding.

RESULTS: Focus group participants had a median age of 58 years; 47% were women and 27% were from rural areas. Three key themes characterized their perspectives of the Kilolani Project: importance of relationships; culturally aware trauma-informed care; and resilience. Participants emphasized the centrality of building trusting relationships or "pilina" with navigators. They valued the navigators' humanistic approach, availability, and persistence, regardless of ethnic concordance. Participants reported a history of unaddressed adverse childhood experiences and expressed how navigators played a significant role in improving mental health. Participants felt a sense of personal responsibility for their health and spoke of the value of tradition and religion as sources of resilience.

CONCLUSION: The Kilolani Project, led by navigators has created a safe space where NH patients living with diabetes feel seen, heard and cared for, thereby improving healthcare experiences and engagement. Giving voice and agency to this vulnerable population is paramount to ensuring cultural values, needs, and priorities drive future navigator based strategies.

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04.02.17 – Poster Session 2 · Chesapeake Suites (MR)

PREVALENCE OF ARBOVIRUSES IN AEDES AEGYPTI MOSQUITOES AND COMMUNITY MEMBERS FROM PONCE, PUERTO RICO.

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Arboviruses are arthropod-borne viruses that have emerged and re-emerged in the Caribbean. Aedes aegypti mosquito as a vector has led to the transmission of flaviviruses (DENV and ZIKV) and alphaviruses (CHIKV and MAYV) causing a significant impact in the Caribbean. Due to the similarities in demographic factors across the Caribbean Islands, there is a high possibility of finding a diversity of arboviruses in Puerto Rico. A cross-sectional study was conducted in four clusters (2 urban and 2 rural) from Ponce, Puerto Rico. We aimed to assess the prevalence of arboviruses in Aedes aegypti mosquitoes and community members from Ponce. It was expected to identify two times more Aedes aegypti mosquitoes infected with arboviruses and a higher predisposition of participants in rural areas compared to urban areas. Recruitment of 25 participants was conducted in each cluster for a total of 100 participants, 50% were females and the mean age was 57y (IQR 21-84y). Most of the participants practiced preventive measures such as the use of screens at windows (64%) and doors (74%), surrounding maintenance (81%), removal of standing waters (69%) and debris (71%); except for mosquito net (6%). Through an environmental assessment, it was observed that participants were exposed to risk factors associated with arboviral diseases such as living near mangroves (22%), rivers and beaches (42%), or having pets (71%). An antibody assessment for alphavirus was performed on participants recruited at Ponce and 34% showed to have antibodies against alphaviruses. Wild-type Aedes aegypti mosquitoes were collected from the four clusters and tested for DENV, ZIKV, CHIKV, and MAYV through an RT-qPCR molecular test. From the molecular assessment, mosquitoes from the urban clusters were positive for DENV-1. This study will provide insight to continue monitoring arboviruses in mosquitoes and community members in Puerto Rico and develop preventive strategies for mosquito control.

5 U54 MD007579-36

04.02.18 – Poster Session 1 · Chesapeake Suites (MR)

LEVELS OF ANXIETY AND DEPRESSION IN RESIDENTS OF A COMMUNITY IN PONCE, PUERTO RICO.

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In Puerto Rico, studies have reported a prevalence of 12.5% for anxiety and 10.4% for depression. It is imperative to design intervention programs tailored to the characteristics of each community to advance in the prevention and control of mental health conditions. This present study aims to estimate the prevalence of anxiety and depression symptoms among members of a community in Ponce, Puerto Rico (PR). Based on Community-Based Participatory Research, this exploratory quantitative study is led by a community leader trained in research. A sociodemographic questionnaire and scales to assess depression symptoms (PHQ-8) and anxiety symptoms (GAD-7) were administered to 105 men and women from a community in Ponce, PR. The participants had an average age of 65 years ± 15.343; 77.1% were women, 53.4% were married/cohabiting, 47.2% had an associate degree or less, and 42.9% had annual family incomes of ≤ $18,000. Results showed that 12.5% reported moderate to severe depression, and 16.5% reported moderate to severe anxiety. Twenty-three percent (23.0%) of the participants reported alcohol consumption, 8.6% tobacco use, and 9.5% used sleep medications (prescribed or not). Of the participants reporting anxiety medication use, 80% did not visit a psychologist or psychiatrist. On the other hand, 29% of those who did not visit a psychologist had at least mild symptoms of depression (6.49%) and anxiety (9.10%). Preliminary results of this study show higher levels of anxiety and depression than those established in island-wide studies, highlighting the need to expand the reach of mental health services.

This work received support from the Research Centers for Minority Institutions (RCMI-U54MD007579).

ABSTRACTS

04.02.20 – Poster Session 2 · Terrace (2nd Floor)

COMMUNITY TRAINING INSTITUTE FOR HEALTH DISPARITIES: BUILDING CAPACITY TO REDUCE HEALTH DISPARITIES

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Community-engaged research has proven to be an essential strategy for reducing health inequities. Correspondingly, community-based participatory research evidence has been reported to bring ample benefits in attending to community health concerns, actively integrating the community in health research, and reducing inequities associated with health, among others. To better support this integration, a Community Training Institute for Health Disparities (CTIHD) was created to capacitate community members in health disparities research and health promotion to aid community-academic partnerships and community-led health promotion intervention development. Capacitation programs were developed and implemented. Evaluation measures for the outcomes of the CTIHD two cohorts include satisfaction, knowledge change, retention rate, completion rate, partnership formation (research proposals), and community health promotion plans. The retention and completion rates were 85% and 80%, respectively. Ten out of sixteen courses (Overall satisfaction rate: 99%) demonstrated a significant change in knowledge ($p<0.05$), and overall, there was an increase in knowledge gained by trainees (N=45). Outcomes include seven formalized community-academic partnerships, the development of research proposals (e.g., obesity, mental health, and cancer), and funding for implementation. Additionally, twenty-six community health promotion plans were developed (e.g., mental health, diabetes, health behaviors), seven were implemented, and funding was received. Findings from this study suggest that the CTIHD was a valuable strategy to provide training, promote the formation of community-academic partnerships, and increase community-led health promotion interventions to increase health disparities research and improve community health outcomes in underserved Hispanic populations.

This work received support from the Research Centers for Minority Institutions (RCMI-U54MD007579).

04.02.21 – Poster Session 1 · Terrace (2nd Floor)

FAITH-BASED COVID RESPONSE FOR AFRICAN AMERICAN OLDER ADULTS

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Purpose: We sought to address the significant health disparities experienced by under-resourced African American older adults, especially those with pre-existing chronic conditions, in South Los Angeles during the COVID-19 pandemic. This study focuses on evaluating the effectiveness of a hybrid (virtual/in-person), community-based participatory intervention, that utilized faith-based lay health advisors within a COVID-19 Health Ambassador Program (CHAP).

Methods: We employed a mixed-methods, pre-post, single-arm quasi-experimental design, recruiting lay health advisors/COVID-19 Health Ambassadors (CHAs) and participants from faith-based organizations. The CHAs led weekly hybrid meetings and follow-up sessions, providing education and support to the participants. To evaluate the intervention's implementation, we used the Consolidated Framework for Implementation Research (CFIR) as a reporting tool and focused on fidelity to the intervention model, challenges encountered, and adaptations necessitated by these challenges. Data was collected via stakeholder interviews and surveys which were subjected to thematic analysis and descriptive statistical analysis using SPSS software.

Results: CHAP was delivered to 152 participants by 19 CHAs from 17 faith-based organizations. CHAs assisted with chronic disease management, resolved medication-related challenges, encouraged COVID-19 vaccination, reduced psychological stress and addressed healthcare avoidance behaviors such as COVID-19 vaccine hesitancy among the participants. Challenges encountered include ensuring participant engagement and retention in the virtual format and addressing technological barriers for CHAs and participants. Adaptations made to better suit the needs of participants included providing communication tools and additional training to CHAs to improve their proficiency in using virtual platforms in addition to adapting scientific/educational materials to suit our participants' diverse cultural and linguistic needs.

Conclusion: The community-centered hybrid approach in addition to our partnership with faith-based organizations and their respective COVID-19 health ambassadors proved to be essential in assisting underserved African American older adults manage chronic health conditions and address community-wide health disparities during the COVID-19 pandemic. Adaptability, cultural sensitivity, and teamwork are key to implementing health interventions especially in underserved populations.

This project was primarily supported by the National Institutes of Minority Health and Disparities/National Institutes of Health Award number R25 MD007610 (PI: M. Bazargan). Additionally, this study received support from the National Institute of Minority Health and Health Disparities under award number U54MD007598 (PI: J. Vadgama). The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

04.02.22 – Poster Session 1 · Terrace (2nd Floor)

ETHICAL DATA PRINCIPLES FOR HEALTH DISPARITY COLLABORATIVE RESEARCH WITH COMMUNITY-BASED ORGANIZATIONS

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PURPOSE: This study addresses the pressing need to develop alternate ethical data management guidelines for health researchers collaborating with community-based organizations or engaging in citizen science projects. Whereas the scientific community increasingly adopts mainstream data management principles such as FAIR (findable, accessible, interoperable, and reusable), community-engaged research indicates the potential for expanding such principles. For example, Indigenous communities across the globe encourage to supplement FAIR with the CARE (collective benefits, authority to control, responsibility, ethics) principles. This project proposes the co-development of alternate data management principles with a community organization that collaborates with scientists and focuses on augmenting energy independence in Puerto Rico to reduce health disparities and better manage chronic diseases in a remote aging community vulnerable to natural disasters.

METHODS: In the first stage of this study, we explored the community organization's past and current data management practices by conducting individual interviews and utilizing participant observation methods. We identified key ethical data management practice themes. The study also aims to compare our bottom-up data principles with other data management strategies used in other global health collaborative research projects and test a pilot implementation of the principles in a data visualization workshop with the community collaborators.

RESULTS/EXPECTED RESULTS: Our preliminary findings identify themes focused on people-centered approaches to data management practices privileging caring interpersonal interactions and low-tech procedures. Our expected final results also suggest that with limited resources available, community organizations prioritize sharing data about the impact of their interventions, facilitating effective emergency response, and building trust and positive engagement with community members.

DISCUSSION/CONCLUSION: This study advances knowledge in ethical data science strategies to support collaborative health research and community-based organizations' decisions in addressing health disparities. By centering alternate data management strategies on the community organization's experiences, needs, practices, values, and uses of data science, this research addresses the limitations of mainstream data principles focused on top-down approaches to data governance.

National Institute on Minority Health and Health Disparities: Md., Md., US; Part of The FIU Research Center in a Minority Institution (FIU-RCMI) (Grant number U54MD012393)

04.02.23 – Poster Session 2 · Terrace (2nd Floor)

MEDICAL MISTRUST AMONG MINORITY PUBLIC HOUSING RESIDENTS

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Purpose: Among African American and Latinx public housing residents, a historical legacy of medical mistrust rooted in slavery and medical experimentation may delay or impair care-seeking. Mistrust experienced by Spanish speaking residents may be more amplified due to a lack of reliable information in Spanish, a preference for multigenerational/ multi-family living, immigration status, and being a frontline health worker. One of the primary goals of this multi-phase study was to examine associations between medical mistrust and provider/patient relationships among African American and Latinx public housing residents in Los Angeles.

Methods: A cross-sectional sample of 252 African American and Latinx individuals were recruited primarily from 9 public housing areas in the City of Los Angeles. Trained bilingual research coordinators administered the structured questionnaire containing demographic items, health information, cultural beliefs, and related factors of trust. Analyses were conducted using multiple linear regression.

Results: Among 252 participants, nearly 20% believe that their ethnic group should be suspicious of information from healthcare providers. Over 16% felt that healthcare providers do not take the medical complaints of people of their identified ethnic group seriously. Nearly 16% reported their belief that healthcare providers and workers sometimes hide information from patients who belong to their ethnic group. Regression analyses revealed that, controlling for other variables, financial strain negatively ($P < .05$) and a positive relationship with their preferred/selected healthcare provider positively ($p < .01$) predicted mistrust towards the healthcare system.

Discussion: Intervention efforts that involve culturally sensitive messaging towards the healthcare system with operation at the individual, interpersonal, societal, and organizational levels may improve trust and increase disclosure of adherence barriers and utilization of preventive care. These findings provide valuable insights into the understudied population of minority public housing residents, which can influence community-based initiatives and innovative engagement strategies to decrease health inequities and overall mistrust.

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ABSTRACTS

04.02.26 – Poster Session 1 · Terrace (2nd Floor)

ASSESSING THE ASSOCIATION BETWEEN SCHOOL VICTIMIZATION AND BINGE DRINKING AMONG SEXUAL MINORITY YOUT

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Purpose: Alcohol use among high school students, particularly high-risk drinking behaviors, is a significant public health concern. Substance use during adolescence is associated with an increased risk of both acute and long-term adverse health outcomes. Sexual minority youth (SMY) are more likely to initiate alcohol use at a younger age and engage in binge drinking when compared to their heterosexual peers. Recent research has suggested that school-based victimization disproportionately impacts SMY and is associated with an increased risk of binge drinking. We aimed to:

(1) Determine the association between binge drinking and sexual identity among high school students.

(2) Assess if school-based victimization mediates the relationship between sexual minority identity and increased risk of binge drinking.

Methods: This cross-sectional study utilized data from a nationally representative sample of United States high school students (n=26,675) collected in the 2017 and 2019 Youth Risk Behavior Survey. Logistic regression was used to assess the association between sexual minority identity and binge drinking. In addition, we tested for mediation of the relationship by school-based victimization.

Results: When compared to their heterosexual peers, bisexual female students were significantly more likely to report binge drinking within the past 30 days. School-based victimization mediated this association.

Discussion: Bisexual females are at a higher risk of participating in binge drinking when compared to their heterosexual counterparts. Our results suggest interventions to reduce school-based victimization may play an important role in addressing risky drinking behavior in this population.

04.02.27 – Poster Session 2 · Terrace (2nd Floor)

USING COMMUNITY ENGAGEMENT TO CONDUCT FOCUS GROUPS WITH BLACK WOMEN AT RISK FOR BREAST CANCER

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Although Black and White women are diagnosed with breast cancer at similar rates, Black women are more likely to die from the disease. Diagnosing breast cancer early coupled with early treatment are the most important strategies to reduce and prevent deaths. About 13-16 percent of women diagnosed with breast cancer have a close female family member who has also been diagnosed. Some studies suggest that the risk of breast cancer among Black women with a first-degree relative (sister, mother, daughter) with a diagnosis is double that of women with no family history. Unfortunately, close relatives of breast cancer survivors are overlooked when it comes to breast cancer prevention. The purpose of this study is to understand the lived experiences of women who are closely related to breast cancer survivors. A snowball sampling strategy was used to recruit 27 adult, black women to participate in a qualitative research study. To participate, women needed to be closely related to a breast cancer patient and cancer-free. We partnered with members of Sisters Network Nashville (SNN), a national support group for African American breast cancer survivors to recruit participants. Based on data from SNN, it was projected that each member would have at least 2 living first-degree female relatives (mothers, daughters, and sisters) who were eligible. SNN members who recruited participants received $10 for each participant who completed a focus group or interview. Participants received a $50 gift card for their time. Five focus group discussions and 2 individual interviews were conducted via Zoom. The community-academic study team collaborated to develop a discussion guide for the focus groups. Although SNN members were trained to conduct focus groups, they decided to participate as observers. Recurring themes were documented in 5 areas: breast cancer knowledge and prevention, the impact of family member's breast cancer diagnosis, lifestyle choices that are linked to breast cancer risk, challenges and barriers of breast cancer prevention, attitudes about and attitudes about genetic testing.

Environmental Science

04.04.01 – Poster Session 1 · Terrace (2nd Floor)

MICROPLASTICS POLLUTION IN THE CHESAPEAKE BAY AND ITS ENVIRONMENTAL HEALTH IMPLICATIONS

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PURPOSE: Microplastic pollution is a global concern that has negative effects on the environment and human health. This study aims to investigate the abundance, distribution, and chemical composition of microplastics in the Chesapeake Bay to provide essential information for assessing the environmental health risks associated with microplastics.

METHODS: Monthly surface water samples were collected at 4 locations on the Chesapeake Bay during the summer of 2023. Microplastic samples were digested with potassium hydroxide (KOH), then subjected to density separation, and finally filtered on silver membrane filters for chemical and physical properties analysis. The Shimadzu AIM 9000 FTIR microscope was used to characterize the abundance, size fraction, and chemical composition of microplastic samples.

RESULTS/EXPECTED RESULTS: The preliminary data revealed significant spatial variability in the distribution of microplastics within the Chesapeake Bay, with an average abundance of 763 ± 411.9 particles per liter of water. Microplastics smaller than 300 µm were the most common, making up over 90% of the total microplastics found. Polyamide was the most abundant (44%) polymer type found in the samples, followed by Polyurethane (21.6%).

DISCUSSION/CONCLUSION: The abundance of microplastics in the Chesapeake Bay was found to be significantly higher than previously estimated, especially for the smaller-size microplastics. Our results indicate that the smaller microplastics (<100 µm) could pose a significant environmental risk by entering the food web and endangering human health.

Funding for this research was partially provided by the NIH National Institute on Minority Health and Health Disparities Award Number U54MD013376 and NSF Award Number 2022887 to Dr. Chunlei Fan

04.04.02 – Poster Session 2 · Terrace (2nd Floor)

RESTRICTED USE PESTICIDE USE AND ETHNICITY IN HAWAII

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PURPOSE: Since 2019 restricted use pesticide (RUP) applicators have been required to submit details about RUP use to the Hawai'i Department of Agriculture. RUP data for 2019 indicate that 337,027 pounds of RUPs were used throughout the state and over 200,000 pounds were carcinogenic fumigants (1,3-dichloropropene (1,3-D) and metam sodium). These highly volatile fumigants have been linked to cancer and asthma with differences found by some races. There is currently no information on pesticide exposure by ethnic groups in Hawai'i. We hypothesize that Filipinos or Native Hawaiian or Pacific Islanders (NHPI) are disproportionately exposed to RUPs compared to other ethnic groups. METHODS: RUP data are currently available by tax map key (TMK); thus, zip codes adjacent to TMKs will be assigned exposure levels based on RUP use and distance from fields. Ethnicity data by zip code will be obtained from the 2020 Census and the American Community Survey. ArcGIS and Stata will be used to assess associations between RUP data and ethnicity including Filipino and NHPI. RESULTS: In the 2021 American Community Survey, Hawai'i's population identified as Asian (38%), white (24%), NHPI (10%). Filipinos are the largest group of Asians (26%). The towns with the highest percentage of Filipinos or NHPIs in Hawai'i either have historical roots in the sugarcane industry or are currently agricultural communities. Thus, these communities are expected to have higher RUP exposures. DISCUSSION: Local food production and consumption is a major priority for the state of Hawai'i. Commercial farming operations have a long-standing practice of using pesticides to manage unwanted pests and ultimately promote crop yield, but these practices may lead to disparities in exposure and health risk to certain communities and ethnic groups. This is the first study to use Hawai'i's RUP data in a public health context.

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Pharmaceutical Sciences / Pharmacokinetics / Drug Discovery and Delivery

04.05.03 – Poster Session 1 · Terrace (2nd Floor)

ASSESSING THE POTENTAIL OF GARCINIA KOLA PLANT EXTRACT IN THE TREATMENT OF BREAST CANCER

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Breast Cancer (BC) is the second most commonly diagnosed and the second most common cancer death among women. Although, screening and patient management have improved significantly, the incidence rate of BC is lower in African American (AA) women than in Caucasian women. However, mortality from BC is higher in AA women. The most common treatments for BC are radiation therapy, chemotherapy, and hormone replacement therapy. Unfortunately, adverse side effects often accompany these treatments. bitter cola also known as Garcinia Kola (G. Kola) is a flowering plant and may contain medicinal properties for cancer cure. Our study aims at assessing the cytotoxic and apoptotic effects of G. Kola on MDA-MB-231 BC cells. To achieve this aim MDA-MB-231 cells were treated with various concentrations of G. Kola at (0, 0.5,1.0,1.5, and 2.0 µg/mL) for 48 hrs. After treatment, the cell viability was measured by performing the MTS and Acridine Orange/Propidine Iodine (AO/PI) fluorescent staining. Apoptosis was assessed through DAPI staining, Annexin V/PI, and Mitochondrial Membrane Potential (JC-1) assays. Results showed reduction in the percentage viability of about 88 % and the IC50 were recorded at 1.35 µg/mL. Treated cell exhibited significant decrease in confluency and number of cells, shrinkage, and detachment from the dish culture, which are signed of early apoptosis. In sum, data showed G. Kola inhibits cell proliferation in concentration dependent manner and early sign of apoptosis were manifested. This preliminary screening demonstrated G. Kola as a potential treatment drug for BC when consumed together.

National Institute on Minority Health and Health Disparities of the National Institutes of Health under Award Number 5U4MD015929-04.

04.05.04 – Poster Session 2 · Terrace (2nd Floor)

TARGETING SKP1 WITH A NOVEL SMALL-MOLECULE COMPOUND IN ADVANCED PROSTATE CANCER

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PURPOSE: Metastatic, castration-resistant prostate cancer (mCRPC) directly contributes to the mortality and morbidity of prostate cancer (PCa). It is an urgent and unmet medical need to identify new therapeutic targets and develop novel targeting strategies against lethal mCRPC.

METHODS: We developed a novel small-molecule compound (GH501) via a "molecular hybridization" approach. The in vitro cytotoxicity of GH501 was evaluated at the National Cancer Institute Developmental Therapeutics Program. The mechanism of action of GH501 was investigated using in silico docking, bio-layer interferometry (BLI) assay, and molecular and cellular approaches. The in vivo toxicity and anticancer efficacy of GH501 against mCRPC were evaluated in animal models. The expression of Skp1 in human PCa specimens was evaluated by IHC staining.

RESULTS: We demonstrated that GH501 exhibits potent cytotoxicity against mCRPC cells and induces apoptosis at nanomolar concentrations in a broad spectrum of human cancer cells. Mechanistically, GH501 disrupts the physical interaction between Skp1 and F-Box proteins (FBPs) and affects multiple Skp, Cullin, F-box containing complex (SCF) oncogenic signaling components implicated in the progression of mCRPC. GH501 suppresses the skeletal and subcutaneous growth of mCRPC in cell- and patient-derived xenograft models. Significantly, Skp1 is overexpressed in human PCa.

CONCLUSION: These results indicated that pharmacological targeting Skp1-FBP interaction represents a promising therapeutic strategy for mCRPC. Considering the higher mortality and morbidity of PCa in African Americans (AA) compared with other racial populations, we are evaluating the capacity of GH501 against mCRPC in representative PCa models of AA origin and demonstrated that GH501 exhibits potent in vitro cytotoxicity in MDA PCa 2b cells of AA origin via inducing apoptosis and cell cycle arrest and inhibiting the SCF complex.

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ABSTRACTS

04.05.05 – Poster Session 1 · Terrace (2nd Floor)

ANALYTICAL METHOD AND FORMULATIONS DEVELOPMENT OF OJT003 FOR BIOAVAILABILITY ENHANCEMENT

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PURPOSE: Even with vaccines, SARS-CoV-2 and new variants remain a challenge. OJT003, a proven drug, effectively reduces the cytopathic effects of both the reference and omicron strains, targeting mechanisms beyond the human recombinant angiotensin-converting enzyme 2 (ACE2) receptor, indicating its potency against emerging variants. However, its oral bioavailability is only 16% compared to intraperitoneal delivery, underscoring the need for a delivery system that improves bioavailability and accessibility.

METHODS: An ultra-performance liquid chromatography (UPLC) technique was devised for quantification of OJT003 utilizing the ACQUITY UPLC H-Class PLUS System, employing a ACQUITY HSS T3 Column with a gradient mobile phase of methanol and 5 mM ammonium acetate at pH 4.73.

To assess the feasibility of co-solvent formulations, OJT003's solubility was examined in 22 different solvents via the shake-flask method. Following this, emulsion formulations for oral administration were concocted using selected solvents with stirring mixture under variable weight ratios. For intraperitoneal delivery, alternative formulations with Tween 80 were prepared through methods including simple suspension, sonication, high-speed homogenization, and a combination of high-speed and high-pressure homogenization, with their size stability appraised using a Zetasizer.

RESULTS: Chromatographic assessment yielded a retention time of 5.5 minutes at a flow rate of 0.4 mL/min, and OJT003 demonstrated a quantification linearity from 1 µg/mL to 200 µg/mL with an R^2 of 0.997. Among the solvents tested, Transcutol HP (5.15 mg/mL) and Labrafac AC CC (2.50 mg/mL) exhibited favorable solubility for emulsion preparation, whereas OJT003 was essentially insoluble in water (<0.07 mg/mL). The formulated concentrations of OJT003 could reach up to 10 mg/mL. The intraperitoneal suspension displayed enhanced size stability after two weeks with the combined homogenization method, maintaining an average particle size 245.4 nm with a polydispersity index (PDI) 0.389 devoid of aggregation.

CONCLUSION/ FUTURE PLANS: This study yielded a new UPLC method to analyze OJT003 and two formulation prototypes: emulsions for oral intake and suspensions for intraperitoneal injection, poised to augment OJT003's bioavailability. Future directives include the development of a spray-drying methodology for crafting micron-sized particles amenable to oral and nasal administration.

GRANT SUPPORT: This study was supported in part by the NIH/NIMHD-Research Centers in Minority Institutions Program (U54MD007605) and Cancer Prevention & Research Institute of Texas (CPRIT) Core Facilities Support Awards (RP180748).

Data Science / Big Data

Artificial Intelligence / Machine Learning

05.01.05 – Poster Session 2 · Terrace (2nd Floor)

A COMPARATIVE STUDY OF MACHINE LEARNING AND NON-MACHINE LEARNING CLASSIFIERS FOR PREDICTING RISK FACTORS FOR TYPE 2 DIABETES

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PURPOSE: The purpose of this study is to identify the risk factors for type 2 diabetes using multiple classifiers and compare their accuracy. Type 2 diabetes is a common chronic disease that is characterized by elevated blood glucose levels. Left untreated, it can seriously affect the circulatory, nervous, and immune systems.

METHODS: Data consisting of 520 people (320 males and 192 females) was analyzed using the UC Irvine Machine Learning Repository. A comparative analysis of risk factors for type 2 diabetes was performed. The performances of Taba regression was compared with logistic regression, probit analysis, along with machine learning methods of artificial neural network (ANN) and decision trees. The accuracy of these methods were assessed using binary classification for the presence or absence of diabetes. The predictive capabilities of age, polyphagia, sex, irritability, itching, obesity, muscle stiffness, partial paresis, polyuria, polydipsia, alopecia, delayed healing, genital thrush, weakness, visual blurring, and sudden weight loss in predicting type 2 diabetes were examined.

RESULTS / EXPECTED RESULTS: The mean age of the patients was 48.03 ± 12.15 years. A total of 16.9% of them were obese while 45.6% had polyphagia, 24.2% experienced irritability, 44.8% had visual blurring, 49.6% had polyuria, 41.7% experienced sudden weight loss, 44.8% had polydipsia, 58.7% felt weakness, 22.3% complained of genital thrush, 37.5% got muscle stiffness, 43.1% showed symptoms of partial paresis, and 34.4% had polydipsia. Taba regression showed the best overall correct classification (96.3%) followed by ANN (94.7% in training sample and 92.5% in testing sample), logistic and probit (tied with 93.3%), and decision tree (87.1%). The most significant risk factors identified by Taba regression were sex (P-value = 0.00068) followed by polyuria (P-value = 0.00202), polydipsia (P-value = 0.00213), irritability (P-value = 0.02440), obesity (p-value = 0.02755), age (P-value = 0.02827), itching (P-value = 0.03551), genital thrush (P-value = 0.04317), and polyphagia (P-value = 0.04956). Based on ANN importance criterion, the importance percentage for polyuria was 75.0%, followed by polydipsia (60.3%) and sex (53.4%).

DISCUSSION / CONCLUSION: Sex, polyuria, and polydipsia were the top three most significant as well as most important risk factors. Taba regression performed well when compared with logistic regression, probit analysis, ANN, and decision tree.

Research Centers in Minority Institutions (Grant Number: U54MD007586)

05.01.07 – Poster Session 1 · Terrace (2nd Floor)

APPLYING ARTIFICIAL INTELLIGENCE AND MACHINE LEARNING TO HEALTH DISPARITIES RESEARCH

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CCHDR - RCMI Program, Medical Sciences Campus, University of Puerto Rico (JSMB, FHN, BGN, ELTR, DCR, ARL)

PURPOSE: Hispanics, constituting 18% of the US population, lack sufficient open data representation and comprise only 8% of enrollees in data science and related fields. Addressing this disparity is crucial for diversifying the NIH-funded workforce skilled in Artificial Intelligence (AI) and Machine Learning (ML). This study aims to enhance diversity by facilitating the creation of Findable, Accessible, Interoperable, and Reusable (FAIR) Hispanic datasets, applying AI/ML to identify and mitigate health disparities in Hispanic populations.

METHODS: To bridge the gap, we developed a bilingual course focused on AI/ML topics, including Jupyter Hub, Python coding, ML libraries, and their application to mitigate Hispanic health disparities. The course was entitled, "Applying Artificial Intelligence and Machine Learning to Health Disparities Research version 2 (AIML+HDRv2),". The didactical materials included 44 presentations, 44 lecture videos, 47 demonstrative videos, and 95 reading materials. The content was presented in English, and the videos were in Spanish with English subtitles. Professors and staff from UPR-MSC and invited speakers from other universities contributed to the course contents.

RESULTS: Sixty-six applicants from UPR and other RCMI institutions applied, with 52 participants selected and enrolled in AIML+HDRv2. Notably, 33 participants successfully earned their certificate by completing the course within the 3-month period during which it was instructed. The evaluation feedback from the students provided valuable insights into the strengths of the course, including its organization, comprehensibility of the work plan, and the effectiveness of the learning activities. The positive feedback and high satisfaction levels met the participants' expectations and professional development needs.

DISCUSSION/CONCLUSION: AIML+HDRv2 represents a vital step towards enhancing diversity in data science education, addressing the underrepresentation of Hispanics. The course's bilingual and asynchronous nature ensures accessibility, fostering the creation and application of AI/ML tools to mitigate health disparities in Hispanic populations.

RCMI grant U54 MD007600 (National Institute on Minority Health and Health Disparities) from the National Institutes of Health.

05.01.08 – Poster Session 2 · Terrace (2nd Floor)

EXPLORING THE INFLUENCE OF CHAIN SIZE OF N297-GLYCAN PEG ON BINDING AFFINITIES TO HER2 MABS USING ALPHAFOLD2 AND FREE ENERGY CALCULATION

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Human epidermal growth factor receptor-2 (HER2) positive breast cancer is a specific type of breast cancer that is known for high levels of aggression, an increased risk of brain metastases, and generally poor prognosis. It is among 20% of breast cancer cases, with a 41% higher mortality rate in older African American women compared to other ethnicities. The glycoprotein HER-2 is part of the ErbB receptor family and is found to be overexpressed on the outer membrane of cancer cells, making it an important therapeutic target for specialized drug treatment. Targeted therapies, such as monoclonal antibodies (mAbs) trastuzumab and pertuzumab, have been in use for over two decades, marking significant progress in treatment. However, a major challenge emerged limiting HER2 targeted therapy efficacy. Nanotechnology presents a promising avenue but has shown degradation in the pegylation of the mAbs binding affinities towards the HER2 receptor. This exploration will go deeper computationally into the PEG length and binding affinity to develop future optimal length conjugations for the nanotechnology toward the anti-HER2 target therapy. This investigation utilizes AlphaFold2, a deep-learning-based program, to build accurate 3-D structures of the anti-PEG mAbs of Pertuzumab and Trastuzumab. We then developed the different weights of the N297-glycan-PEG conjugates located in the FC region of the mAbs. With pLDDT (>70), pTM (>0.7), PAE, and RMSD (<1) scores, our structures were found to be accurate. The full mAbs were assembled using a fit-to-map method with atomic structural fragments of IGg1 antibodies from both Protein Data Bank and Electron Microscopy Data Bank, resulting in high scores >0.7. Protein-protein docking was then employed to known binding paratopes and epitopes of HER2 receptor and mAbs complexes, which were late subjected to Binding Affinity software (PRODIGY) according direct correlations of the number of interfacial contacts (ICs) and free energy algorithmic. The anti-PEG antibodies showed a ΔG of -18 kcal/mol compared to a 2KPEG-antibody conjugate ΔG of -14 kcal/mol. This is correlated to experimental data studies showing reduced binding between Pertuzumab-2KPEG conjugates and HER2. Further usage and experimental data validation are underway. The outcome of this research would be critical to the HER2 Pegylated-mAbs, giving an optimal PEG length during the developmental stage to nanotargeted therapy and insight into FC region.

ABSTRACTS

05.01.09 – Poster Session 1 · Terrace (2nd Floor)

ETHNIC DIFFERENCES IN HPV: A FOCUS ON HISPANIC WOMEN VULNERABILITY

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PURPOSE: Cervical cancer is a major global public health issue, with disparities in incidence and mortality rates especially high among Hispanic women, suggesting the need for targeted research. Studies show significant differences in health conditions like diabetes and cancer among Hispanics, Caucasians, and African Americans. This study hypothesizes that Hispanic women exhibit a higher incidence of HPV-related clinical conditions compared to non-Hispanics. METHODS: Using data from the All of Us database, this study analyzed 3,848 HPV-positive women across Hispanic (n=1,189), non-Hispanic White (n= 2,013), and non-Hispanic Black (n= 872) groups, focusing on 22 HPV-relevant conditions identified from 220 distinct conditions reported by at least 10% of participants. Statistical analyses, including One proportion Z-test and One sample t-test for age, were conducted to identify significant differences among ethnic groups. These findings intended to select most relevant features for Machine Learning model training to predict comorbidities associated with Hispanics. RESULTS: Hispanic participants had a significantly (p-value < 0.01) lower average age (48 ± 12.67) compared to their non-Hispanic White and Black counterparts. Analysis of 22 medical conditions revealed that 19 conditions were more prevalent in Hispanics than in non-Hispanic Whites, and 15 were more prevalent compared to non-Hispanic Blacks (p-value < 0.01). Notably, 13 conditions showed higher prevalence in Hispanics across both comparison groups. DISCUSSION / CONCLUSION: Hispanics have an onset of the evaluated medical conditions at younger ages, translating into a burden to their lifestyles and medical history. The analysis indicates a significant difference in clinical conditions across ethnic groups, underscoring the presence of intrinsic factors unique to each ethnicity that influence health outcomes. GRANT SUPPORT: This project is supported by RCMI grant U54 MD007600 from the National Institutes of Health and AIM-AHEAD Research Fellowship 2nd Cohort (AWARD NUMBER: 1OT2OD032581-1-31-305).

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05.01.10 – Poster Session 2 · Terrace (2nd Floor)

A SEMI-SUPERVISED THIGH CT TISSUE SEGMENTATION NETWORK

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PURPOSE: Segmentation is an essential tool for quantification and characterization of tissue properties, with applications including assessment of body composition and disease diagnosis. In this work, we propose a semi-supervised automated system for segmentation of bone tissues, muscle and adipose tissue from CT scans in the mid-thigh. These tissues play a key role in quantification of fat depositions in the adipose tissue that are significant predictors for type-2 diabetes, sarcopenia and age-related diseases.

METHODS: We introduce a deep learning framework of U-Net architecture for automated segmentation of the subcutaneous adipose tissue (SAT), muscle, intermuscular adipose tissue (IMAT), cortical bone and trabecular bone to 2D thigh CT scans. We propose a model that employs auto-labels along with manual annotations to train the network. We divide the training in two steps. In the first, the network is trained on 50% of the 66 samples with manual labels, and tested on the remaining. Next, the trained net segments another 33 samples and generates auto-labels. In the second stage, we re-train the network with manual labels and auto-labels from first step. We also apply bootstrapping methods to bone tissues, to reduce class imbalance in the train data. The trained net is evaluated on the same test samples from step one.

RESULTS: For segmentation performance evaluation, we calculated the Dice similarity coefficient (DSC) between the tissue segmentation masks and corresponding reference masks. We achieved an overall DSC score of 0.91 for segmentation of mid-thigh regional tissues.

CONCLUSION: The introduction of auto-labels along with manual annotations generated results with good accuracy that are competitive with current methods. Addition of auto-labels increases the training size for datasets with limited manual annotations to increase accuracy. Future work will focus on tuning the hyperparameters to improve the segmentation results.

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05.01.11 – Poster Session 1 · Terrace (2nd Floor)

AUTOMATED BREAST DENSITY PREDICTION IN DIGITAL MAMMOGRAMS

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PURPOSE Breasts with high density are known to increase the risk of breast cancer. Evaluating breast cancer is challenging and typically requires trained radiologists to visually assess mammograms. However, dense breast tissue can obscure lesions, complicating this assessment. Despite promising outcomes from deep learning techniques, the scarcity of annotated medical imaging data poses a challenge, particularly with increasing network model sizes. Here we develop deep learning-based techniques for breast density prediction using clinical and simulated mammographs.

METHODS This study investigates the impact of incorporating simulated mammograms into deep learning and sparse approximation approaches for breast density prediction. We utilize breast tissue regions of interest (ROIs) from clinical full-field digital mammography images from the VinDr-Mammo dataset including cases with no abnormality findings and cases with abnormalities. Simulated mammography images were generated with representation of all breast density grades. We evaluate convolutional neural network (CNN) and sparse coding classifiers for the binary classification task of high versus low breast density.

RESULTS/EXPECTED RESULTS Preliminary results demonstrate high classification performance by CNN classifiers trained solely on clinical data using transfer learning techniques. Specifically, DenseNet-201 classification reached a breast density classification accuracy (ACC) of 95.20% and an area under the ROC curve (AUC) of 0.9888 when using solely clinical mammograms for training and testing. Additionally, our conventional machine learning approach, referred to as label-specific sparse representation classification (LS-SRC), demonstrated strong classification performance, achieving an ACC of 86.40% and an AUC of 0.8855 using ROIs from clinical data. Furthermore, we evaluate the inclusion of simulated images in the training stage to enrich the training dataset and potentially improve generalizability of classification.

DISCUSSION/CONCLUSION Our research indicates that CNNs effectively learn and classify breast density patterns. Incorporating simulated mammograms may have the potential to enhance breast density prediction models, thereby improving the accuracy of breast cancer risk assessment.

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05.01.12 – Poster Session 2 · Terrace (2nd Floor)

PRECISION AND SPEED IN MICROGLIA ANALYSIS USING YOLO DEEP LEARNING MODEL

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INTRODUCTION Microglia, essential immune cells in the central nervous system, undergo morphological changes in reaction to injuries and diseases, transitioning from a ramified to an amoeboid shape during neuroinflammation. To analyze these transformations, the YoloV8 deep learning models were employed, facilitating the detection and classification of microglia within brain slice images from both normal and cardiac arrest rat brain tissues through immunohistochemistry, achieving notable accuracy and efficiency.

METHOD Long Evans rats were exposed to 12 minutes of asphyxial cardiac arrest, with brain sections collected 24 hours later. These sections, 40 µm thick, were stained with anti-Iba1 and imaged using 20X magnification bright field microscopy. The YoloV8 model then quantified and sorted microglia into six types: ramified, hypertrophic, bushy, amoeboid, rod, and hyper-rod, using colored bounding boxes on the immunohistochemically stained images to create the morphological map for clear visualization of each category.

RESULTS The YoloV8 models efficiently identified multiple microglia types, processing over 40,000 cells and generating detailed maps in under 20 minutes, with a mean Average Precision exceeding 0.8 across six classes at IOU50:95. Observations in brain tissue affected by cardiac arrest revealed a higher presence of busy and amoeboid microglia in the cortex and hyper-rod cells in the corpus callosum, signaling severe neuroinflammation.

CONCLUSION This research presents the Yolov8 model for analyzing microglia morphology, highlighting significant improvements in speed and accuracy, showcasing its utility in neuroscience. It opens avenues for subsequent research to refine deep learning approaches in neurobiology, deepening insights into microglia's contribution to the brain's immunity and their impact on neurologic diseases.

NIMHD U54MD007597, NINDS R01NS112294, R01NS123442, NICHD P50HD105328, HRD 2200489 and CNS 2200585.

ABSTRACTS

05.01.13 – Poster Session 1 · Terrace (2nd Floor)

PROFILING OF URINARY VOLATILE ORGANIC COMPOUNDS IN PROSTATE CANCER BIOPSY PATHOLOGIC RISK STRATIFICATION USING LOGISTIC REGRESSION AND MULTIVARIATE ANALYSIS MODELS

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PURPOSE: Prostate cancer (PCa) is the second leading cause of cancer-related death in American men after lung cancer. The current PCa diagnostic method, the serum prostate-specific antigen (PSA) test, is not specific. Alternatives are needed to avoid unnecessary biopsies and over-diagnosis of clinically insignificant PCa. Metabolomics has emerged as an alternative method for early disease diagnosis. We hypothesized that changes in metabolite concentrations, such as volatile organic compounds (VOCs), in urine could be indicative of alterations in individuals' physiological state, making them valuable markers in diagnosing cancer.

METHODS: Urine samples were collected from 386 male adults, including 247 patients with biopsy-proven PCa and 139 with biopsy-proven negative results. The PCa-positive group was further subdivided into two groups: low-grade (ISUP Grade Group = 1; n = 139) and intermediate/high-grade (ISUP Grade Group ≥ 2; n = 108). VOCs in urine were extracted and analyzed by gas chromatography and mass spectrometry. We used machine learning tools to identify significant VOCs and further to develop and evaluate models for PCa diagnosis and prognosis.

RESULTS: In total, 22,538 VOCs were identified in the urine samples. With regularized logistic regression, a model for PCa diagnosis yielded an area under the curve (AUC) of 0.99 and 0.88 for the training and testing sets respectively; while the models for differentiating between low-grade and intermediate/high-grade PCa yielded an average AUC of 0.78 based on a repeated test-sample approach for cross-validation.

CONCLUSION: A novel method using urinary VOCs and logistic regression was developed to fill gaps in PCa screening and assessment of PCa grades prior to biopsy. Our findings provide a promising alternative to current PCa screening and diagnostic methods to better target patients for biopsy and mitigate the challenges associated with over-diagnosis and over-treatment of PCa.

U54MD007592, SC1CA245675

05.01.14 – Poster Session 2 · Terrace (2nd Floor)

MACHINE LEARNING PREDICTIONS FOR PROSTATE CANCER PROGRESSION

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As one of the most prevalent cancer in males within the United States, prostate cancer (PrCa) has recorded a significant decline in survival rate for metastasized cases. Worldwide, Black men have an increased risk of dying from PrCa compared to other races, underscoring the critical need to enhance diagnostic and prognostic accuracies and to streamline treatment decisions. In this work, we leverage machine learning (ML) models to identify clinical factors associated with progression-free status in patients with PrCa. Using the CBioPortal for Cancer Genomics, a dataset comprising 22 well-defined clinical variables for 494 patients was extracted. Algorithms from multiple imputation by chained equations (MICE) were used to assess and rectify deficits in the data. With progression-free survival (PFS) time as response, we trained and tested two machine learning models: the penalized Cox model (PCM) and random survival forest (RSF) to select important clinical variables for predicting PFS outcomes. Initial analysis revealed that iterations from different imputation algorithms of MICE produced reasonable results consistent with the unimputed clinical data distribution. Among the top 10 most important variables identified by both PCM and RSF with a concordance index greater than 0.80, neoadjuvant treatment, new tumors after initial treatment, and neoplasm cancer status were the three most important clinical factors contributing to PFS. Additionally, mutation count (MC) and tumor mutation burden nonsynonymous (TMBns) were rated important by both models. The high concordance index obtained by predictions using the selected important clinical variables suggested that the PrCa progression status can be predicted by ML tools. Since MC and TMBns are considered important predictors, we are currently incorporating genomic variant data and extending our analysis to use other deep ML methods to predict PFS outcomes to support the development of customized healthcare routines and help reduce PrCa disparities.

Biomedical Informatics

05.02.01 – Poster Session 1 · Terrace (2nd Floor)

SCREENING WITH THE BILATERAL CORENAL SYMMETRY 3-D ANALYZER

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PURPOSE To assess the performance of an innovative platform (the Bilateral Corneal Symmetry 3-D Analyzer - BiCSA) and a novel cornel symmetry index (the Volume Between Spheres – VBS) in distinguishing normal corneas from cases with subtle corneal abnormalities.

METHODS The Pentacam imaging data matrices (~20,000 elevation points for each exam) of 30 patients with healthy corneas and 30 keratoconus patients were extracted and analyzed. BiCSA was used to determine the VBS for each individual. Statistical analysis included calculating the mean VBS in each group, as well as the sensitivity, specificity, and positive predictive value (PPV).

RESULTS Patients with keratoconus had significantly higher VBS scores compared to healthy controls. This difference was most pronounced in the central 4.0 mm zone (6.3 versus 11.4, 5.1 points higher, p=9.0 x 10^4), but became weaker in the 6.0 mm zone (3.4 points higher, p = 0.11). Using a VBS threshold of 11.3 in the central zone identified all keratoconus cases (100% PPV) but only captured 40% of the cases. Lowering the threshold to 10.4 increased case detection to a majority (90% specificity) while maintaining a high PPV (84.2%). This suggests that VBS, particularly when focused on the central 4.0 mm zone, could be a valuable tool for keratoconus screening, and identifying cases in their early stages.

CONCLUSION Overall, our data demonstrate that corneal asymmetry is significantly increased in the setting of keratoconus and detection may be most effective when focusing on the central 4mm zone. In practical use, we envision that this technique can flag abnormalities beyond keratoconus for an eye doctor to examine, as various conditions may affect the anterior cornea. Given that no control corneas in this sample exceeded the VBS threshold of 11.4 at 4mm, values higher than this can be marked for further review.

NIMHD/NIH U54MD013376; Maryland Innovation Initiative MII_0922-002_2

05.02.03 – Poster Session 2 · Terrace (2nd Floor)

INTEGRATIVE BIOINFORMATICS ANALYSIS AS A PIONEER TOOL IN STUDYING CDC20 EXPRESSION AND GENE REGULATION NETWORK IN BREAST CANCER AGGRESSIVE SUBTYPES.

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Cell division cycle 20 homolog (CDC20) is a well-known regulator of cell cycle progression. Abnormal expression of CDC20 leads to mitotic defects, which play a significant role in cancer development. The oncogene CDC20 is overexpressed in various tumors, including breast cancer (BRC). It is a biomarker that has been linked to poor patient outcomes. In this study, we investigated the association of CDC20 with BRCA prognosis and immune cell infiltration by using multiple online databases, including The University of Alabama at Birmingham cancer data analysis portal (UALCAN), Kaplan-Meier plotter, Tumor Immune Estimation Resource (TIMER2.0), The Human Protein Atlas (HPA), Tumor Normal-Metastatic (TNM)-plot, bc-GenExMiner, LinkedOmics, Search Tool for the Retrieval of Interacting Genes/Proteins (STRING), Gene Expression Profiling Interactive Analysis (GEPIA). The results demonstrate elevated CDC20 expression in tumor tissues compared with the adjacent normal tissue. BRCA patients with overexpressed CDC20 had a median survival of 63.6 months compared to 169.2 of its counterparts with low expression. Prognostic analysis indicated that elevated expression of CDC20 was associated with poor prognosis and a reduction of overall survival in BRCA patients. These findings were even more prevalent in patients with triple negative breast cancer (TNBC) with chemotherapy resistance. Furthermore, the Gene Set Enrichment Analysis tool indicated that CDC20 plays a key role in the regulation of the cell cycle and apoptosis in BRC cells. Additionally, CDC20 also strongly correlates with increased levels of infiltrating levels of B cells, CD4+ T cells, neutrophils, and dendritic cells in BRCA. Our findings suggested that CDC20 may play a vital role in regulating immunomodulation in the tumor microenvironment. These findings support the role of CDC20 as a promising prognostic biomarker for BRCA. Future studies will focus on CDC20 inhibition as a potential therapeutic option for BC patients with CDC20 overexpression.

NIMHD U54 MD 007582

05.02.04 – Poster Session 1 · Terrace (2nd Floor) 🏆

THE ROBUST RIBOSOMAL SUBUNIT DERIVED PIRNAS DISTINGUISH NON-SMALL CELL LUNG CANCER ACROSS DIVERSE POPULATIONS FROM TISSUE TO PLASMA EXOSOME

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Non-small cell lung cancer (NSCLC) is a lethal cancer and lacks robust biomarkers for non-invasive clinical diagnosis. Our study stands as the first comprehensive analysis of piRNAs in the context of NSCLC diagnostics, pioneering the exploration of this type of small non-coding RNA as biomarkers. For the first time, we identified five novel piRNAs within a large-scale transcriptome sequencing dataset of 2,050 samples, employing machine learning techniques such as Random Forest and Logistic Regression. These piRNA were identified through the complexity of heterogeneity inherent in samples from multiple sources, underscoring the real-world applicability of our findings. Five piRNA signatures derived from ribosomal subunits identified to be tumor specific exhibited robust diagnostic ability and were combined into a piRNA-Based Tumor Probability Index (pi-TPI), demonstrating a promising area under the curve (AUC) value at 0.81 in training set. Subsequent validations underscored its efficacy in tumor diagnosis within tissue samples, including successful independent validations with AUC values above 0.80. Notably, this diagnostic tool showed remarkable performance in detecting early-stage tissue samples across various tissue cohorts, consistently achieving AUC values in excess of 0.80. The pi-TPI system also exhibited exceptional efficacy in diagnosing conditions using plasma validations reaching an AUC value of 0.85. In plasma-exosome diagnosis for distinguishing between healthy and cancerous conditions, it achieved an even more impressive AUC of 0.96. Moreover, our research marks the inaugural inclusion of benign samples of exosome studies for NSCLC diagnosis discovery. The pi-TPI indicated outstanding diagnostic precision, evidenced by AUC values of 0.82 in mixed sample test and 0.78 in benign assessment. This model is particularly advantageous for the classification of indeterminate cancer samples. Consequently, our findings hold substantial clinical value, positioning the five piRNA signatures as a potent diagnostic tool for NSCLC, especially in the realm of non-invasive cancer diagnostics, highlighting their significant potential.

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ABSTRACTS

05.02.05 – Poster Session 2 · Terrace (2nd Floor)

MICROGLIA CLASSIFICATION WITH ELO-RATING

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PURPOSE Microglia express diverse phenotypes and their morphology is key to understanding their role in neurological diseases. Previous studies have suggested classifying cells into discrete categories, such as ramified, hypertrophic, and amoeboid cells. Categorizing cells with the human eye, however, may yield inconsistent results, necessitating a new curation method to avoid noisy human factors. This study aims to utilize the Elo-Rating system to classify cell morphology based on instinctive judgement of cell activation levels.

METHODS 20X bright field microscopy images were obtained on 40 µm thick brain sections stained with anti-Iba1 from Long Evans rats, 24 hours post-12-minute asphyxia cardiac arrest. A Python-based web application employs an Elo-Rating grading system that classifies microglia activation levels by comparing two cell images simultaneously. Once the user has selected the image of the more inflamed cell and classified both cell images, the program ranks the images using Elo-rating.

RESULTS This app aims to generate a unified classifier that efficiently labels microglia. It features additional classification buttons, including six activation categories, “Clusters” and “Debris” to minimize classification error. A file is generated that records image pairings, the selected images, and image classifications. The Elo-Rating of an image increases after selection and decreases when unselected. The amount it changes depends on individual image rankings within a comparison. After collecting adequate curator data, the program determines the cells more likely to be classified into an activation category based on a higher Elo-Rating score.

DISCUSSION This research introduces a novel curation method enhancing cell labeling accuracy. It mitigates the bias from the standard approach of visually determining cell classification by addressing ambiguity. Classifying both images, not only the selected image, reduces bias in correlating inflammation level and classification, preventing skewed results. The app enables precise microglia classification and builds a comprehensive database for deep learning model training.

This study was supported by NIH/NIMHD U54MD007597, NIH/NICHD 1P50HD105328, NIH/NINDS 1R01NS123442, NIH/NINDS 5R01NS112294, NSF 2200489 and NSF 2200585.

05.02.06 – Poster Session 1 · Terrace (2nd Floor)

LEUKEMIA MUTATIONAL BURDEN COMPARISION AMONGST GO TERMS

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PURPOSE: Acute lymphoid leukemia (ALL) is a malignancy caused by uncontrolled proliferation of immature B or T lymphocyte precursors. Epidemiological studies have found increased ALL mortality in Hispanic Americans. Gene Ontology (GO) terms group sets of genes by cellular components, biological processes and molecular functions. The purpose of this study is to leverage Genomics Data Common (GDC) ALL data to explore differences in the calculated tumor mutation burden (TMB) within GO terms between Hispanic and non-Hispanic whites.

METHODS: Clinical and demographic data was obtained for each patient by making API calls to the GDC endpoint by requesting fields of interest while applying filters specific for the TARGET-ALL-P2 study. Variant call formatted (VCF) files containing mutational data from GDC were downloaded and fed into the UTEP OncoMiner pipeline. Only mutations in coding regions of genes were isolated for this study. For each sample, a list of genes with their individual TMB was constructed and used to construct sample specific GO term TMB. GO term TMB subsetted by various clinical and demographic information were then analyzed for differences by comparing between Hispanic and non-Hispanic samples.

RESULTS: 534 patients (20.2% Hispanic, 79.6% non-Hispanic) were included in the study. While overall mean TMB values were lower in the Hispanic subgroup compared to non-Hispanic, comparison of individual GO terms revealed 27 sets of proteins contained higher TMB in the Hispanic group while only one GO term was significantly higher in the non-Hispanic subgroup.

DISCUSSION/CONCLUSION: Comparisons revealed important differences in TMB values amongst GO term between the two groups. Survival analysis and transcriptomic differences are being performed to determine if any set of genes can be predictive markers for ALL patient outcome. An in-depth understanding of such differences could also significantly impact ALL prognosis and treatment options.

NIH-MIMHD (5U54MD007592) to UTEP’s Border Biomedical Research Center

Computational Biology

05.03.02 – Poster Session 2 · Terrace (2nd Floor)

EXPLORING DESTABILIZING P53 MUTATIONS BY COMPUTATIONAL TOOLS

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PURPOSE The tumor suppressor protein p53 activates several genes to transcribe hundreds of response elements that are important for fixing DNA damage and controlling abnormal cell growth. The p53 mutations are more common in African Americans (43.9%) than Caucasians (27.6%), which may increase the risk of the incidence and progression of aggressive types of cancers, like triple-negative breast cancer (TNBC), among them. The purpose of this study is to identify deleterious mutations in the p53 protein and explore how these mutations destabilize the protein structure and reduce DNA binding.

METHODS Potential mutations in the DNA binding domain (DBD) of the p53 protein, selected from the UniProt database, are studied with sorting intolerant from tolerant (SIFT), polymorphism phenotyping v2 (Polyphen-2), predictor of human deleterious single nucleotide polymorphisms (PhD-SNP), and MutPred2. The most deleterious mutations identified by these tools were further investigated by molecular dynamics simulations, using AmberTools20 to identify the impact of mutation on protein structure and to calculate MM/GBSA binding free energies of p53 with DNA.

RESULTS C141Y, C238S, and L265P were identified as the most deleterious p53 mutations that may impact protein structure. MD simulations showed an increase structural flexibility in these mutant proteins compared to the native protein. The MM/GBSA binding affinities of all three p53 variants demonstrated significantly reduced binding interaction with DNA due to the alteration in mutant p53 protein structures. Moreover, pairwise decomposition analysis revealed significantly reduced interactions in LYS120-ADE1104, LYS120-THY1105, and SER121-THY-1106 pairs in mutant protein structures, which contribute to higher DNA binding affinities in wildtype protein.

CONCLUSION This in-silico study identified C141Y, C238S, and L265P as deleterious p53 mutations and explored how they alter protein structures and reduce interaction with DNA. These findings assist to explain tumorogenesis caused by p53 mutations and will aid in the development of targeted therapies.

This work used Anvil at Purdue University through allocation [CHE210078 to S.M.I] from the Advanced Cyberinfrastructure Coordination Ecosystem: Services & Support (ACCESS) program, which is supported by National Science Foundation grants #2138259, #2138286, #2138307, #2137603, and #2138296. This research has been funded by RCMI (U45MD015959).

05.03.03 – Poster Session 1 · Terrace (2nd Floor)

COMPUTATIONAL SATURATION MUTAGENESIS OF TARGET PROTEINS ASSOCIATED WITH HUMAN DISEASES

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PURPOSE: Utilizing state-of-the-art machine learning techniques like AlphaFold, accurate structure models can be generated. The ongoing progress in these advanced bioinformatics methods enables the exploration of how protein mutations affect systemic functions by mapping them onto computational structure models. This study aims to develop and utilize the computational approach to investigate the consequences of disease-causing mutations on both protein stability and protein-protein interactions.

METHODS: In this study, we developed computational saturation mutagenesis techniques integrating structure-based energy calculations and sequence-based machine learning predictions to analyze the effects of missense mutations on protein structure and function. Genome editing and RNA-seq were employed for experimental validation of mutation effects associated with human diseases.

RESULTS: We effectively evaluated the systemic consequences of viral mutations on the functional attributes of the coronavirus spike protein function and probed the effects of genetic variants associated with mental disorders on AlphaFold-generated structural models. Furthermore, we utilized our computational platform to identify potentially pathogenic missense mutations in peroxidases, elucidating their influence on wing phenotypes and gene expression in transgenic fruit flies.

CONCLUSION: This computational platform offers a fast and effective method for studying the functional impacts of mutations in specific proteins, assisting biomedical researchers in comprehending how missense mutations contribute to the development of diseases. These findings could lead to the identification of potential target sites for drug and vaccine development against various human diseases.

This study is supported by the National Science Foundation (DBI 2000296) and in part by the National Science Foundation (IIS 1924092 and HRD 2011933), National Institute on Minority Health and Health Disparities of the National Institutes of Health (2U54MD007597).

ABSTRACTS

05.03.04 – Poster Session 2 · Terrace (2nd Floor)

NANOBODY DESIGN MAY TARGET EGFR TO CONTROL TNBC

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PURPOSE Epidermal growth factor receptor (EGFR) is a cell surface receptor comprising a 170 kD polypeptide chain of 1210 amino acids. EGFR has been reported to be overexpressed in up to 78% of triple-negative breast cancer (TNBC). Approximately 20 to 40 percent of breast cancer diagnosed in African American women are triple negative. EGFR plays a major role in TNBC by having a downstream signal path that increases cell proliferation, survival, and migration. The purpose of this research is to identify a nanobody to inhibit EGFR activation.

METHODS Visual Molecular Dynamics was used to analyze different structures of EGFR in complex with the nanobodies. It was also used to identify critical residues for binding between the nanobody and EGFR. Single and combined mutagenesis are run with the intention to enhance the binding affinity between nanobody and EGFR. Molecular dynamics simulations were also run to calculate the MMGBSA binding free energy.

RESULTS Analyzing the structure of numerous nanobodies in complex with EGFR has yielded valuable insights for enhancing their efficacy. Leveraging computational design techniques, several nanobodies have been engineered. Various computational methodologies have demonstrated enhanced binding affinity between these nanobodies and EGFR. Consequently, it is anticipated that the nanobodies will exhibit reduced experimental KD values.

DISCUSSION This in-silico study is expected to enhance the binding affinity of a nanobody that will keep EGFR inactive. If EGFR is inactive then it will not be able to promote cell oncogenesis. Ultimately, the expected results from this in-silico study will help to inhibit the growth of TNBC.

This work used Anvil at Purdue University through allocation [CHE210078 to SMI] from the Advanced Cyberinfrastructure Coordination Ecosystem: Services & Support (ACCESS) program, which is supported by National Science Foundation grants #2138259, #2138286, #2138307, #2137603, and #2138296. This research has been funded by RCMI (U45MD015959).

05.03.05 – Poster Session 1 · Terrace (2nd Floor)

IN SILICO SATURATION MUTAGENESIS OF SARS-COV-2 ORF3A PROTEIN

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PURPOSE: Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), has been causing a global health emergency. The viral ORF3a protein plays a crucial role in the pathogenesis of SARS-CoV-2, contributing to cell and tissue damage, disease severity, and the cytokine storm associated with COVID-19-related deaths. Thus, the analysis of ORF3a protein mutations is useful for understanding the mechanism of pathogenesis of SARS-CoV-2.

METHODS: In this study, we applied the in silico saturation mutagenesis approaches, including structure-based energy calculations and sequence-based machine learning predictions, to investigate the effects of ORF3a coding mutations on protein stability and protein-protein interaction.

RESULTS: We observed that G188W, P138W, and P159W had the highest destabilizing values in the monomer. G188H, G187W, and P159Q decreased binding affinity in the dimer structure while N119M, S58Q, and R122F displayed an increase in binding affinity. Moreover, we did both sequence and structure alignments of ORF3a-SARS-CoV2 and ORF3a-SARS-CoV1 proteins, which showed high similarity. Besides, we compared ORF3a-SARS-CoV2 and ORF3a-SARS-CoV1 proteins and found that G188, G187, and P159 have the highest destabilizing values on both proteins.

CONCLUSION: These findings enhance our understanding of the molecular mechanisms underlying ORF3a's role in the pathogenesis of SARS-CoV-2.

This study is supported by the National Science Foundation (DBI 2000296) and in part by the National Science Foundation (IIS 1924092 and HRD 2011933), National Institute on Minority Health and Health Disparities of the National Institutes of Health (2U54MD007597).

05.03.06 – Poster Session 2 · Terrace (2nd Floor)

MUTATIONAL CHANGES IN RECEPTOR-BINDING DOMAIN OF SARS-COV-2 VARIANTS AND STRUCTURAL STABILITY OF THE RBD–ACE2 INTERACTION

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Texas Southern University (KAI, SW, OAO)

PURPOSE Every virus, including SARS-CoV-2, the virus that causes COVID-19, change over time. Most changes have little to no impact on the virus's properties. However, some changes may affect the virus's properties such as transmissibility, the associated disease severity, molecular interaction with host receptors and more. More infectious SARS-CoV-2 variants have emerged globally since SARS-CoV-2 pandemic e.g. XBB.1.5, XBB.1.16, EG.5, BA.2.86 are currently circulating variants of interest (VoIs). This study evaluates the impact of mutational change(s) on receptor binding domain (RBD) of various variants of SARS-CoV-2 on the molecular interactions between the viral Spike protein and human angiotensin converting enzyme-2 (hACE-2), structural stability of the complex and binding affinity between the proteins.

METHODS The RBD of different variants was docked with the hACE-2 using haddock servers. To understand and establish the effects of the mutations on the structural stability and flexibility of the RBD-hACE-2 complex, molecular dynamic (MD) simulation of the docked complexes was performed (using TSU-BioRACC computing cluster) and evaluated after 50 ns trajectory.

RESULTS The result of the binding energy showed that RBD of variants BQ.1.1 (-48.45 Kcal/mol), CH.1.1 (-39.54 Kcal/mol), EG.5 (-42.90 Kcal/mol), EG.5.1 (-43.75 Kcal/mol), XBB.1 (-44.41 Kcal/mol), XBB.1.5 (-41.01 Kcal/mol), XBB.1.9.1 (-42.48 Kcal/mol), XBB.2.3 (-46.92 Kcal/mol), and BA.2.75 (-48.37 Kcal/mol) have higher binding affinity towards hACE-2 than the wide type (WT) with binding energy of -35.24 Kcal/mol. The study further showed that increase in the binding affinity of the variants is directly associated with increase in the number of Hydrogen (r = 0.51), Van der Waal (r = 0.56 and electrostatic (r = 0.30) bonds that exist between the complexes.

DISCUSSION/CONCLUSION The structural stability and flexibility of variants' systems as evidenced by the decreased average RMSD values showed that mutations on the variants (except XBB.1.5, XBB.1.9.1 and XBB.1.9.2) does not disturb the stability of RBD-hACE-2 complex. This study, therefore, assumed these variants have high receptiveness towards hACE-2 than the BA.5, BQ.1, XBB.1.6.1 and BA.2.86 variants and the WT, and thereby, responsible for their increase in transmission. This study provides molecular insight on impact of the mutational changes associated with each variant on stability and molecular interactions between viral protein and hACE-2

This project is sponsored by the NIH-RCMI (U54MD007605) grant.

Genomics

05.05.01 – Poster Session 1 · Terrace (2nd Floor)

GENETIC TESTING FIRST APPROACH FOR RARE DISEASES IN PUERTO RICANS

EM ALBINO; E Farrow; F Velez-Bartolomei; C Chapel-Crespo; F Scaglia; S Carlo; A Santiago-Cornier; CJ Buxo
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Purpose: Diagnosing rare diseases is complex due to diverse clinical symptoms, including neurogenetic phenotypes. Our goal is to develop and apply a genetics-first testing algorithm to streamline the identification of genetic variants contributing to rare diseases, particularly mitochondrial disorders, among Puerto Ricans. Additionally, we aim to explore patients' perspectives on the diagnostic process and their access to molecular testing.

Methods: This cross-sectional study aims to characterize clinical laboratory results from metabolic disease profiles in individuals suspected of mitochondrial disorders from 2018 to 2023. We will recruit a subset of 200 individuals for comprehensive analysis, including medical and family history, metabolic biomarkers in blood and urine, hearing tests, imaging, and chromosomal microarray. Genetic testing utilizing whole genome and mitochondrial DNA sequencing will be performed on a subset of 100 randomized trios (probands and parents). Descriptive and multivariate analyses will be conducted to identify associations between variants and reported phenotypes, adjusting for potential confounders.

Results: Altered biochemical profiles in pediatric Puerto Ricans suspected of rare diseases will help differentiate mitochondrial or metabolic causes from other conditions. Implementing a testing algorithm combining whole genome sequencing and mitochondrial DNA aims to identify disease-causing variants, enhancing rare disease diagnosis in Puerto Ricans. Additionally, we aim to identify rare or novel variants specific to our Hispanic population. Exploring patients' perspectives on their diagnostic journey will illuminate challenges of limited molecular testing access and living through a diagnostic odyssey.

Conclusions: Our findings aim to investigate the application of genetic testing algorithms to comprehend the genetic factors influencing disease susceptibility in our population. Additionally, we aim to explore the establishment of a biorepository for storing samples to facilitate future rare disease research. The documentation of participants' diagnostic journeys will shed light on the challenges faced by individuals lacking access to molecular testing, advocating for enhanced healthcare services.

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ABSTRACTS

Proteomics

05.07.01 – Poster Session 2 · Terrace (2nd Floor) 🏆

PROTEOMIC ANALYSIS OF TUSC2 KNOCKOUT MOUSE HIPPOCAMPI

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Meharry Medical College (VMP, SVI, TF, JT, AS, AVI)

PURPOSE Compare to general population, older Black Americans have twice higher risk of Alzheimer's disease (AD), the most common type of dementia with no cure. As mitochondrial function is critical for neuronal health during aging, mouse models of mitochondrial dysfunction may provide valuable insights into how AD and other neurodegenerative diseases can be timely diagnosed and treated. In our mouse model, inactivation of Tusc2, a small mitochondrial protein involved in calcium signaling, caused premature aging and cognitive decline, which is similar to the Tusc2 related findings in humans. Our proteomic study is aimed to determine how Tusc2 inactivation affects mitochondrial health, calcium signaling and neurodegeneration in hippocampus (HC), the most vulnerable to dementia brain area.

METHODS Tusc2 knockout (KO) and wild type (WT) mouse HC protein extracts were analyzed using Multi-dimensional Protein Identification Technology (MudPIT) and Orbitrap Exploris nano-LC/MS (liquid chromatography/mass spectrometry) platform.

RESULTS A total of 3,279 protein groups were identified in HC extracts obtained from male Tusc2 KO and WT mice. Label-free quantification has shown 1047 diferentially expressed proteins including 894 proteins down-regulated and 153 proteins up-regulated in Tusc2 KO mice. Gene enrichment analysis showed Tusc2 KO associations with neurodegenerative disorders (Parkinson, Huntington, prion diseases, amyotrophic lateral sclerosis and AD) and depletion of mitochondrial oxidative phosphorylation proteins. Proteins up-regulated in Tusc2 KO were linked with synaptic dopamine-, glutamate- and GABAergic signaling and long-term potentiation/depression.

CONCLUSION Results of our proteomics analysis suggest that Tusc2 plays a critical role in maintaining mitochondrial activity and neuronal health. Tusc2 levels in blood present a potential biomarker for early detection of age-related dementia. Tusc2 KO mouse model appears useful for better understanding of molecular mechanisms of dementia and development of diagnostic and therapeutic tools for AD treatment urgently needed for minority patients.

Meharry RCMI program U54MD007586 (VMP, AVI, AS), NCI grant U54CA163069 (AS), and NIH grant SC1CA182843 (AS)

05.07.02 – Poster Session 1 · Terrace (2nd Floor)

A COMPREHENSIVE GENE ENRICHMENT ANALYSIS OF BRAC1 INTERACTORS' NETWORK.

Bishnu Sarker; Jaylin Dyson; Aleesa Mann; Sara Taylor; Jamaine Davis
Meharry Medical College(Bishnu Sarker, Jaylin Dyson, Aleesa Mann, Sara Taylor, Jamaine Davis)

Protein-protein interaction (PPIs) are essential to almost every process in a cell. Uunderstanding PPIs is crucial for understanding physiology in normal and diseased states. Protein-protein interaction networks are mathematical representations of the physical contacts between proteins. A typical protein can interact with hundreds to thousands of other molecules within the cell. Computational tools offer the ability to rapidly test thousands of PPI of key proteins. The Breast Cancer Susceptibility protein 1, BRCA1, is an important protein for preventing tumor formation. This protein has functions across a variety of cellular processes. In this work, we sought to determine the variety of PPI specific for protein domains within BRCA1, termed the BRCA1 C-terminal domains. Here we present a comprehensive gene set enrichment analysis of the BRCA1 interactors. As a first step, we identified sources of biomedical data relating to BRCA1 sequences, structures, functions, interactions, DNA-damage response, and cell signaling to characterize the network of interactors of breast cancer causing BRCA1 gene. We retrieved the interactor proteins from BIOGRID database. There is a list of 1157 unique interacting proteins mapped to 1175 unique genes. We accessed Enrichr program programmatically using Python GSEAPY to perform gene set enrichment analysis. A comprehensive gene enrichment analysis was performed that includes functional enrichment (Gene Ontology), pathway enrichment (Reactome, KEGG), molecular signature (MSigDB), domain enrichment (InterPro, Pfam). A detail report was generated to show the signigicantly enriched characteristics. Additionally, a network visualization of the 1175 interactors of BRCA1 is generated using STRING database to help elucidate the intiricate relationship as well as to identify closely knitted clusters of the genes of high similarity. This analysis presents an unprecedented structure- and context-dependent view of protein interaction networks. These structure-informed networks will reveal mechanistic insights regarding cellular processes underlying human diseases ranging from cancer to those resulting from viral and bacterial infection. The results also provide a framework for the development of new hypotheses in understanding BRCA1 genotypes and associated phenotypes, as well as strategies for drugs that can target proteins in these networks.

RCMI Sub Award

05.07.03 – Poster Session 2 · Terrace (2nd Floor)

PROTEOMICS OF SARS-COV-2 VIRION REVEALED PROTEIN PHOSPHATASE-1

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PURPOSE Severe acute respiratory syndrome coronavirus 2 (SARS CoV 2) has led to over 566 million confirmed cases and caused over 6.4 million deaths worldwide and continues to evolve as more pathogenic and infectious variants of the viruses. Despite the progress in the role of host kinases in the viral lifecycle, understanding how the virus exploits the protein phosphatases for its propagation is largely incomplete.

METHODS To address this gap, and to better understand the biology of SARS-CoV-2, SARS-CoV-2 virions were purified from infected Vero-E6 cells and their protein composition and protein phosphorylation was analyzed by high resolution liquid chromatography-linked tandem mass spectrometry (nano LC-MS/MS).

RESULTS We detected several viral proteins including M, N, S and open reading frames (ORFs). Over 500 phosphorylation sites are predicted for SARS-CoV-2 viral proteins. Among them 83 serine phosphorylated peptides belong to M, N, S and ORFs viral proteins. Within N protein, there were also 16 threonine phosphorylated sites. We also detected 6580 phospho-modifications of host proteins packaged in SARS CoV-2 virions. Of all the host proteins identified CAVIN2, DIMT1, LARP1B, H1-5, MOV10, NOP16, RASSF7 have been previously shown to interact only with the viral N protein. We also detected protein phosphatase-1 (PP1) and its interacting proteins that included MAP3K, TRIM21, PP1 Inhibitor-1 (PPP1R), PLCL2, GRB2.

DISCUSSION / CONCLUSION To identify PP1 binding sites on N viral protein we analyzed the presence of potential PP1 binding motifs within N sequence and found 4 motifs which have the lowest p-value. We identified an RVxF motif, 14RITF17, MyPhone motifs, 36RSKQRRPQ43 and 80PDDQIGYY87, and SILK motif, 129GIIW132. The most statistically significant potential binding site found was a 14RITF17 motif on the N-terminus of N protein. SARS-CoV-2 analysis showed presence of PP1 that may be recruited by N protein or PP1-binding proteins packaged in the virion.

This work was supported by NIH grant 5U54MD007597

Health and Healthcare Policy Research

Health Policy

06.02.01 – Poster Session 1 · Terrace (2nd Floor) 🏆

ASSESSING 30-YEAR TRENDS IN SUBSTANCE USE DISORDERS: THE EVOLVING BURDEN, STATE DISPARITIES, AND POL

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Purpose: Utilizing data from the Global Burden of Disease Study (GBD), this research investigates trends in Substance Use Disorders (SUDs) in the United States from 1990 to 2019, focusing on opioids, alcohol, cannabis, cocaine, and amphetamine use disorders. We explore these trends by sex, age, and year, and also align state SUDs policies and mental health budget in the states with the three highest and three lowest SUDs burdens.

Methods: We used the Python Programming Language within the Jupyter Notebook interface. We utilized Disability-Adjusted Life Years (DALYs) to evaluate the burdens of SUDs by considering sex, age, and years. Our methodology involved referencing the Trust for America's Health (TFAH) report and accessing states' mental health budgets. This allowed us to align states demonstrating both the lowest and highest burdens in terms of substance use and alcohol use disorders DALYs with their respective policies and mental health budgets.

Results: Our findings reveal a significant increase in SUD burdens from 1990 to 2019, with a concurrent decrease in alcohol use disorder burdens. The gender gap in SUDs has narrowed, and the 20-39 age group bears the highest burden. West Virginia, Kentucky, Ohio, New Mexico, Alaska, and the District of Columbia exhibit the highest SUD-related DALYs, while Nebraska, South Dakota, North Dakota, New Jersey, Maryland, and Texas demonstrate the lowest. We observed variations in the burden of SUDs, SUD policies and mental health budgeting among states and regions with the lowest and highest burdens in the United States.

Discussion: The use of DALY estimates in our study revealed notable difference in the burden of SUDs across sex, age, years, and states. Aligning these findings with the states policies and corresponding mental health budgets provided us with valuable insights, underscoring the importance of implementing more robust policies to address SUDs.

ABSTRACTS

Health-Related Technology Application

Health-Related Technology Application in Minority Health and Health Disparities

07.01.02 – Poster Session 1 · Terrace (2nd Floor) 🏆

TELEMEDICINE RELATED OPIOID USE DISORDER SERVICES IN UNDERSERVED POPULATIONS: A QUALITATIVE EVALUATION OF THE WAIVER ERA

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Introduction: This study examined access to opioid use disorder (OUD) related telemedicine in Houston's underserved communities, and the impact of OUD-related telemedicine on treatment initiation and retention during the waiver era (before July 2023).

Methods: Partnering with local OUD treatment clinics, participants were recruited through targeted emails to providers, flyers posted in the clinic, and snowballing sampling. A total of 14 in-depth qualitative interviews with 5 treatment providers, and 9 self-identified Black or Hispanic patients were conducted via Zoom between August-October 2023. Informed consent was obtained from all participants, and they were offered grocery gift card incentives for their time. Patients were asked about their previous experiences with telemedicine in general, as well as their experiences with and preferences for telemedicine as part of their OUD treatment. Providers were asked about their experiences providing OUD treatment services via telemedicine and their perception of patients' attitudes toward this modality. Both groups were asked about their experiences prior to and directly following the end of the waiver era. A rapid qualitative analysis approach was conducted by the qualitative research team members.

Results: Subjects indicated overwhelmingly that they were often not offered telemedicine options for OUD but did express a general comfort with telemedicine and technology for other healthcare needs. Patients highlighted their comfort with using telemedicine platforms, as well as the convenience in terms of transportation and time-saving potential as facilitators to using telemedicine. The digital divide was not a reported barrier, although language barriers for Spanish-speaking patients was noted as a potential barrier. Providers expressed a willingness to provide telemedicine services but cautioned that each patient requires a personalized plan based on needs and that no one-size-fits-all approach should be adopted. Both patients and providers acknowledged the potential value and opportunities of telemedicine for future OUD treatment. Neither group noted any major changes to their treatment experiences since the waiver elimination.

Discussion: Our study highlights the underutilization of telemedicine for OUD treatment and initiation in underserved communities in Houston, despite provider willingness and demonstrated comfort and acceptance of technology by patients.

NIMHD NOSI 3U54MD015946-04S2

07.01.03 – Poster Session 2 · Terrace (2nd Floor)

IMPLEMENTATION OF THE FAMILY HISTORY AND CANCER RISK STUDY (FOREST) AT MEHARRY MEDICAL COLLEGE

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PURPOSE: Family Health History (FHH) is a key factor in assessing cancer risk, yet health providers often do not have adequate time or resources to collect FHH systematically. African Americans and other medically underserved populations suffer significantly higher cancer incidence and mortality. These populations would benefit if their cancer risk were better defined. The Family History and Cancer Risk Study (FOREST) aims to implement a patient-facing web-based FHH cancer risk assessment platform called MeTree in a clinic with a high percentage of underserved patients at Meharry Medical College (MMC) and a cohort at Vanderbilt University Medical Center.

METHODS: Partnering with the MMC Community Engagement Core (CEC), we conducted two virtual studios with 12 Nashville minority community members. Topics of concern were medical data privacy, potential benefits, and proper informed consent. CEC recommendations informed our pre-implementation planning. Recruitment methods consisted of a staffed table outside of and, later, inside the MMC Family Medicine Clinic waiting room. Patients could also request assistance from the study research coordinator (in person or virtually).

RESULTS: 139 potential participants were invited to FOREST from MMC. 44 patients were interested, 34 were eligible, 32 patients consented, and 18 patients completed MeTree. Six patients utilized in-person assistance from the research study coordinator. Three patients who completed MeTree were determined to be at high-risk for cancer.

CONCLUSION: We observed a 31% enrollment rate and 40% completion rate. Six of 32 patients requested and received assistance. In-person recruitment had the highest volume of potential enrollments (36 interested), yet lower completion rates (33%) compared to the pamphlet QR code (5 interested with 60% completion). We realize that these numbers are not large enough to show statistical significance at this early stage, but do expect this trend to continue.

U54MD007586, U01CA232829

07.01.05 – Poster Session 1 · Terrace (2nd Floor)

REMOVING ALGORITHMIC BIAS AND EVALUATING CLEFT SPEECH THERAPY GAME

JS DUVAL; TA Ikwunne; M Vigil-Hayes; JB King
Northern Arizona University (JSD, TAI, MVH, JBK)

PURPOSE: This project leverages SpokeIt, a telehealth cleft speech therapy game, to enhance speech therapy access and effectiveness for children with orofacial clefts in the Southwestern United States. The project aims to improve clinical outcomes, bridge the speech therapy health equity gap, and assess potential algorithmic biases against Indigenous and Hispanic accents.

METHODS: The research employs a comprehensive, mixed-methods approach to assess and refine SpokeIt. Initially, the project will thoroughly evaluate the game's machine-learning algorithms for potential biases against dialects and accents prevalent among the target populations via comparing linguistic analysis of the game's recorded audio files by speech-language pathologists and the predictions produced by our models to compute agreement across multiple variables, including language spoken at home, accent, and types of speech errors (e.g., articulation, nasal emissions, resonance, compensatory), with a goal of 85% agreement for each. Parallel to these efforts, the project will engage in community outreach and partnership development with Indigenous communities and organizations to co-create culturally sensitive and accessible refinements.

EXPECTED RESULTS: The project is expected to yield significant findings on the performance and inclusivity of SpokeIt by identifying and correcting any algorithmic biases, thus enhancing the game's diagnostic accuracy and therapeutic relevance for a diverse user base. Furthermore, through collaboration with Indigenous communities, the project anticipates developing a model for culturally sensitive health technology development. The expected outcomes include improved speech therapy access, higher engagement rates among children, and, ultimately, better user speech outcomes.

DISCUSSION: This project represents a critical step forward in applying telehealth and gamification to address longstanding healthcare access and outcomes disparities exacerbated by geographical, financial, and cultural barriers. Integrating technology with traditional therapeutic practices offers a scalable model for expanding access to specialized healthcare services with an emphasis on cultural sensitivity and community partnership for a holistic approach to healthcare innovation.

GRANT SUPPORT: Supported by the Southwest Health Equity Research Collaborative (#5U54MD012388-07) and building upon foundational work funded by the National Science Foundation (#1617253), this project exemplifies a collaborative, interdisciplinary approach to tackling health disparities through innovation. The support from these grants not only validates the project's scientific merit and potential impact but also underscores the commitment to advancing health equity through research and technology.

07.01.06 – Poster Session 2 · Terrace (2nd Floor)

PROTOTYPE OF A PERSONALIZED FITTING CERVICAL COLLAR

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University of Puerto Rico Medical Sciences Campus, San Juan, Puerto Rico (RN, CC, WF, EFR, AS) University of Puerto Rico Rio Piedras Campus San Juan, Puerto Rico (VRV, JR, SP); Ponce Health Sciences University, Ponce, PR (GL)

PROBLEM: There are several pathologies requiring neck immobilization. The general availability for achieving neck immobilization is relatively thick, heavily padded collars in small, medium, and large sizes. The objective of this project is to produce personalized open-cell 3D-printed cervical collars that are created from the measurements of each patient. METHODS: Various prototypes were made in our facilities using a high-resolution Artech 3D Eva scanner that was able to obtain virtual models of the head and shoulders that matched the 3D dimensions of the subject within several millimeters. The virtual STL model of the open-cell collar generated by Rhino 6 Grasshopper software, with an offset Voronoi tessellation mesh, was printed with an Anycubic Kobra 2 Max 3D printer and fitted to the subject. Myosignal amplitude kits were built to detect strain in specific muscle groups in the neck. Initial evaluation of these collars was made by monitoring the myosignals of the sternocleidomastoid muscle group of the neck with and without wearing the open-celled collar. RESULTS: Preliminary results showed a reduction of activity in this muscle group of approximately sixty-five percent (65%) while wearing the collar. Although the preliminary methodology and data are very promising, having access to a high-resolution 3D scanner to obtain a model for the patient is time-consuming and expensive. Currently, we are engaged in developing a computer model using direct-selected measurements of subjects to improve the existing model and reduce the price. CONCLUSION: We expect that by using personalized cervical collars patients will be able to experience greater comfort during neck immobilization, reducing the rehabilitation period and benefiting minority populations with limited health benefits. Future efforts will also focus on developing open-cell collars that will allow for a greater quantity of fresh air to circulate through the neck area preventing severe allergic contact dermatitis.

Infrastructure support provided by RCMI- NIMHD Grant U54-MD007600.

ABSTRACTS

Research in Special Population Sub-Groups

Child and Adolescent Health

08.02.01 – Poster Session 1 · Terrace (2nd Floor)

DEMOGRAPHIC DIFFERENCES IN THE VISUAL FIRE PERCEPTION OF YOUNG CHILDREN

JW Bonny
Morgan State University (JWB)

Purpose In the United States, demographic disparities are present in residential fire casualty rates. Along with the elderly, casualties are more likely with young children. In addition, higher casualty rates have been observed with minority children and those from lower socioeconomic backgrounds. The present study investigated whether such differences are also present in young children's visual perception of fire. Identifying whether a real threat is present is crucial for initiating a response to a fire. Adults have been found to use visual cues, such as flame size, to perceive the risk posed by fires. Between three to six years of age, children become better able to detect small differences in the sizes of objects. Perceptions of fire cues may follow a similar developmental trend. The present study examined the following hypotheses with young children: the precision of fire perception improves with age and demographic disparities will be present.

Methods Eighty children and parents completed a task where they judged which of two trains contained more fire. The fires were presented as videos, generated by simulation software. The relative difference between the intensity of fires was varied across trials. Parents provided sociodemographic information.

Results Older children were more likely to accurately identify the train that had more intense fires. Although no significant racial differences were observed, children from the youngest age group, three-year-olds, from lower socioeconomic households tended to have lower accuracy.

Discussion The developmental improvement in fire precision paralleled trends in size perception. This novel research suggests that socioeconomic disparities may extend to fire perception in young children. Future research should examine whether such disparities relate to socioeconomic differences in fire knowledge of children or associated cognitive processes. This can aid in identifying new approaches to fire prevention training with children from vulnerable groups.

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08.02.02 – Poster Session 2 · Terrace (2nd Floor)

BILINGUAL SUPPORT FOR VIETNAMESE CHILDREN IN THE US

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San Diego State University (GTP, NTD)

PURPOSE: Communication is a human right. Children in the US who speak a minoritized first language need two languages to communicate in the home, school, and society. Bilingualism/biculturalism provides opportunities for children to engage in larger society and their ethnic community, increasing social capital and promoting self-esteem and academic success. Yet 1 in 4 children with bilingual exposure end up speaking only English. Continued development of the minoritized first language critically relies on social and educational support. Being the second most spoken language in the US, Spanish has been the focus of most bilingual school programs. The present study focuses on a bilingual program for speakers of Vietnamese, spoken by 2 million in the US and 100 million worldwide.

METHODS: This study reports on the bilingual outcomes of children attending a dual immersion school in which they receive instruction in Vietnamese and English. Over 50 children, aged 4 to 9 years, completed measures of Vietnamese and English vocabulary, grammar, and narratives. Parents and teachers completed surveys of children's language history and current proficiency. Data collection is completed, and analysis is pending.

RESULTS: We will compare children's comprehension and production across measures and in both languages. Based on the literature, we anticipate that children will comprehend more than they can produce. We expect English outcomes will be robust i.e., increase with age and relatively stronger than Vietnamese outcomes for older participants. We also anticipate increases in Vietnamese because children are receiving school instruction in both languages.

DISCUSSION/CONCLUSION: For many bilingual children, the first language is the main connection to one's identity and heritage. When provided with adequate support, children have the capacity to develop two (or more) languages. Positive examples of bilingual support, like in the present study, highlight what is working to address minority health disparities in the US.

NIH-NIDCD R01DC019335 (PI: G. Pham)

08.02.03 – Poster Session 2 · Terrace (2nd Floor)

VEGGIE METER: DIET ASSESSMENT TOOL FOR PARENTS AND CHILDREN

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PURPOSE: The VeggieMeter (VM) is an objective measure of skin carotenoids, a biomarker to evaluate fruit and vegetable (FV) intake. VM overcomes issues related to estimating FV consumption of parents and their children. We hypothesized that FV intake would be correlated with VM scores for parents and children, with stronger correlations among parents vs children. The objective of this study was to quantify the correlation between parent and child VM scores and FV intake.

METHODS: We evaluated FV consumption of parents and children using the Dietary Screener Questionnaire (National Cancer Institute) and skin carotenoid content using the VM at baseline enrollment in a produce prescription trial for children ages 2 to 12 years (n= 59 parent-child dyads). Correlations between 1) parent and child FV consumption, controlling for age, 2) parent and child VM reading, controlling for age, 3) FV consumption and VM readings of parents, and 4) FV consumption and VM readings of children were conducted.

RESULTS: There was a strong, positive correlation between parent (2.23 ± 1.40 servings/day) and child (2.02 ± 1.26 servings/day) FV consumption while controlling for child age (5.49 ± 2.72 years), r(56)=.703, n=59, p<.001. Correlation between parent (220.8 ± 88.2) and child (168.0 ± 71.3) VM reading was slightly weaker, but still statistically significant while controlling for age, r(56)=.591, n=59, p<.001. There was a moderate correlation between parent FV consumption and VM reading (r=.44, p<.001), but for children the correlation was weak and non-significant (r=.13, p=.32).

DISCUSSION/CONCLUSION: These findings support the utility of VM as a biomarker for FV consumption among parents and children. The VM may be particularly useful when relying upon surrogate reporters for child diet.

National Institute of General Medical Sciences, National Institutes of Health (Grant #P20GM139753)

08.02.04 – Poster Session 1 · Terrace (2nd Floor)

FARM TO EARLY CARE AND EDUCATION (ECE) PROGRAMMING: ASSESSING CURRENT ACTIVITIES, RESOURCES, OPPORTU

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Purpose Farm to Early Care and Education (ECE) programming is a promising innovative policy, systems, and environment strategy to address health disparities, improve diet, increase food security, and develop healthy eating habits among children and their families. Farm to ECE activities enhance the ECE nutrition environment, offer nutrition education, and connect children and families to local food and farms. This study provides an understanding of current ECE activities and resources, facilitators and barriers to program implementation, and preferences and knowledge to expand and sustain farm to ECE programming.

Methods An online survey was distributed to all ECE providers in Louisiana through a statewide ECE newsletter. The survey addressed current activities, facilitators, barriers, resources, interest in future activities, and demographic characteristics. Descriptive statistics were calculated and reported.

Results Participants included providers of 104 ECEs from 62 zip codes. One-third reported current engagement in farm to ECE programming. While most participants did not report engagement, respondents recognized participation related activities: teaching children how food is grown (41%); purchasing local food (33%); planting edible gardens (29%); conducting field trips to gardens or farmers markets (18%); and holding taste tests of local food (18%).

Almost all (95%) respondents were interested in engaging in farm to ECE programming, and many perceived a variety of benefits to participation. Barriers included lack of funding (62%), knowledge (47%), and space (41%). Participants indicated that farm to ECE training (73%), especially through webinars (69%), and technical assistance (49%) would facilitate implementation.

Discussion/Conclusion This study provides insights into the current state of farm to ECE programming, highlights challenges to implement farm to ECE activities, and gives guidance on strategies to engage centers. The results informed the Louisiana Farm to ECE strategic plan to implement, sustain, and expand programming and may be similarly used by other states and regions.

NIH U54 MD007595-17, WK Kellogg Foundation

People with Disabilities

08.09.01 – Poster Session 2 · Terrace (2nd Floor)

CANNABIS CONNECTION: PATIENT PERSPECTIVES OF MEDICINAL CANNABIS USE

Nailah Smith, Valencia Perry
Howard University

This study aimed to gather insight into patient perspectives about remediating symptoms associated with neurological conditions that affect communication and related functions using medicinal cannabis, and how speech-language pathologist (SLPs) can support their patients while remaining in the scope of practice. The investigation involved a mixed methods design that drew upon data collected from ethnographic interviews and a single case intervention involving a pretest-posttest design. The interviews aimed to gain insight into the perspectives, feelings, and attitudes of adult patients and/or caregivers of people with neurological conditions who are taking or recommended to take some form of medication to address symptoms associated with focus, communication, and/or learning. The intervention portion of the study used a single-case research design that involved the presentation of an educational video lecture to subjects to inform them about medicinal cannabis.

National Institute of Health

ABSTRACTS

08.09.02 – Poster Session 1 · Terrace (2nd Floor)

DETERMINANTS OF DISPARITIES AMONG YOUTH WITH ASD AND/OR ID

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Florida International University (RA, AB, AMD, MFV, DMB, JWP, ARL)

PURPOSE Transition-aged youth (TAY) with autism (ASD) and/or intellectual disability (ID), especially those from racial and ethnic minority groups experience poor outcomes in postsecondary achievement, employment, independent living, and social integration. Given that caregivers play a pivotal role in their child's life, this novel study uses the ABCX Model to qualitatively explore the determinants and types of resources, strategies, coping mechanisms, and parenting styles caregivers employ that may influence youth outcomes.

METHODS We conducted one-on-one 60-minute semi-structured interviews with 30 caregivers of TAY (12 to 25 years old) with ASD/ID. Sessions were available in-person or via Zoom, and in English or Spanish. All sessions were recorded and transcribed. Caregivers were largely female (90%), between 45 to 54 years old (72%), and identified as belonging to a racial/ethnic minority group (76%).

RESULTS / EXPECTED RESULTS Analyses suggest that caregivers largely utilized a proactive parenting approach to seek out resources and emphasized the need for routine to support positive youth outcomes. In addition, several factors influence parenting behaviors, such as parents' own upbringing, family structure and dynamics, unexpected events such as COVID-19, severity of the TAY's disability, and cultural norms. For example, many Hispanic/Latino caregivers shared the need to accept that their TAY may not attend college as expected. Caregivers also reported that the support they received did not extend beyond the family circle, and many relied on their faith to cope with ongoing stress.

DISCUSSION / CONCLUSION Findings suggest the importance of aligning resources and parenting styles with the unique needs of each TAY, and enhancing support for families. By examining the intersectionality of disability, race, and ethnicity, this study highlights underlying mechanisms that may contribute to growth and explain disparities in TAY outcomes. Moreover, it sheds light on necessary yet missing intervention/prevention programs for caregivers.

FIU-RCMI Grant #U54MD012393

Rural Health

08.10.02 – Poster Session 2 · Terrace (2nd Floor)

CHILDREN GUT MICROBIOME DURING COMPLEMENTARY FEEDING PERIOD

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Morgan State University (AK, LY); University at Buffalo (GJ); Johns Hopkins University (DD); University of Maryland (MP)

PURPOSE: Investigating the human gut microbiome is essential to understanding microbiota homeostasis and disease predisposition. The gut microbiome plays an important role in childhood development, and dysbiosis has been associated with many diseases. We studied how breastfeeding practices and age affect the gut microbiome in children.

METHODS: We analyzed 16S rRNA microbiome data of 778 stool samples of Peruvian children aged 6, 12, 18, and 24 months. The samples were classified into the Breastfeeding group (BF) who received complementary foods in addition to breastmilk and Non-Breastfeeding group (NBF), who had been weaned completely (NBF). Faith Phylogenetic Diversity and Pielou's Evenness measurements were employed to examine within-sample diversity, also called Alpha Diversity. Weighted UniFrac phylogenetic distance followed by PERMANOVA tests was used to quantify the dissimilarities of the microbial communities between samples. Microbial composition relative abundance was measured to compare taxon abundance to taxa abundance observed.

RESULTS: We found that breastfeeding is crucial for shaping gut microbiome during complementary feeding period. We also found that the gut microbiome changes over age, but the effect of age on gut microbiome depends on breastfeeding practices. We characterized the bacterial composition of a healthy Peruvian cohort in the MAL-ED study and identified three enterotypes: Actinobacteria, Firmicutes, and Bacteroidetes within this population.

CONCLUSION: Breastfeeding plays a critical role in shaping the gut microbiome for children of 2 years old or younger. Although the gut microbiome naturally changes with age, our findings indicates that the impact of age on the gut microbiome is heavily influenced by breastfeeding practices. To our knowledge, this is the first study to identify enterotypes and characterize the bacterial composition in a large group of healthy Peruvian children. The findings contribute to a better understanding of how different breastfeeding practices shape gut microbiome during complementary feeding period.

GRANT SUPPORT: National Institute on Minority Health and Health Disparities (U54MD013376 to O.V. and H.Y.)

Sexual and Gender Minorities

08.11.01 – Poster Session 1 · Terrace (2nd Floor)

LGBTQ MINORITY STRESS, ALLOSTATIC LOAD, AND SUBSTANCE USE

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PURPOSE: Sexual minority (SM) adults experience disproportionately high rates of substance use. Substance use among SMs is linked to chronic stress resulting from their minority sexual orientation (i.e., minority stress), such as discrimination and internalized homonegativity. In addition, emerging research has demonstrated links between minority stress and stress physiology dysregulation. However, no studies to date have examined stress physiology and substance use in LGBTQ samples. Research in other populations suggests that stress physiology dysregulation—specifically, the concept of allostatic load (AL)—may be a promising avenue for understanding substance use vulnerability and trajectory. The purpose of the current research is to conduct a pilot feasibility test and provide proof of concept for the examination of longitudinal links between SM stress, AL, and substance use outcomes.

METHODS: A total of N=40 LGBTQ adults aged 18-60 will be recruited in Houston, TX, to complete three assessments over the course of one year. Assessments include self-report of minority stress, mental health, and alcohol, tobacco, and other drugs; blood draws to assess for immune and metabolic functioning (e.g., C-reactive protein, HbA1c); and anthropometric measurements (e.g., BMI, blood pressure). AL will be calculated using clinical cutoffs (0 or 1) and summing each of 17 biomarkers. In addition, acceptability will be measured by self-report and feasibility will be measured through recruitment, enrollment, and attrition data.

EXPECTED RESULTS: It is expected that data collection will be completed by spring 2025 and that the study will be rated as acceptable by participants and will demonstrate feasibility by successful recruitment and enrollment and minimal attrition. The study will also provide estimates of effect size that will be used to propose a fully-powered subsequent R01 proposal.

CONCLUSION: Understanding the links between SM stress, AL, and substance use will provide unique insights into the biopsychosocial mechanisms underpinning LGBTQ substance use.

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08.11.03 – Poster Session 2 · Terrace (2nd Floor) 🏆

FORMATIVE RESEARCH TO INFORM AN INTERVENTION FOR PREP UPTAKE AMONG LATINO MSM IN PUERTO RICO

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University of Puerto Rico-Medical Sciences Campus (UPR-MSC)

PURPOSE Pre-exposure prophylaxis (PrEP) is an effective biomedical tool to prevent HIV infection when used as recommended. Men who have sex with men (MSM) in Puerto Rico are at increased risk for HIV infection. Puerto Rico has the lowest PrEP uptake rate in the US, highlighting health disparities in this population. This qualitative analysis aims to inform the adaptation of a behavioral intervention to reduce barriers along the PrEP care continuum and increase uptake among MSM in Puerto Rico.

METHODS Following the ADAPT-ITT model, we are collecting formative data to inform the adaptation of a culturally sensitive intervention to improve PrEP uptake in Puerto Rico. Semi-structured interviews are conducted in Spanish and explore content, design, and recommendations for the intervention. Qualitative interviews with potential PrEP users and providers began in October 2023. Content analysis is ongoing.

RESULTS A total of 12 MSM participants (mean age 45.3) and six healthcare providers (mean age 38.2) answered the interviews. The main topics of interest of MSM regarding PrEP uptake include side effects, drug-drug interactions, how PrEP works, benefits of using PrEP, eligibility, and the current research on PrEP. Providers concur that side effects, as well as costs and insurance coverage, are a primary interest. The proposed intervention design was well accepted, and participants have not yet provided substantial recommendations. Both groups insisted on the importance of incentivizing participation, recruitment strategies, and constant follow-ups to increase intervention retention.

CONCLUSIONS Preliminary findings suggest that the intervention design is acceptable and responsive to MSM needs in Puerto Rico. Supporting MSM to overcome barriers to PrEP uptake is critical to prevent HIV transmission. Targeted behavioral interventions have shown effectiveness in promoting healthier practices. We aim to implement and evaluate the effectiveness of a PrEP intervention for eligible Latino MSM in a priority EHE jurisdiction.

NIMHD-RCMI U54 MD007600

ABSTRACTS

Women's Health

08.12.01 – Poster Session 1 · Terrace (2nd Floor)

YOUNG BLACK WOMEN ANTICIPATE IMPACTS OF DOBBS V. JACKSON

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Florida International University (AG, SS, MJT); Boston University (KMN)

PURPOSE: Young Black women face increased risk for STIs, HIV, and unintended pregnancy in the United States (US). The US Supreme Court case Dobbs v. Jackson Women's Health Organization overruled federal protection for abortion care access in 2022. However, widespread consequences on a broader set of sexual and reproductive contexts are expected, and young Black women are likely to be among those most affected. This study assessed anticipated impacts of Dobbs v. Jackson among this population.

METHODS: Young Black women (N = 500; 18–22 years) recruited across the US participated in an online sexual/reproductive health survey in Oct. and Dec. 2023. Participants responded to demographic and psychosocial items, and rated the extent to which they anticipated negative impacts of Dobbs v. Jackson on their sex life and decisions related to prescription birth control, emergency contraception, STI testing, and abortion ("No impact" to "A lot of impact"). A composite score was calculated and categorized as low, moderate, and high. Multivariable ordinal logistic regression was conducted between participant characteristics and the categorized anticipated impact scores.

RESULTS: Most anticipated moderate (43%) to high (30%) negative impacts of Dobbs v. Jackson, while 27% anticipated low impacts. Increased perceived childhood SES was associated with greater odds of a moderate anticipated impact score (aOR = 1.54, 95% CI [1.11, 2.14]). Increased medical mistrust (aOR = 1.63, 95% CI [1.02, 2.61]) and being aware of the Dobbs decision prior to participation (aOR = 8.90, 95% CI [2.68, 29.54]) were associated with increased odds of a high anticipated impact score.

DISCUSSION/CONCLUSION: Young Black women anticipate widespread negative impacts of Dobbs v. Jackson within the contexts of their sexual and reproductive experiences. Culturally-responsive sexual/reproductive health care and support for this population are crucial for preventing further disparities in Black women's health.

National Institute on Minority Health and Health Disparities (Award Number U54MD012393, FIU Research Center in Minority Institutions (FIU-RCMI))

08.12.02 – Poster Session 2 · Terrace (2nd Floor)

RACIAL DISPARITIES IN ADMISSION TO A RESIDENTIAL TREATMENT PROGRAM FOR SUBSTANCE USE DISORDERS AMONG UNDERSERVED PREGNANT OR POSTPARTUM WOMEN

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Department of Psychiatry and Behavioral Sciences; Department of Biomedical Data Science; Meharry Medical College, Nashville, TN

Purpose This study seeks to explore the presence of racial disparities among pregnant/postpartum women from underserved communities who experience Substance Use Disorders (SUDs) and co-occurring psychiatric disorders, upon admission to a residential treatment program.

Methods We conducted a retrospective crossover study for pregnant/postpartum women enrolled in the residential treatment program at Elam Mental Health Center (EMHC) at Meharry between 2017 and 2022. Clinical charts were reviewed and patient characteristics were extracted for analysis. This patient cohort was compared to pregnant/postpartum women treated at Meharry's outpatient clinics who had at least one SUD diagnosis using Electronic Health Records.

Results We reviewed 106 clinical charts for 98 patients who were admitted into the EMHC residential treatment program. The majority were White (n=60) and Black (n=33) with a median age of 29 (IQR: [26,34]). Most were unmarried (n=71), with highest education level of high school (n=69) and college (n=21). They suffered SUDs including opioid (n=79), cocaine (n=39), cannabis (n=37), amphetamine (n=30), and alcohol (n=20), along with comorbid psychiatric disorders of depression (n=29), anxiety (n=21), PTSD (n=18), and bipolar (n=15). Additionally, 93 pregnant/postpartum women were identified who had at least one type of SUDs from Meharry outpatient EHRs, including Black (57%), White (28%), with a median age of 35 (IQR: [29,43]). A Chi-Square test was conducted to compare the proportions of White versus Black women between these two patient cohorts, yielding significant difference ($p<0.001$).

Conclusion The study indicates that Black women were less likely to grain admission to the residential treatment program compared with White women. A contributing factor could be the source of referrals. When pregnant women test positive for drugs, in Davidson County and rural counties in East Tennessee, White women were more likely referred for drug treatment while Black women were more often referred to the Department of Children's Services.

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08.12.03 – Poster Session 2 · Terrace (2nd Floor)

NEUREGULIN-1 (NRG1) SIGNALING IN HUMAN ENDOMETRIUM.

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PURPOSE Neuregulin 1 (NRG1), a member of the EGF-like factor family that mediates its effect through the erythroblastoma (ErbB) family. NRG1 is well recognized in neurodevelopmental and cardiac function, neurological and psychiatric disorders, and cancer. However, the physiological role of NRG1 in the uterus has not been well documented. Therefore, we examined the expression levels of NRG1 and its receptors in human endometrium in relation to proliferative marker (PCNA).

METHODS Briefly, slides carrying human uterine tissue sections were de-waxed in xylene and rehydrated in a descending ethanol gradient at room temperature. NRG1, ErbB3 and PCNA were co-localized in tissue samples with CD105 (Endoglin) and epithelial cadherin (E-cadherin) (n=3 different uterine sections/group). Negative controls were performed by omitting the primary antibody or using an isotype-matched control antibody derived from the same species. Also, uterine sections were stained with hematoxylin and eosin (H&E). Mounted slides were examined using an Olympus microscope with an Optronics Magnifier digital camera.

RESULTS Our results showed a differential pattern of NRG1, ErbB3, PCNA, CD105, and E-cadherin expressions in the uterus. However, no detectable immunostaining was observed when the primary antibodies were replaced with IgG, confirming the specificity of the staining procedures. Interestingly, strong immunoreactive signals of NRG1, ErbB3, PCNA, CD105, and E-cadherin in the luminal epithelium and superficial and deep glands of endometrium were observed, whereas weak immunostaining in myometrium was noticed.

CONCLUSION These findings suggest that NRG1 and ErbB receptor may play an important intracellular role in uterine physiology.

Nothing to Disclose: TK; MA; SB; IC.

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08.12.04 – Poster Session 1 · Terrace (2nd Floor)

BENEFITS OF APP-DELIVERED MINDFULNESS MEDITATION FOR PREGNANCY

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San Diego State University (DB); University of California, Irvine (DTB, AMR, AN)

PURPOSE Stress and anxiety during pregnancy are highly prevalent, and associated with numerous adverse outcomes, among the most serious are increased rates of preterm birth and low birth weight infants. Mindfulness is a strategy to reduce stress and anxiety, however barriers to formal training include availability, accessibility, cost, and time. We conducted a study to evaluate if a more accessible (app-delivered) version of mindfulness training could impact stress and anxiety levels during pregnancy, or had any other benefits.

METHODS We conducted a month-long mindfulness intervention using the Headspace app, with 20 participants who were instructed to meditate twice/day. We collected pre/post self-report data with validated measures, a post-intervention questionnaire, and physiological measures of stress (sleep and heart rate variability [HRV]) using the Oura ring.

RESULTS Pre-to-post intervention reductions were found in self-reported stress (p=0.005), anxiety (p=0.01) and pregnancy-specific anxiety (p=0.0001). Sleep improved by 2% (p=0.09). Hierarchical linear modeling showed statistically significant changes reflective of stress reduction in 1 of 6 HRV metrics, the low-frequency power band, which decreased by 13% (p=.006). 95% of study participants reported that learning mindfulness positively impacted other aspects of their lives. A quasi-qualitative analysis of participant narrative data revealed the following impacts for study participants: improved patience, improved perspective, improved focus, improved conflict management, reduced emotional reactivity, and a greater focus on self-care.

DISCUSSION/CONCLUSION There is a paucity of research investigating the benefits of mindfulness apps during pregnancy. Results showed that mindfulness meditation training via the Headspace app is effective to reduce stress and anxiety during pregnancy, and participants reported numerous additional benefits, including improved sleep. This study contributes to the literature by supporting the benefits of app-delivered mindfulness training during pregnancy, which improves accessibility, and may reduce disparities for this vulnerable population.

ABSTRACTS

08.12.05 – Poster Session 2 · Terrace (2nd Floor)

RACIAL DISPARITES OF CERVICAL CANCER SURVIVAL RATES IN USA

S MILLER; E Abdalla
Tuskegee University (SM, EA)

PURPOSE: According to recent cancer statistics, in the USA, Cervical Cancer (CerCancer) five-year relative survival rate (RSR) is 66%. The objective was to assess racial differences in CerCancer RSRs by age and stage at diagnosis, between Blacks and Whites, living in the USA. METHODS: Data for 2389 Blacks and 13386 Whites diagnosed with CerCancer were extracted from the 2015 to 2020 Surveillance, Epidemiology, and End Results (SEER) database. We incorporated age groups, stages, and years of diagnosis to compare the RSRs between Blacks and Whites, using SEER*Stat software. RESULTS: Whites diagnosed with the localized stage of CerCancer always had better chances of survival because their RSRs were always more than 68%, compared to Blacks. The only exception was in Blacks aged 45-54, who had a higher RSR of 89.5% (95% CI, 80.3-94.5). Which was almost the same as in Whites in the same age group and aged 55-64 (89.4% (95% CI, 85.8-92.2). This was because of the precision of the statistics, which depended on their sample size and variability. Whites diagnosed with regional stage CerCancer had better chances at survival than Blacks. Their RSRs decreased as age increased for both Black and White. However, Whites aged 15-44 had a higher RSR of 66% (95% CI, 62.3-68.8) compared to Blacks aged 75 and older who had the lowest RSR of 37.2% (95% CI, 15.5-59.1). Whites 15-44 aged diagnosed with the distant stage of CerCancer had an RSR of 25% (95% CI, 19.8-30.1) compared to Blacks aged 75 and older who had no survival. Their RSRs decreased as age increased for both Blacks and Whites of any age group that's diagnosed with distant stage. Blacks aged 15-44 diagnosed with the unknown stage had an RSR of 74% (95% CI, 39.2-90.5) compared to Whites who had a slightly higher RSR of 77% (95% CI, 69.2-83.7) among the same age group. Blacks aged 45 and older had significantly low RSRs compared to Whites in any age group excluding 75 and older. DISCUSSION/CONCLUSION: There were significant racial differences in the RSRs of CerCancer. Remarkably, Black women experienced the worst RSRs compared to their White counterparts.

This work was supported by the MSM/TU/UAB Comprehensive Cancer Center Partnership [NCI]: Tuskegee University – U54 CA118623 grant. The Tuskegee University Center for Biomedical Research/Research Centers in Minority Institutions (TU CBR/RCMI) Program at the National Institute of Health (NIH). The CBR/RCMI U54 grant number MD007585.

08.12.07 – Poster Session 1 · Terrace (2nd Floor)

RACIAL DISPARITIES IN MATERNAL MORTALITY ACROSS TEXAS

CM Torres; OA Olaleye
Texas Southern University (CMT, OAO)

PURPOSE: The aim is to complete a scoping review of maternal mortality in Texas and assess the racial disparities present across various social determinants of health. The goals are to describe the trends of racial disparities in maternal mortality, highlight the influence of social determinants of health on racial disparities in maternal mortality, and assess areas of improvement in tracking maternal mortality. The main objective is to centralize the most up-to-date maternal mortality data so it can be utilized to improve maternal health, promote the need for maternal health programming, and serve as a toolkit for policy creation and advancement.

METHODS: PubMed, TSU Library, Google Scholar, and organizational websites at the federal, state, and county levels were utilized to compile literature assessing racial disparities and social determinants of health surrounding maternal mortality across the State of Texas and Harris County.

RESULTS: Despite societal advancements and housing the world's largest medical center (Texas Medical Center), Texas and Harris County continue to experience increased maternal mortality rates that are disproportionately impacting the non-Hispanic Black population. These racial disparity trends in maternal mortality are seen despite controlling for various social determinants of health. Through the literature, we observe that in Texas non-Hispanic Black women have a 2.3- and 4.4-times higher pregnancy-related mortality rate than their non-Hispanic White and Hispanic peers respectively despite variables such as income, education, urbanization, zip code, and age.

CONCLUSION: The reported findings highlight the urgent need for a synergistic effort to address maternal mortality in African Americans and contribute to the knowledge of women's health by centralizing maternal mortality data related to racial disparities across Texas and Harris County and demonstrating the need for up-to-date data to be provided by state and local health departments.

This project is supported by the National Institute on Minority Health and Health Disparities of the National Institutes of Health (NIH) under award 2 U54 MD007605-27A1 and Health Resources and Services Administration (HRSA), Maternal Health Research Collaborative for MSIs – Research Centers Grant Award 1 UR6MC50354-01-00.

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Nicole Sylvina Arnold is a Postdoctoral Fellow in Studies in Health Disparities at Morgan State and Wayne State Universities (2021-present). She holds a Ph.D. in Bio-Environmental Sciences from Morgan State University school of computer, mathematics and natural science. Dr. Arnold's undergraduate and master's degrees were obtained from Towson University. Her bachelor's degree (2011) is in Biological Science with a Functional Biology track. Dr. Arnold's master's degree (2017) is in Biological Sciences with a Molecular and Cellular track. She joined Morgan State University's PhD Bioenvironmental Sciences program in August 2017. Her research focused on unraveling the association between environmental factors and gene expression patterns linked to health disparities. Dr. Arnold's work in differential gene expression has been featured in the American Society of Human Genetics 2021 press release.

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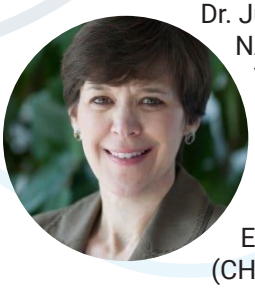

Dr. Julie Baldwin is the NARBHA Institute Vice President for NAU Health, the Executive Director of the Center for Health Equity Research (CHER), and a Regents' Professor in the Department of Health Sciences at Northern Arizona University (NAU). She earned her doctorate from the Johns Hopkins Bloomberg School of Public Health. From 1994-2004, she served as a tenured faculty member at NAU. She joined the faculty at the University of South Florida College of Public Health in 2005. She returned to NAU in August 2015 to be the founding director of CHER. Dr. Baldwin's research has focused on both infectious and chronic disease prevention. She is the PI of the Southwest Health Equity Research Collaborative and a member of the National Academy of Medicine. As a citizen of the Cherokee Nation of Oklahoma, she has made a life-long commitment to advocating for health promotion programs for children, adolescents and families.

MICHAEL BANYAS

Commander Michael Banyas is a Senior Officer in the U.S. Public Health Service and a Health Specialist in the National Institute of Minority Health Disparities (NIMHD). The mission of NIMHD is to lead the nation's scientific research to improve minority health and reduce health disparities. In his role, he is the Program Director for NIMHD's SBIR/STTR program and oversees an award budget of almost $20.5 million and over 100 awardees. CDR Banyas specializes in underserved health care and public health systems with a focus on implementation science. Previously, he served as Public Health Analyst in NIH's All of Us Research Program, where he led the Federally Qualified Health Center (FQHC) Pilot Project and Co Led the Tribal Engagement Strategic, as well as operational process improvement. Additionally, he served as a Project Officer in the Health Resources Services Administration for FQHCs and as the Communications Lead for the Office of Health IT and Quality. Additionally, he served as a Fellow on the U.S. Senate Health, Education, Labor, and Pensions Committee's Health Policy subcommittee and has worked in three academic medical centers. He has a Bachelor of Arts from the University of Vermont, a Masters in Public Administration in Health Management and Policy from New York University's Wagner School of Public Service, graduate work in health informatics from Columbia University, and a Masters of Arts at the U.S. Naval War College. As a UVM political science student, he was able to grow his interests and career experiences in how politics and policy affect each other, utilize political theory for philosophically analyzing problems, and explore political and historical areas, ranging from African security issues to Vermont town halls politics. His UVM political science and liberal arts education were invaluable in helping him develop critical thinking for policy formation and analysis, augment his ability to connect theory and policy to present and future political situations, and understand how to align interests with objectives. These skills sets have been invaluable in furthering his work in variety of health policy and political settings at state and Federal levels.

NONI BYRNES

Dr. Noni Byrnes is Director of the Center for Scientific Review (CSR) at the National Institutes of Health (NIH). She leads a staff of about 600 and is responsible for overseeing a majority of the NIH peer review process. As Director, Dr. Byrnes has launched multiple initiatives to strengthen peer review including CSR's signature enquire initiative to ensure that study sections evolve to include emerging scientific areas, the Simplified Review Framework for research project grants and changes to the review criteria for individual fellowships. She has prioritized efforts to ensure the integrity and fairness of peer review and has led the development and implementation of bias awareness training and review integrity training, required for all NIH reviewers. Prior to being appointed Director in 2019, Dr. Byrnes served in a variety of roles at CSR in positions of increasing responsibility, including scientific review officer in Chemistry and Biophysics, Branch Chief in Cell Biology, Division Director in Basic Sciences, Acting Deputy Director and Acting Director of CSR. Dr. Byrnes holds a

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WILSON COMPTON

Wilson M. Compton, M.D., M.P.E. is Deputy Director of the National Institute on Drug Abuse (NIDA) of the National Institutes of Health, where he has worked since 2002. Dr. Compton received his undergraduate education at Amherst College and medical education, including psychiatry training, at Washington University in St. Louis. Over his career, Dr. Compton has authored over 250 publications and often speaks at high-impact venues. He was a member of DSM-5's Revision Task Force and has led, for NIDA, development of the Population Assessment of Tobacco and Health Study, jointly sponsored by NIDA and the U.S. Food and Drug Administration (FDA), with 45,971 participants. Dr. Compton has received multiple awards, including FDA awards for collaboration in 2012, 2013 and 2017, and the Health and Human Services Secretary's Awards for Meritorious Service in 2013 and Distinguished Service in 2015, 2018 and 2019.

EMILY COPE

Dr. Cope is an Associate Professor in the Department of Biological Sciences and Assistant Director of the Center for Applied Microbiome Sciences at the Pathogen and Microbiome Institute (PMI) at Northern Arizona University (NAU). She earned a PhD at Northern Arizona University where she studied the effect of tobacco smoke on the respiratory microbiome. After her PhD, she was a postdoctoral scholar at the University of California San Francisco (UCSF), where she characterized the sinonasal microbiome in patients with CRS, cystic fibrosis, and asthma. The primary focus of her research is to understand the role of host-microbiome interactions in chronic and progressive diseases, focusing on CRS, asthma, and Alzheimer's Disease. Her translational work will contribute to an increased understanding of the role of the microbiota in chronic inflammation and will ultimately lead toward rational development of therapeutics aimed at manipulation of microbiome to treat these important and costly diseases.

ARIA CRUMP

Aria Davis Crump, Sc.D. is a social and behavioral scientist and the Deputy Director of NIDA's Office of Research Training, Diversity and Disparities. She has previously served as a Program Official and Deputy Branch Chief for NIDA's Prevention Research Branch, specializing in the social, cognitive, and developmental aspects of risk-taking in adolescence and applications to preventive interventions. Throughout her career, she has been dedicated to promoting prevention science, empowering the next generation of NIH researchers, advancing health equity, and supporting diversity in the research workforce.

GENE D'AMOUR

Dr. D'Amour begin his career as a professor at West Virginia Uiversity in the field of Philosophy of Science and Mathematical Logic. There he was Instrumental in enhancing a new approach to teaching problem solving and developed the "Nature of Evidence" course called by Change Magazine "One of most notable improvements in American undergaduate education." He then was invited to become a rotator for 2 years at the National Science Foundation, after which he was hired by Tulane Univerity as vice president for research (non medical) to create an Office of Research. During this tenure Tulane increased its Federal R&D expenditures more than seven-fold and its total R & D expenditure ranking in the nation by twenty-three places. He played a principle role in organizing the Coalition of EPSCoR States expanding the EPSCoR program to 6 federal agencies. He also Chaired the Louisiana's State-wide EPSCOR committee for 15 years. During this period, Louisiana's per scientist funding grew from 38% to 90% of the US average. In 2002 after helping to create the Louisiana Cancer Research Consortium which receives $10M per year from the State of Louisiana, he retired to become Sr. Vice President for Resource Development at Xavier Univeristy where he developed a sponsored research office and reorganied Xavier's Institutional Advancement Office. Xavier is now among the top 10 HBCus in the nation in NIH funding. He has Published one book, "The Nature of Evidence," numerous articles and been a Consultant to more than thirty universities, foundations and government agencies.

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Monica is a resident of Kaneohe, Oahu she is a wife, daughter and mother to Victor and Teresa. She is an associate professor and dietetics program director at the University of Hawaii at Manoa. In this role she is interested in supporting Filipino, Native Hawaiian and Pacific Islander students in pursuit of becoming Registered Dietitians and on research that can improve the health and well-being of individuals and communities through food and system interventions.

Bios and photos as received at time of production

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Stacey L. Gorniak, Ph.D., F.A.H.A., is currently an Associate Professor in the Department of Health and Human Performance at the University of Houston. She earned her B.S. in Physics and M.S. and Ph.D. in Kinesiology, focused in Biomechanics and Motor Control (with a minor in Statistics) from the Pennsylvania State University. Dr. Gorniak's research interests focuses on evaluating both the central and peripheral contributions to sensory, motor, and cognitive deficits due to chronic health conditions and movement disorders. She is the current Director of the Investigator Development Core of UH's HEALTH Research Institute's NIMHD.

AYALA GUADALUPE

Guadalupe X. Ayala, MA, PhD, MPH, is a Professor of Public Health at San Diego State University. She also is the Director of the Institute for Behavioral and Community Health, Director of the SDSU HealthLINK Endowment, Co-Director of the SDSU HealthLINK Center for Transdisciplinary Health Disparities Research, and Co-Director of the Imperial County Clinical Research Network, the last three funded by the NIMHD. Trained in both clinical psychology and public health, her research focuses on developing new and adapted interventions to reduce Latino health disparities in obesity, diabetes, and asthma. This has included the development of multi-level interventions to improve diet, physical activity, and other behavioral, social (e.g., parenting), and environmental (e.g., food stores) determinants of health.

GEORGES HADDAD

Dr. Haddad is a tenured full professor in the Physiology & Biophysics department, College of Medicine, Howard University. Dr. Haddad research spans the mechanisms and treatments of multiple cardiovascular diseases from hypertension, heart failure, cardiac hypertrophy, alcoholic cardiomyopathy, and cART HIV treatment cardio-effects. Dr. Haddad is reviewer and on editorial board for many peer-reviewed journals and on NIH study sections. He has mentored more than 75 underrepresented minority students and post-doctoral fellows as well as coached around 30-40 faculty, mostly within the NRMN SETH and other programs. Dr. Haddad is also a published music composer!

CHERISE HARRINGTON

Cherise B. Harrington, PhD, MPH is a Professor and Senior Researcher in the Department of Public Health Education (PHE) at North Carolina Central University in Durham, NC. Her doctorate degree is in Medical Psychology, and she also holds a Master of Public Health degree both from the Uniformed Services University of the Health Sciences in Bethesda, MD. Her research involves identifying and developing interventions that improve health literacy by targeting social drivers of health using innovative methods including community-based approaches and mHealth technologies. A significant portion of her research addresses health disparities and seeks to identify 1) the variable influence of race on psychosocial and environmental factors as it relates to health and 2) approaches/ interventions to address these health disparities through improved health literacy. Her work also includes designing and conducting needs assessments and program evaluations focused on prevention behaviors, health literacy, disease management, and overall health.

MELISSA HARRINGTON

Melissa Harrington has been at Delaware State University (DSU) since 2001 where she started as a faculty member in the Department of Biological Sciences, and she is currently the Associate Vice President for Research and the director for the Delaware Institute of Science and Technology, the first research institute created at DSU.
Currently, Dr. Harrington is the co-director of the RCMI -supported Interdisciplinary Health Equity Research Center and the director of the NIH-funded Delaware Center for Neuroscience Research. She is also a co-director of NIH-funded training grants that support undergraduates for a summer research program and support students in DSU's neuroscience PhD program.

JERRIS HEDGES

Dr. Jerris Hedges is Dean Emeritus of the University of Hawai'i at Manoa's John A. Burns School of Medicine (JABSOM). After serving as dean for 15 years, he now leads an NIH-funded research program to address health disparities that disproportionately affect Hawai'i's citizens who share less advantaged cultural and ethnic backgrounds, especially the rural, the poor, and those of Native Hawaiian, other Pacific Island and Filipino ancestry. Dr. Hedges is known internationally as the founding co-editor of one of the leading texts in emergency care, Roberts and Hedges' Clinical Procedures in Emergency Medicine, now in its seventh edition. Dr. Hedges has

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served in national emergency medicine leadership roles including the Society for Academic Emergency Medicine President, and Association of Academic Chairs of Emergency Medicine President. He was inducted into the United States' National Academy of Medicine in 2000. In Hawai'i, he is also recognized as a leader who has strengthened the medical school by building vital bridges between JABSOM's community partners and collaborators. In 2013, the Hawai'i Medical Association (HMA) named him "Physician of the Year" and in 2023, he received the HMA "President's Award".

CHRISTINE HOHMANN

Christine Hohmann completed her PhD in Neuroscience at Brown University. Following a postdoc and faculty appointment at Johns Hopkins University School of Medicine, she joined the faculty of Morgan State University in 1993 and rose through the ranks to full professor. Dr. Hohmann's research interest has been to understand mechanism of brain development involved in neurological and psychiatric disorders. To that end she has studied brain structure and molecular function, as well as behavior, in experimental mouse models. At MSU, Dr. Hohmann has contributed to the research training of nearly 300 undergraduates as long-standing Director and PI of the NIGMS RISE Program and Core Director, PI of the BUILD/ASCEND Program and in her own lab. Dr. Hohmann's current focus is on faculty, program, and institutional development. Dr. Hohmann is an elected Fellow of the American Association for the Advancement of Science and the International Behavioral Neuroscience Society.

WENDY JIA MEN HUANG

Dr. Wendy Jia Men Huang holds a PhD in Biomedical Sciences from the University of California San Diego and completed a postdoctoral fellowship in immunology at the New York University in 2015. Between 2016 and 2023, Dr. Huang was an Assistant Professor at the University of California, San Diego, and studied the role of inflammation in autoimmune diseases and cancers. Dr. Huang took the leading role in the Center Research Capacity Core and the Center's Cost Recovery Service efforts in 2023 to support the Center's mission to advance minority health and health disparities research.

MUHAMMED IDRIS

Dr. Idris is an Assistant Professor in the Department of Medicine at Morehouse School of Medicine (MSM). Trained as a computational social scientist, his work combines data science and community-based research methods to study how structural and environmental factors impact health disparities. In addition to research, he contribute to multiple efforts to build educational programming and developing curriculum to leverage data science, machine learning, and artificial intelligence for health disparities research, including serving as the lead investigator developing a new U24 training program to enhance data science capacity across 25 NIMHD-Funded Research Centers in Minority Institutions (RCMI). Prior to joining MSM, Dr. Idris led interdisciplinary teams building, deploying, and maintaining machine learning solutions for a variety of clients, including a large hospital system, United Nations Refugee Agency, and Garmin. His work has been funded by the National Institutes of Health and Microsoft Research, and has been presented on various academic, policy, and industry platforms and encompasses a TED talk on AI-driven social service delivery that garnered around 1.8 million views. Dr. Idris graduated from the University of Washington and the Pennsylvania State University.

RAPHAEL ISOKPEHI

Dr. Raphael Isokpehi is a Program Director in the Training, Workforce Initiatives, and Community Engagement (TWICE) team of the National Institutes of Health's Office of Data Science Strategy (ODSS). Prior to joining NIH, Dr. Isokpehi held faculty and director positions in biology, bioinformatics and data analytics at Jackson State University in Mississippi and Bethune-Cookman University in Florida. At Jackson State University, he was a Pilot Project Investigator at the Center for Environmental Health funded by the NIHMD Research Centers in Minority Institutions (RCMI) program. In addition, He co-chaired the Bioinformatics & Computational Biology Working Group of the RCMI Translational Research Network (RTRN). Dr. Isokpehi's program focus areas at NIH ODSS emphasizes enhancing institutional data science capacity through growing human capital, expanding infrastructure, and building partnerships.

NANCY JONES

Dr. Nancy Jones is a Program Officer in the Division of Community Health and Population Sciences at NIMHD. Dr. Jones' research interests include the ethical, legal, and social ramifications that research, medicine, and healthcare have on underserved populations. Another interest is to support research to improve the ability of theoretical constructs and

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conceptual models to explain the causes of health disparities. Dr. Jones' portfolio includes place-based disparities, measurement of constructs of minority health and health disparities, and population-level health trajectories and intergenerational transmission of risk and resilience. She developed a code of ethics for life sciences and a curriculum to teach ethics and professionalism for biomedical science and engineering graduate students. Dr. Jones joined NIMHD in 2012 and served as co-chair on the Etiology of Health Disparities for the Science Visioning as well as several trans-NIH committees on bioethics.

SEAN KIMBRO

K. Sean Kimbro is a Microbiology, Biochemistry, and Immunology professor at the Morehouse School of Medicine in Atlanta, Georgia. He is currently the lead PI on a National Institutes of Health Transformative R01, the first time this type of grant has been awarded to an HBCU, and the Director of the Center for Translational Research in Health Disparities, an NIH Research Center in Minority Institutions. Dr. Kimbro received his undergraduate degree from Washington University in St. Louis, Missouri, and his Ph.D. in Molecular and Microbiology from Indiana University, Bloomington, Indiana. He was a postdoctoral fellow at Harvard Medical School and the National Institutes of Health, National Institute of Environmental Health Sciences. Dr. Kimbro became an assistant professor at Clark Atlanta University, Department of Biological Sciences, in Atlanta, Georgia. He later directed the NIH Center of Excellence, the Georgia Center for Health Equality at Winship Cancer Institute, Emory University. He was recruited to North Carolina Central University as the second Director of the Julius L. Chambers Biomedical/ Biotechnology Research Institute. In 2014, Dr. Kimbro received funding for cancer health disparities research and returned to the lab to study immunity and breast/prostate cancers, including type 2 diabetes and obesity. Today, Dr. Kimbro trains multiple Ph.D. and Master's students in his laboratory and actively addresses health disparities in metro Atlanta and rural Georgia.

STACEY MCRAE

Stacey McRae serves as the Budget Director for the Howard University Research Centers in Minority Institutions (HU RCMI) Program, located within the College of Medicine, where she has served in various capacities to grow the program over several years. Ms. McRae has over 19 years of experience in administrative and programmatic processes in the clinical and biomedical areas, including 12 years working in program management for the current HU RCMI Program. She holds a Molecular/Cellular Biology degree from Hampton University, along with Program Management certificates. Ms. McRae has also served as the RCMI Program Administrators Secretary, helping to coordinate and present valuable information to her fellow administrators and PI's.

MARTIN MENDOZA

Martin Mendoza, PhD, serves as the director of health equity for the All of Us Research Program. In this role, he provides leadership and high-level expertise to improve inclusion and equity in precision medicine and leads the program's efforts to promote health equity. Before joining All of Us, Martin led extramural research for minority health in the Office of the Commissioner at the U.S. Food and Drug Administration (FDA). He is a recognized expert in clinical trial diversity and has testified on it before Congress. He is also the primary author of the pivotal FDA guidance recommending that clinical trial sponsors be required to submit a diversity and inclusion plan to FDA. Martin's original idea and recommendation became federal law in December 2022. Martin has also served as director of the Division of Policy and Data in the Office of Minority Health in the Office of the Secretary at the U.S. Department of Health and Human Services, as well as in the Division of Clinical Research at the National Institute of Neurological Disorders and Stroke. He conducted his primary research training in the National Cancer Institute's Pediatric Oncology Branch and helped to map chromosome 7 as part of the Human Genome Project during his tenure at the National Human Genome Research Institute. Martin is a graduate of the University of Maryland, Baltimore County, and received his Ph.D. in cancer biology from Johns Hopkins University.

GEORGE MENSAH

Dr. George Mensah is a clinician-scientist who currently serves as the Director of the Center for Translation Research and Implementation Science at the National Heart, Lung, and Blood Institute (NHLBI), a part of the National Institutes of Health (NIH). In this role, Dr. Mensah leads a trans-NHLBI effort to advance late-stage translational research and implementation science to address gaps in the prevention, treatment, and control of heart, lung, and blood diseases and the elimination of related health inequities. His goal is to maximize the population health impact of advances made in fundamental discovery science and pre-clinical or early-stage translational research. Dr. Mensah is an honors graduate of Harvard University. He obtained his medical degree from Washington University and trained in Internal Medicine and Cardiology at Cornell. His professional experience includes more than 20 years of public health service between the U.S. Department of Veterans Affairs,

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the Centers for Disease Control and Prevention (CDC), and the NIH. In addition to his public service, Dr. Mensah had 15 years of experience in direct patient care, teaching, and research at Cornell, Vanderbilt, and the Medical College of Georgia (MCG). He was a full professor with tenure at MCG and is currently a Visiting Full Professor at the University of Cape Town, South Africa. Dr. Mensah has been admitted to fellowships in several national and international societies including the American Heart Association, American College of Cardiology, and the European Society of Cardiology. He is an Honorary Fellow of the College of Physicians of South Africa. He maintains active collaboration with several international groups to advance research on the global burden of diseases and risk factors.

NOREEN MOKUAU

Noreen Mokuau, DSW, serves as MPI of the NIMHD Specialized Center Ola HAWAII whose objective is to lead and advance minority health and health disparities research in Hawai`i. Ola HAWAII is located at the University of Hawai`i at Mānoa. Dr. Mokuau is a social work leader whose scholarship and teaching are grounded in social justice and health for underserved populations, with an emphasis on Native Hawaiians. As Professor Emerita and former Dean of the Thompson School of Social Work & Public Health, she has numerous grants and publications in these areas, and continues to engage in scholarship and teaching organized around indigenous practices that support Native Hawaiians in health and wellness. Ka Māno Wai, a recent book, with co-authors, Kukuna Yoshimoto and Kathryn Braun, details Native Hawaiian ancestral practices that have potential meaning for social justice and health.

NANI MORGAN

Dr. Morgan serves as a primary care physician and teaching attending at Queen Emma Clinics and Clinical Assistant Professor at the John A Burns School of Medicine. Dr. Morgan is passionate about advancing health equity among Native Hawaiians and other Pacific Islanders and training Hawaii's future primary care physicians.

SERGEI NEKHAI

Dr. Nekhai has been at Howard University's Center for Sickle Cell Disease since 2000. He conducts basic and translation studies on Sickle Cell Disease, HIV-1 and Ebola virus infections. He also investigates iron metabolism with the focus on ferroportin, an iron export protein, which mutations might pose a risk for iron. Dr. Nekhai currently serves as Deputy Director for Center for Sickle Cell Disease. Dr. Nekhai also leads Howard RCMI Proteomics Program. Dr. Nekhai is also a Director for Basic Science for Washington DC Center for AIDS Research (CFAR). Dr. Nekhai's current and past funding includes NIH and NSF grants RO1, U19, P50 and G12 for which he has served as a PI, co-PI or PD. He has over 150 publications in basic virology and hematology journals.

RICHARD NOEL

Richard J. Noel Jr., PhD, is Professor and Chairman of the Department of Basic Sciences in the School of Medicine at Ponce Health Sciences University. His research is focused on understanding the chronic inflammation caused by HIV proteins which is associated with significant morbidity in clinically suppressed HIV-positive individuals. Recent work using an animal model his lab developed has shown that production of early HIV proteins by a small number of astrocytes in the brain produce local and systemic inflammation. Dr. Noel serves as the PI for the RCMI-Specialized Center for Health Disparities at PHSU, the founder and Director of the Strategic Academic Research Training Program (investigator development core) at PHSU, and Director of the Molecular Biology Core Laboratory at PHSU.

OMONIKE OLALEYE

Omonike Arike Olaleye, Ph.D. MPH. is the Senior Associate Vice President for Research and Innovation, and Professor of Pharmacology at Texas Southern University (TSU). By the grace of God, under her leadership, TSU maintained and was reaffirmed High Research Activity "R2" status by the Carnegie Classification on January 26, 2022. Presently, Omonike serves as an American Council on Education Fellow, (2023-2024) at The University of Texas System in the Office of the Chancellor, where Chancellor JB Milliken oversees 14 UT institutions, 250,000 students and 120,000 staff. Omonike's formal training in pharmacology and epidemiology, were at Johns Hopkins University School of Medicine and Harvard University respectively. Omonike has a strong background and expertise in biomedical research and public health spanning over a combined 21 years, working on research programs focused on diseases that disproportionately affect underrepresented minorities and/or underserved populations. Omonike is passionate about mentoring the next generation of scientists. To date, Omonike has trained up to 220 trainees/interns/doctoral graduates/fellows and published several papers/abstracts. Recently, Omonike received the Health Resources and Services Administration $2.42M Award to support and establish "The Gulf Coast Collaborative Center for Maternal Health Research, Education,

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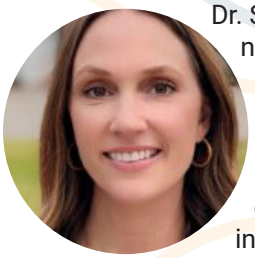
Advanced Training, Community Engagement, Health Equity and Justice at TSU (MH-REACHTSU)." Omonike provides institutional oversight and leadership to the newly formed Texas Health Equity Alliance for Breast Cancer (THEAL), a strong partnership with MD Anderson Cancer Center that will address the long-standing health disparities in breast cancer outcomes among our communities. Presently, she leads the $8.63 million NIH-funded Center for Biomedical and Minority Health Research.

EMILY SCHMEID

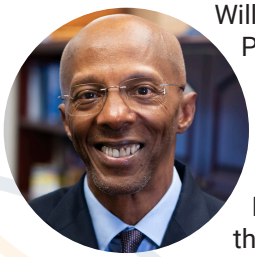


Dr. Schmied has nearly fifteen years of experience conducting health promotion interventions and epidemiological investigations in community, clinical, and military settings. Among Dr. Schmied's many research interests are mental health and chronic illness management, and the bidirectional relationships between the two. She is an expert in the design and implementation of health promotion interventions and the study of health influences and healthcare utilization within traditionally underserved communities. She has collaborated with various types of healthcare organizations, including Federally Qualified Health Centers. She has also led numerous Department of Defense-funded research studies designed to promote resilience and mental health among military service members.

JEAN SHIN

Jean H. Shin, Ph.D., is Deputy Director in NIH's Chief Officer for Scientific Workforce Diversity (COSWD) office, where he provides administrative oversight and subject matter expertise for data-related projects, communication tools, virtual conferences and events, and DEIA-oriented committees and working groups. Prior to joining the NIH staff, he served as Director of Diversity and Inclusion at the American Sociological Association (ASA) in Washington, DC. He joined the ASA Executive Office staff from McDaniel College in Westminster, MD where he was Associate Dean of Academic Affairs for First Year Students and an Associate Professor of Sociology. He has been a co-PI for NSF-funded research projects on the links between teaching innovation and social networks, as well as the impact of mentoring and networks on the trajectories of early-career STEM faculty. Dr. Shin received a B.A. from the University of Virginia and an M.A. and Ph.D. from Indiana University-Bloomington, all in sociology.

WILLIAM SOUTHERLAND



William M. Southerland, PhD is Professor of Biochemistry at the Howard University College of Medicine. He serves as the Director of Howard University's Center for Computational Biology & Bioinformatics (CCBB), Interim Director of the Howard University Center for Applied Data Science and Analytics (CADSA), and Principal Investigator of the Howard University Research Centers in Minority Institutions (RCMI) Program. He attended North Carolina State University where he earned a bachelor's degree in chemistry and subsequently, He subsequently earned the PhD in Biochemistry from Duke University. His research interests include utilization of data science principles to better understand the differing chronic disease burdens among different ethnic groups in the Washington, DC area. His interests also include investigating the association between allele frequencies and chronic disease expression among different ethnic groups. Earlier interests include molecular dynamics approaches to investigate the recognition and binding between small molecule ligands and their macromolecular targets.

PAUL TCHOUNWOU

Dr Paul Tchounwou currently serve as Dean of the School of Computer, Mathematical and Natural Sciences (SCMNS) at Morgan State University (MSU). In this capacity, his primary responsibilities include overseeing the academic enterprise and guiding the continued advancement of SCMNS's research, education, and training programs. He is also the current PI of the RCMI Center for Urban Health Disparities Research and Innovation at MSU. Prior to joining MSU in January 2023, he served as Presidential Distinguished Professor; Associate Dean for Research, Graduate Studies and International Programs in the College of Science, Engineering and Technology, and Executive Director of RCMI Center for Health Disparities Research the at Jackson State University (JSU) where he was associated with the RCMI Program since its establishment in 1998; initially a PI of a biomedical research project, and later as Center PI/PD for 15 years. Currently serving as MPI of the RCMI Coordinating Center and providing leadership for the coordination of its Research Infrastructure/Capacity Core domain, Dr. Tchounwou has been a very active leader of the RCMI Consortium where I initially served as Co-PI of RCMI Translational Research Network and Director of RTRN Data Coordinating Center from 2017 to 2020. For over 20 years, he has mentored, trained and provided excellent career development opportunities to over 100 BS, 8 MS and 49 PhD students, 10 post-docs, and 13 junior faculty. Resultantly, I was awarded the 2013 AAAS Mentor Award. In 2018, he was selected by the White House and the National Science Foundation as a recipient of the Presidential Award for Excellence in Science, Mathematics and Engineering Mentoring (PAESMEM). The primary research focus in his laboratory is to elucidate the mechanisms of action of selected chemotherapeutic drugs.

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His research endeavors in this area have led to the discovery of many molecular targets for the treatment of cancer and other health disparity diseases. He is author of 317 publications in the areas of biomedical science, environmental medicine, and public health. He ranked among the top 2% of world scientists. He is a 2023 Fellow of the American Association for the Advancement of Science.

JAYDUTT VADGAMA

Dr. Jay Vadgama is a Full Professor of Medicine at Charles R. Drew University of Medicine and Science (CDU) and the UCLA David Geffen School of Medicine in the Department(s) of Internal Medicine. Over the last three decades, he was responsible for providing leadership and sustaining research at CDU. He served as the Vice President for Research and Health Affairs (2012 – 2023) where he set the foundation for biomedical and clinical translational research and built excellent networks and partnerships with NIH, academic institutions, local communities, biotech, and pharmaceuticals. Dr. Vadgama continues to serve as AXIS Center PI, Chief of the Division of Cancer Research and Training, Director for the Center to Eliminate Cancer Health Disparities, Director of the Molecular Oncology Program, Endowed Chair for Cancer Research, Director of the Cancer Pillar, , serves on the senior leadership team of the UCLA CTSI Program, and Executive Director for CDU Center of Excellence for Clinical Trials. As Cancer Division Chief, his team has obtained more than $93.3M since 2009 in extramural funding and more recently secured funding for 10 yrs. at $5.7 Million to establish a Center of Excellence for Clinical Studies at CDU where he will serve as Executive Director.

HONGMEI WANG

Hongmei Wang, PharmD, PhD, BCIDP, is an associate professor of Pharmacy Practice at Texas Southern University and is also an infectious diseases clinical pharmacist practicing at Houston Methodist Texas Medical Center. Her research focuses on access, adherence, and therapeutic drug monitoring in care for adults with HIV prevention and treatment for minority communities through the implementation science strategies. She received grants from the NIMHD through the NIH supplement award to implement pharmacy-based HIV prevention services and through the RCMI Coordination Center to support minority older adults in the transition of care.

MONICA WEB HOOPER

Dr. Monica Webb Hooper is Deputy Director of the National Institute on Minority Health and Health Disparities (NIMHD) at the National Institutes of Health (NIH). She is an internationally recognized licensed clinical health psychologist and translational behavioral scientist, with a 20+ year history of working every day to improve the health and quality of life among underserved communities. Her collaborative, community engaged science seeks to prevent or reduce the impact of chronic illnesses on populations with health disparities. Through her work, Dr. Webb Hooper has directly improved the health of thousands of racial and ethnic minority group adults and families, developing and delivering successful treatments for overcoming addictions, such as tobacco smoking, achieving personal weight management goals, reducing distress and mental health concerns (e.g., anxiety or depression), and improving partner and family relationships. NIMHD leads and supports cutting edge science to improve minority health, reduce health disparities, and promote health equity. As NIMHD Deputy Director, Dr. Webb Hooper partners with the Director on overall executive direction and scientific leadership of the institute. Dr. Webb Hooper is also highly committed to the equitable and inclusive training of the next cadre of scientists who are invested in improving population health, community health, and global health. Overall, Dr. Webb Hooper is dedicated to the scientific study of minority health and racial and ethnic disparities, and interventions to reduce them. She has published over 100 articles and book chapters and has been featured in numerous editorials throughout her career. Indeed, the mantra of her work is "science and partnerships that benefit and serve communities." Academic Influence has identified Dr. Webb Hooper as one of 25 Influential Black Psychologists from the Last 30 Years, and one of 50 most cited and searched Black anthropologists (including the social sciences, biological sciences, physical sciences, and the humanities) over the past 30 years.

KRISTEN WELLS

Dr. Wells has nearly 20 years conducting research focused on improving the quality of healthcare delivered to underserved populations. Her research specialty is in patient navigation. Dr. Wells has led or contributed to numerous studies which have developed and evaluated patient navigation interventions to improve quality of cancer, HIV-related care, suicide prevention, and COVID-19 vaccination including among diverse and minoritized populations. She also leads studies developing technological solutions to improve adherence to recommended cancer care and oral medications for cancer. These include the use of mobile sensing technologies and data to understand medication-taking behaviors, predict individual risk

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factors, and deliver interventions to improve adherence that are needed by the individual at the optimal time, place, and in the optimal context.

LEANNE WOODS-BURNHAM

Dr. Leanne Woods-Burnham is an assistant professor in the Department of Physiology at Morehouse School of Medicine in Atlanta, GA. Her team focuses on prostate cancer health disparities using a translational approach. Dr. Burnham obtained a B.S. in biology from The University of Akron, and a Ph.D. in physiology from Loma Linda University School of Medicine. Her research evaluates ancestry-associated HER2 expression as it relates to worse clinical variables and survival outcomes for Black men with prostate cancer. She is currently funded by the Department of Defense Prostate Cancer Research Program, Prostate Cancer Foundation, the Georgia CTSA KL2 Scholars Program and Pilot Award Program, and an NIH/NIMHD Research Centers for Minority Institutions U54 award. In addition to bench and preclinical studies, Dr. Burnham has fostered several multidisciplinary collaborations with clinicians and pharma to conduct translational race-stratified research studies and clinical trials. She co-directs the Prostate Cancer Precision Prevention Program (PCP3) at Morehouse School of Medicine which leverages community partnerships to provide health education and free prostate-specific antigen (PSA) tests to at-risk men in the greater Atlanta area and rural Georgia. Dr. Burnham has been recognized by Cell's #FacesofCell Twitter campaign to increase visibility of talented Black scientists, as well as The Cancer Health 25: Black Lives Matter, as a "remarkable individual breaking down racial barriers to better cancer care."

YONG WU

Yong Wu, M.D., Ph.D., is an Associate Professor and Core Director for the Drug Discovery Program in Charles Drew University of Medicine and Science. He also holds faculty positions at David Geffen School of Medicine at the University of California, Los Angeles (UCLA). Dr. Wu has a broad background in pharmacology, molecular and cellular biology of diabetes and cancer, and has experiences in anti-cancer drug design and discovery. He is a member of the American Association for Cancer Research and American Heart Association, among others. Currently, He is engaged in investigating the links between metabolic syndrome and cancer, specifically focusing on the fundamental mechanisms by which elevated blood glucose and fatty acids increase breast cancer risk and progression. This is a key area of interest in the Division of Cancer Research and Training. His current research has also been focused on (1) elucidating a safe and effective therapeutic strategy to preferentially kill the malignant cells that are dependent on glycolytic pathway with a minor effect on normal cells; (2) Design, synthesis, modification, and biological evaluation of small molecule anti-cancer compounds for breast cancer therapeutic development.

HUAN XIE

Dr. Huan Xie is a Professor of Pharmaceutics at Texas Southern University (TSU). She has over 20 years of experience in preclinical drug development. She serves as the Founding Director of the Institute of Drug Discovery and Development (iD3) at TSU, which is an NCI-designated subcontractor to provide service for investigators across the United States. She is the PI of the RCMI Center for Biomedical and Minority Health Research (CBMHR), and the co-Director of the GCC Center for Comprehensive PK/PD and Formulation (CCPF) funded by the Cancer Prevention & Research Institute of Texas (CPRIT). She is also the Program Director of the Graduate Program in Pharmaceutical Sciences at TSU. Dr. Xie had 4 years of industry experience, and she is an inventor of 3 patents and has over 40 peer-reviewed publications. Dr. Xie has successfully obtained grants for over $30 million, completed over 200 collaborative research projects/services, taught over 1000 Pharm.D. students, and personally mentored 10 research scientists/postdoctoral fellows, and over 50 Ph.D., Pharm.D., undergraduate and high school students, most of whom were underrepresented minorities.

RCMI2024

Acknowledgments

The 2024 RCMI Consortium National Conference Planning Committee, the Conference Organizing Committee consisting of RCMI Principal Investigators and NIMHD Program Officials, would like to thank the RCMI Centers' faculty, trainees, and staff for contributing their best science to this conference.

We are grateful to our abstract reviewers, speakers, and moderators for due diligence.

We thank the staff of the RCMI Coordinating Center for programmatic support.

We are especially indebted to the staff at Morehouse School of Medicine: Dr. Tandeca King Gordon, Geannene Trevillion and Mohamad Malouhi for administrative and resource support; and the sponsored research administration and finance team.

We thank the 1Joshua Group team for excellent execution of conference meeting management.

KEY TAKEAWAYS

NOTES

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Daniel F.K. Sarpong, PhD

Yale University School of Medicine

4 MAJOR EVENTS

3 VIRTUAL SYMPOSIA

- March 20, 2024
- June 19, 2024
- September 18, 2024

1 CONFERENCE

- Culminating In-Person Meeting in Accra, Ghana

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