CLEVELAND HIGH SCHOOL STUDENT SCIENTIFIC ENRICHMENT & OPPORTUNITY PROGRAM AND YOUTH ENGAGED IN SCIENCE PROGRAM

2022 STUDENT RESEARCH POSTER PRESENTATION

CASE WESTERN RESERVE UNIVERSITY SCHOOL OF MEDICINE

Participating High Schools

Andrews Osborne Academy, Avon HS, Beachwood HS, Charles F. Brush HS, Cleveland Heights HS, Cleveland School of Science and Medicine, Copley HS, Facing History New Tech, Gilmour Academy, Harrisburg Academy, Hathaway Brown School, Hawken School, John F. Kennedy HS Lake Ridge Academy, Laurel School, Mayfield HS, Orange HS, Padua Franciscan HS, Revere HS, Saint Edward HS, Saint Ignatius HS, Shaker Heights HS, Shaw HS, Solon HS, Stow Munroe Falls HS, Twinsburg HS, University School, Westlake HS

Sponsored by

CWRU Center for Science, Health and Society

10900 Euclid Avenue, Cleveland, Ohio 44106-4971

July 28, 2022

WELCOME

Welcome to the nineteenth annual Scientific Enrichment and Opportunity (SEO) and Youth Engaged in Science (YES) Program - High School Student Research and Poster Capstone Presentation sponsored by the Case Western Reserve University School of Medicine, Center for Science, Health and Society, and the Case Comprehensive Cancer Center. This year 80 high school students and six high school teachers participated. Thanx to effective COVID-19 vaccines, mitigation strategies, and anti-viral agents, we were able to return to an onsite, in person research and education program. While the virtual programs of the past two years were productive, all students and faculty mentors agree there is nothing like the excitement of hands on research. And the ability of students to interact on a regular basis goes a long way towards establishing a community of scholars.

The SEO Program was initiated in 2004 to focus on connecting students from the Cleveland Metropolitan School District with outstanding research and clinical faculty and staff at the CWRU School of Medicine. Over the years, the program has expanded to more broadly include students from a greater area of northeast Ohio. In 2018, with support from the National Cancer Institute Youth Engaged in Science (YES) grant, the program further increased to specifically include underrepresented minority students interested in cancer research and health care.

The SEO and YES programs provide Cleveland H.S. students with a unique opportunity to engage in biomedical research under the supervision of expert CWRU Medical School and Case Comprehensive Cancer Center faculty, to mentor and motivate students to complete H.S., attend college, and pursue careers in the biomedical sciences and health professions, and to enrich Cleveland by transforming students into enlightened members of the community who are prepared, enthusiastic and eager to participate in the growth of the biomedical sciences, the health care delivery systems and the elimination of health care disparities. Those students that have completed high school are currently enrolled in college, most are pursuing studies in science and some have now advanced to biomedical and healthcare schools.

We gratefully acknowledge the help of the dedicated counselors and leadership from the Cleveland area High Schools who guided the application process and worked along with committed CWRU faculty members to complete the student selection process.

This program would not be possible without the dedication of the faculty and staff of CWRU School of Medicine and the Case Comprehensive Cancer Center, who have volunteered their time as seminar speakers, mentors and coordinators, taking the high school students into their labs to show them the excitement associated with scientific investigation and discovery. We hope that their efforts will contribute to the students' success and to the future of health, health care and biotech development in Cleveland and around the globe.

We extend our special compliments to the students, who have worked diligently on their research projects, to understand the scientific method and to contribute their talents to solving a variety of fundamental and clinical biomedical challenges. We also extend our appreciation to the students' families for supporting and encouraging their engagement in these academic pursuits.

We thank all of you for your support, your participation, and your encouragement. It is our hope and expectation that, in the near future, we all will benefit from what you have enabled these students to accomplish this summer.

Sincerely,

Nathan A. Berger, M.D.
Distinguished University Professor
Hanna-Payne Professor of Experimental Medicine
Professor, Medicine, Biochemistry, Oncology, Genetics & Genome Sciences
Director, Center for Science, Health & Society
Case Western Reserve University School of Medicine

SEO/YES DONORS & SUPPORTERS

NAME

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University School

Mt. Sinai Health Foundation

ACKNOWLEDGEMENTS

Program Organizer
Center for Science, Health & Society
Nathan A. Berger, MD, Director
J.T. Render, Program Manager

Advisory and Selection Committee
Nathan A. Berger, MD, Center for Science, Health & Society
April Archer-Bailey, Euclid Middle School
Jennifer Cullen, PhD, MPH, Department of Population and Quantitative Health Sciences
Cynthia Dalveren, Cleveland School of Science and Medicine
William Dunn, Cleveland Metro School District
Mike Ford, M.Ed, PhD, Andrews Osborne
Damian Junk, PhD, Case Comprehensive Cancer Center
Sarah Laux, PhD, University School
Crystal Miller, PhD, Hathaway Brown
Cynthia Owusu, MD, MS, Department of Medicine
John Pink, PhD, Case Comprehensive Cancer Center

CWRU Faculty Research Mentors
Drew Adams, PhD, Department of Genetics and Genome Sciences
Kristian Baker, PhD, Department of Genetics and Genome Sciences
James Basilion, PhD, Department of Biomedical Engineering
Nathan Berger, MD, Case Comprehensive Cancer Center
Andrew Blum, MD, PhD, Case Comprehensive Cancer Center
Walter Boron, MD, PhD, Department of Physiology and Biophysics
Mark Cameron, PhD, Department of Population and Quantitative Sciences
Bryan Carroll, MD, PhD, Department of Dermatology
Kenneth Chavin, MD, PhD, Department of Surgery
Fabio Cominelli, MD, PhD, Department of Medicine
Jennifer Cullen, PhD, MPH, Department of Population and Quantitative Health Sciences
David Danielpour, PhD, Case Comprehensive Cancer Center
Michael Decker, PhD, Department of Physiology and Biophysics
Thomas E. (Ted) Dick, PhD, Department of Neurosciences
Agata Exner, PhD, Department of Radiology
Stephen Fink, PhD, Case Comprehensive Cancer Center
Chris Flask, PhD, Department of Radiology
Thomas Gerken, PhD, Department of Biochemistry
Stan Gerson, MD, Case Comprehensive Cancer Center
Mahmoud Ghannoum, PhD, Department of Dermatology
Brian Grimberg, PhD, Case Comprehensive Cancer Center
Kishore Guda, DVM, PhD, Case Comprehensive Cancer Center
Sanjay Gupta, PhD, Department of Urology
Peter Hovmand, PhD, Center for Community Health Integration
Alex Huang, MD, PhD, Department of Pediatrics
Stanley Huang, PhD, Case Comprehensive Cancer Center
Ge Jin, PhD, Case Comprehensive Cancer Center
Siran M. Koroukian, PhD, Department of Population and Quantitative Health Sciences
Allison Kraus, PhD, Department of Pathology
John Letterio, MD, Department of Pediatrics

ACKNOWLEDGEMENTS Continued

CWRU Faculty Research Mentors

Alan Levine, PhD, Department of Molecular Biology and Microbiology
Anant Madabhushi, PhD, Department of Biomedical Engineering
Ganapati Mahabaleshwar, PhD, Department of Pathology
Danny Manor, PhD, Department of Nutrition
Sanford Markowitz, MD, PhD, Departments of Medicine, Genetics
Thomas McCormick, PhD, Department of Dermatology
Lin Mei, MD, PhD, Department of Neurosciences
Helen Miranda, PhD, Department of Genetics and Genome Sciences
Lalitha Nayak, MD, Case Comprehensive Cancer Center
Quintin Pan, PhD, Department of Otolaryngology
Reshmi Parameswaran, PhD, Department of Pathology
Paul Park, PhD, Department of Ophthalmology
Andrew Pieper, MD, PhD, Department of Psychiatry
Theresa Pizarro, PhD, Department of Pathology
Aaron Proweller, MD, PhD, Department of Medicine, Cardiology
William Schiemann, PhD, Case Comprehensive Cancer Center
Alvin Schmaier, MD, Departments of Medicine and Pathology
Fredrick Schumacher, PhD, Department of Population and Quantitative Health Sciences
Can Shi, PhD, Department of Medicine, Cardiology
Neena Singh, MD, PhD, Department of Pathology
Andrew Shoffstall, PhD, Department of Biomedical Engineering
Evi Stavrou, MD, Case Comprehensive Cancer Center
Blanton Tolbert, PhD, Department of Chemistry
Erica Trapl, PhD, Department of Population and Quantitative Health Sciences
Horst Von Recum, PhD, Department of Biomedical Engineering
Satish Viswanath, PhD, Department of Biomedical Engineering, Radiology
David Wald, MD, PhD, Department of Pathology
John (Zhenghe) Wang, PhD, Department of Genetics & Genome Sciences
Aaron Weinberg, DMD, PhD, Department of Biological Sciences, Dental Medicine
Jordan Winter, MD, Department of Surgery
Anthony Wynshaw-Boris, MD, PhD, Department of Genetics & Genome Sciences
Rong Xu, PhD, Center for Artificial Intelligence
Vivien Yee, PhD, Case Comprehensive Cancer Center
Hung-Ying Kao, PhD, Department of Biochemistry
Mei Zhang, PhD, Department of Biomedical Engineering
Xiongwei Zhu, PhD, Department of Pathology

ACKNOWLEDGEMENTS Continued

2022 SEO/YES Lunch & Learn and Career Café Seminar Speakers

Stanley Adoro, PhD, Department of Pathology
Nathan Berger, MD, Case Comprehensive Cancer Center
Debra Bruno, MD, Case Comprehensive Cancer Center
Arnold Caplan, PhD, Department of Biology
Amitabh Chak, MD, Department of Medicine, Gastroenterology
Jennifer Cullen, PhD, MPH, Department of Population and Quantitative Health Sciences
David Danielpour, PhD, Case Comprehensive Cancer Center
Afshin Dowlati, MD, Department of Medicine, Oncology
Damian Junk, PhD, Case Comprehensive Cancer Center
Emmitt Jolly, PhD, Department of Biology
Andrew Pieper, MD, PhD Department of Psychiatry
Kristina Knight, PhD, Department of Population and Quantitative Health Sciences
John Letterio, MD, PhD, Department of Pediatrics, Hematology & Oncology
Andrew Sloan, MD, Department of Neurological Surgery
Kurt Stange, MD, PhD, Center for Community Health Integration
Erika Trapl, PhD, Department of Population and Quantitative Health Sciences
Robert Salata, MD, Department of Medicine
George Yendewa, MD, MPH, Department of Medicine
Joe Willis, PhD, Department of Pathology

2022 SEO/YES Near Peer Mentors

Alicia Aguilar
Yaw Asante
Liz Anderson
Emily Arzola
Oscar Bautista
Danielle Browne
Yuli Buckley
Kevin Felt
Rachael Gowen
Allison Grenell
Alex Gurgis
Ethan Honeycutt
Peinan Hu
Kayla Kindig
Raquel Lopez de Boer
Ben Mittman
Otis Pinkard
Eric Prileson
Jerrik Rydbom

2022 Participating High Schools

Andrews Osborne Academy
Avon High School
Beachwood High School
Charles F. Brush High School
Cleveland Heights High School
Cleveland School of Science and Medicine
Copley High School
Facing History New Tech
Gilmour Academy
Harrisburg Academy
Hathaway Brown School
Hawken School
John F. Kennedy High School
Lake Ridge Academy
Laurel School
Mayfield High School
Orange High School
Padua Franciscan High School
Revere High School
Saint Edward High School
Saint Ignatius High School
Shaker Heights High School
Solon High School
Stow Munroe Falls High School
Twinsburg High School
University School
Westlake High School

SEO/YES PROGRAM OUTCOMES

Overall, 2004-2022

496 High School Student Participants
93% High School Graduation
88% College Matriculation

Most Recent 5 Years, 2018-2022

186 High School Student Participants
100% High School Graduation
97% College Matriculation

Colleges Entered by SEO/YES High School Graduates 2018-2022

CWRU - 21
The Ohio State University – 10
Cuyahoga Community College – 4
Harvard – 2
University of Akron - 2
Ursuline College - 2
Columbia University
University of Michigan
Northwestern University
Johns Hopkins University - 2
Washington University in St. Louis
Yale University - 2
University of Notre Dame - 3
University of Pennsylvania - 3
Walsh University
Bowling Green
Xavier of Louisiana
Marist College
Duke University
College of Wooster
University of Richmond
Muskingum College
Kenyon College
Oberlin College
University of Dayton
United States Naval Academy
Nova Southeastern University
University of Maryland
Vanderbilt
Cornell
University of Rochester
University of Cincinnati
Arizona State
Phillips Exeter
Carleton College
Spellman College

SEO & YES ALUMNI and COLLEGES

Student	High School	College
Marie Abdul-Karim	James F. Rhodes High School	Penn State Cuyahoga Community College CWRU Cleveland State University
Nichele Abeyesundere	Shaker Heights High School	Notre Dame
Amal Aboumerhi	Westlake High School	
Henrietta Abrams	East Technical High School	Cuyahoga Community College
Adesewa Adeweso	Mayfield High School	
Nneka Adigwe	John F. Kennedy High School	Cuyahoga Community College Kent State University
Madeline Adler	Laurel School	
Nassim Aidja	Mayfield High School	
Jordan Alexander	John F. Kennedy High School	
Rama Al Ghalayini	Westlake High school	
Manal Alkabani	Cleveland School of Science and Medicine	Case Western Reserve University
Raneem Almhana	Saint Joseph Academy	
Hussein Al Raheel	Cleveland School of Science and Medicine	
Dominic Anderson	John F. Kennedy High School	Cuyahoga Community College
Anushree Aneja	Solon High School	University of Pennsylvania
Katherine Antepara	James F. Rhodes High School	Youngstown State Cuyahoga Community College
Zain Anwar	University School	
Marangely Aponte	James F. Rhodes High School	Cuyahoga Community College
Shruthika Araselvan	Hathaway Brown School	University of Rochester
Alexis Armstead	Glenville High School	Cuyahoga Community College Hiram College

Student	High School	College
Dylan Arnold	Cleveland School of Science and Medicine	Cuyahoga Community College Case Western Reserve University
Omer Ashruf	University School	NEOUMED/Univ. of Akron
Zehra Ashruf	Hathaway Brown	Case Western Reserve University
Zaid Ashruf	University School	
Vivek Aslot	Westlake High School	Case Western Reserve University
Abdur At-Thababi	Glenville High School	Cleveland State University
Rithvik Ayyagari	St. Ignatius High School	University of Cincinnati
Audreanna Bailey	Glenville High School	Cuyahoga Community College
De'va Baker	James F. Rhodes High School	Clark State Community College
Nathan Ballman	Shaker Heights High School	
Anusha Bangalore	Westlake High School	Case Western Reserve University
Sergio Banks	Glenville High School	Bryant & Stratton College Cuyahoga Community College
Rhycordia Barner	John F. Kennedy High School	
Derricka Barron	Cleveland School of Science and Medicine	John Carroll University Ursuline College
Rachel Bart	Cleveland School of Science and Medicine	
Crisharon Beale	Collinwood High School	Abilene Christian University University of Toledo
Abigail Beard	Shaker Heights High School	College of Wooster
Anna Beck	Laurel School	The Ohio State University
Julian Berger	University School	
Laneisha Berry	Glenville High School	Lakeland Community College
Mercedes Beverly	James F. Rhodes High School	The Ohio State University

Student	High School	College
Ramon Bhambra	Twinsburg High School	Kent State University
Sahaj Bhambra	Twinsburg High School	Kent State University Hiram College Case Western Reserve University
Ian Bhatia	Shaker Heights High School	University of Vermont
Sharan Bhatia	University School	Cleveland State Purdue University
Aarshvi Bhatt	Walsh Jesuit High School	The Ohio State University
Aaruni Bhatt	Walsh Jesuit High School	The Ohio State University
Josh Bickerstaff	University School	Washington University in St. Louis
Kayla Blake	Cleveland School of Science and Medicine	Cuyahoga Community College
Thomas Blossom	University School	
Cashalynn Bolden	Glenville High School	Cleveland State University
Emily Boron	Shaker Heights High School	
Anise Bowman	Cleveland School of Science and Medicine	University of Maryland Case Western Reserve University
Alisha Boyce	Glenville High School	
Lavontae Bradford	Glenville High School	Kent State University
Luke Brandon	University School	
Peter Breen	Saint Ignatius High School	SUNY Finger Lakes Community College
Sha'nya Brightharp	John Hay Early College	University of Akron
Anaria Britt	Hathaway Brown School	
Amber Brown	James F. Rhodes High School	Sanford Brown College South College
Kenaisha Brown	John F. Kennedy High School	Kent State University
Safwaan Brown	Glenville High School	Montgomery College/U.Toledo

Student	High School	College
Taquita Brown	Glenville High School	Cuyahoga Community College
David Buchinsky	University School	Washington University
DaQuan Bush-Pierce	Glenville High School	Kent State University
Janae Camargo	Andrews Osborne	Cornell University
Brittany Camp	Glenville High School	Cuyahoga Community College Cleveland State University
Keelin Carrocia	James F. Rhodes High School	John Carroll University
David Carter	Cleveland School of Science and Medicine	Case Western Reserve University
Michael Castellanos	University School	U.S. Naval Academy
Cara Castro	Hathaway Brown School	
Faye Catacutan	James F. Rhodes High School	The Ohio State University University of Toledo
Neha Chellu	Beachwood High School	Johns Hopkins University
Amy Chen	Beachwood High School	University of Pennsylvania
DeAndra Childress	John F. Kennedy High School	The Ohio State University
Maia Childress	Nathan Hale High School	
Woochul Choi	Revere High School	Northwestern University University of Akron
Suhas Cingireddi	University School	Boston College
Desire Clark	Cleveland School of Science and Medicine	
Katherine Clark	Laurel School	Miami of Ohio
Candi Closson	James F. Rhodes High School	Bryant & Stratton College Kent State University Indiana Wesleyan University
Javan Cobb	University School	Vanderbilt University
Melanie Moreno Colon	James F. Rhodes High School	Cleveland State University
Cyril Creque-Sarbinowski	Cleveland School of Science and Medicine	M.I.T John Hopkins University

Student	High School	College
Danyel Crosby	John Hay Early College	Cleveland State Case Western Reserve University
Tyreshea Crumedy	John F. Kennedy High School	Cuyahoga Community College Central State University
Vareliz Cruz	James F. Rhodes High School	Cuyahoga Community College
Katherine Dai	Solon High School	The Ohio State University
Imani Dalton	Glenville High School	Cuyahoga Community College The Art Institute of Pittsburgh
Dhweeja Dasarathy	Hawken School	Harvard University
Nikita Davidenko	University School	Case Western Reserve University
Jeremiah Davis	Glenville High School	Cleveland State University
Michael Davis	Glenville High School	Kent State University
Landon Dawson	Avon High School	The Ohio State University
Maxinae DeJesus	James F. Rhodes High School	
Jade Del Orbe	Facing History New Tech	Bowling Green
Manzili Denis	University School	
Denisha Derrick	Glenville High School	Wilkes University Chamberlain University
Alex Devastey	Glenville High School	Cleveland State University
Katelyn Devereaux	Walsh Jesuit High School	Colgate University
Mary Draper	John F. Kennedy High School	Indiana Wesleyan University
Amy Duan	Solon High School	
Latisha Duncan	James F. Rhodes High School	Cleveland State University Walden University
Claire Dunn	Shaker Heights High School	
Tommy Dunn	Shaker Heights High School	Phillips Exeter
Jeaney Durand	John F. Kennedy High School	The Ohio State University

Student	High School	College
Adrik Dutta	Shaker Heights High School	
Le'Aona DySart	Cleveland School of Science and Medicine	Eastern Michigan
Chloe Echols	Hathaway Brown School	
Samantha Edwards	Glenville High School	Ohio State University
Simone Edwards	John F. Kennedy High School	Kent State University
Ahmed Elsharkawy	St. Edward High School	The Ohio State University
Karim Elsharkawy	St. Edward High School	
Amanda Rae Erickson	James F. Rhodes High School	
Kaitlyn Ernst	Laurel School	
Parker Ernst	University School	University of Richmond
Adam Esa	Saint Edward High School	
Mary Estafanous	Laurel School	
Jamila Evans	James F. Rhodes High School	Bismark State College Cuyahoga Community College
Adora Ezepue	Campus International High School	The Ohio State University
Jenny Fan	Revere High School	Columbia University
Julia Fan	Solon High School	Case Western Reserve University Cornell University
Anna Ferro	Cleveland School of Science and Medicine	Oberlin College
Abem Fetene	University School	Tufts University
Emanual Fetene	University School	Wesleyan University
Sydney Fields	Twinsburg High School	Xavier of Louisiana
Clyde Fisher	Benedictine High School	Saint Leo University

Student	High School	College
La'Mia Flowers	John F. Kennedy High School	Miami University
Victoria Fort	Glenville High School	John Carroll University
Dennae Foster, Jr.	Ginn Academy	Ursuline College
Britany Fulcomer	James F. Rhodes High School	Cuyahoga Community College
Jazmine Fulton	John F. Kennedy High School	University of Toledo
Fahness Freeman	Cleveland Heights High School	
Benjamin Frostino	Padua Franciscan High School	Notre Dame
Anish Ganesh	University School	The Ohio State University
Amie Garcia	James F. Rhodes High School	University of Alaska Cleveland State University
Emilie Garcia	James F. Rhodes High School	University of Toledo Cleveland State University
Rohan Garg	University School	Yale University
My'Desire George-Wiggins	Shaw High School	
Debolina Ghosh	Hathaway Brown	Harvard University Case Western Reserve University
Isaiah Gilbert	University School	
Anthony Gillespie Jr.	Gilmour Academy	Hampton University
Deshawna Gilmore	John F. Kennedy High School	Cuyahoga Community College
Tesha Gilmore	John F. Kennedy High School	Ursuline College
Wiktor Golczak	Mayfield High School	Case Western Reserve University
Tarini Gowda	Revere High School	
Kevin Gramajo	John Marshall High School	The Ohio State University
Adrien Grant	Glenville High School	Cuyahoga Community College
Cory Grant	Glenville High School	Cuyahoga Community College Kent State University
Jarod Graves	Glenville High School	J. Sargeant Reynolds CC Bowling Green State Univ. US Marine Corps

Student	High School	College
Kalita Griffin	Glenville High School	Cuyahoga Community College Bowling Green State University
Nalin Gupta	Solon High School	
Nikki Haab	John F. Rhodes High School	Cleveland State University
Jaida Hadley	Cleveland Metropolitan Remote School	
Kenneth Hale	Cleveland School of Science and Medicine	Bates College
Bruce D. Hale, Jr.	Cleveland School of Science and Medicine	University of Toledo
Quinta Hamilton	Glenville High School	Kent State University
Trevon Hamilton	John F. Kennedy High School	Purdue University
Madison Hampton	Cleveland School of Science and Medicine	
April Hardaway	John F. Kennedy High School	Bryant & Stratton College Eastern Gateway Community College
Jason Hardeo	Facing History New Tech	Cuyahoga Community College
Justin Hardeo	Facing History New Tech	Cuyahoga Community College
Connor Harris	University School	
Gia Harris	John F. Kennedy High School	Cuyahoga Community College Hiram College
Isabel Hart	Shaker Heights High School	
Lauren Harville	John F. Kennedy High School	Cleveland State University
Ali Hasan	James F. Rhodes High School	The Ohio State University
Charity Henderson	Glenville High School	Cuyahoga Community College Cleveland State University
Joshua Hill	Cleveland School of Science and Medicine	University of Toledo
Brittny Hines	Campus International High School	The Ohio State University
Lagia Hinton	John F. Kennedy High School	Kent State University Cleveland State University

Student	High School	College
Hannah Holt	Charles F. Brush High School	
Devona Hopgood	Glenville High School	University of Phoenix
Nathan Hsiao	Westlake High School	Case Western Reserve University
Janae Hughes	Cleveland School of Science and Medicine	Harvard University
Manith Humchad	Brecksville-Broadview Heights High School	University of Akron
Le'Shai Hunt	Glenville High School	The Ohio State University
Antuoine Hunt-Strong	Glenville High School	Waldon University Ohio University College of Wooster
Marko Iskander	James F. Rhodes High School	Cuyahoga Community College Baldwin Wallace College
Ahmad Islambouli	Cleveland School of Science and Medicine	Case Western Reserve University
Sabrina Jackson	Glenville High School	Malone University
Sha'Niya Jackson	Shaw High School	
Ta'nea Jackson	Shaw High School	
ShaRayne Jackson	Glenville High School	Miami University Saint Louis University
Valerie Jackson	Glenville High School	Cuyahoga Community College Case Western Reserve University
Rahul Jagetia	University School	Princeton University
Rahul Jain	Westlake High School	University of South Florida
Rohan Jaiswal	Solon High School	The Ohio State University
Anushree Jakate	Solon High School	The Ohio State University
Srujan Jaladi	Solon High School	Cuyahoga Community College
Benjamin Jamal	Shaker Heights High School	
Suhib Jamal	Cleveland School of Science and Medicine	Case Western Reserve University

Student	High School	College
Isaac Jang	Orange High School	Case Western Reserve University
Jonathan Jang	University School	The Ohio State University
Che Jarvis	University School	University of San Diego
Asha Jha	Shaker Heights High School	
Kevin Jiang	Shaker Heights High School	Duke University
Davionna Johnson	Euclid High School	
Kwanza Johnson	Cleveland School of Science and Medicine	Bethune-Cookman University
Cheyenne Jones	Hathaway Brown	
Jasmine Jordan	Glenville High School	Case Western Reserve University
Mariah Jordan	Shaker Heights High School	UNC Chapel Hill The Ohio State University
Vishwum Kapadia	University School	
Timofii Karamalak	Facing History New Tech	Cleveland State
Sai Karnati	University School	Brown University
Hannah Kassaie	Mayfield High School	Lakeland Community College
Elisa Katz	Shaker Heights High School	
Sukmani Kaur	Hathaway Brown	University of Pennsylvania
Shria Kavaturu	Copley High School	
Ella Kazazic	Hathaway Brown	Massachusetts Institute of Technology
Alicia Keely	James F. Rhodes High School	Bowling Green State University
Allison Kennedy	John F. Kennedy High School	Cleveland State University Case Western Reserve University
Julia Kiefer	Charles F. Brush High School	Franklin and Marshall College
Donghan (Daniel) Kim	Hudson High School	Brown University
Minjun Kim	St. Edward High School	

Student	High School	College
Kareem King	Charles F. Brush High School	Harvard University
Veronica Kissoon	North Olmsted High School	Cleveland State
Rashon Knight	Benedictine High School	Allegheny College
Wyson Kong	Cleveland School of Science and Medicine	The Ohio State University
Ishita Kopparapu	Hathaway Brown	
Ajay Krishnaney	University School	Washington University
Nikhita Kumar	Hathaway Brown	SUNY Albany
Prathna Kumar	Hathaway Brown	Dartmouth University
Rohan Kumar	University School	
Lily Kwiatkowski	Cleveland School of Science and Medicine	Case Western Reserve University
Adlai Kwofie	Cleveland School of Science and Medicine	The Ohio State University
Graham Lane	University School	University of Chicago
Rayyan Laryea	Cleveland School of Science and Medicine	
Mya Lavender	John F. Kennedy High School	
Bauldwine Lazare	Cleveland Early College	
Timothy Lett	Glenville High School	Cuyahoga Community College Kent State University
Arthur Li	Lawrenceville School	University of Pennsylvania
Kate Lindley	Harrisburg Academy	
Patricia Lindsey	Cleveland Heights High School	Cleveland State University
Tamika Littlejohn	Glenville High School	The Ohio State University University of Toledo
Karis Liu	Solon High School	Northwestern University
Laura Llapa	James F. Rhodes High School	Miami University

Student	High School	College
Arik London	Cleveland School of Science and Medicine	
Noah Lockhart	John F. Kennedy High School	
Andrew Loney	Shaker Heights High School	
Ivana Macazana	Bedford High School	Case Western Reserve University
Alyssa Macko	James F. Rhodes High School	Ohio University
Rhea Mahajan	Hathaway Brown School	University of Akron
Sarisha Mahajan	Revere High School	University of Michigan
Omar Mahmoud	Cleveland School of Science and Medicine	Dartmouth College
Yousef Mahmoud	Cleveland School of Science and Medicine	Case Western Reserve University
Charvi Malhortra	Western Reserve Academy	Case Western Reserve University Drexel University
Diana Malkin	Hathaway Brown	Boston University
Cheyenne Marolt	Cleveland School of Science and Medicine	
Ashley Martin	John F. Kennedy High School	
Natalie Martinez	James F. Rhodes High School	Bryant & Stratton College Cleveland State University
Henry Massey	University School	College of William & Mary
Kortney Mave	Berea Midpark High School	Cuyahoga Community College The Ohio State University
Atreya McCall	John F. Kennedy High School	Cleveland State University
Michael McCarthy	James F. Rhodes High School	Cuyahoga Community College Cleveland State University
Quinn McDermott	Shaker Heights High School	
Shay McDermott	Shaker Heights High School	Case Western Reserve University
Nichola McDowell	Cleveland School of Science and Medicine	Case Western Reserve University

Student	High School	College
Tayla McKenzie	Cleveland School of Science and Medicine	Spellman College
Antoinne McKinney	Glenville High School	Cleveland State University
DeVaughn McNary	Glenville High School	ITT Technical Institute
Akhil Medarametla	University School	Case Western Reserve University
Ella Meges	Padua Franciscan High School	
Arul Mehta	St. Ignatius High School	Case Western Reserve University
Ira Mehta	Lakeridge Academy	
Rafael Mercado	James F. Rhodes High School	
Beverly Mercedes	James F. Rhodes High School	Kent State University
Kyimani Miller	Beachwood High School	Ursuline College
Toussaint Miller	University School	Harvard University
Ebenezer Minaya	James F. Rhodes High School	Cuyahoga Community College
Yaqueline Miranda	James F. Rhodes High School	Cuyahoga Community College
Pratistha Mishra	Cleveland School of Science and Medicine	John Carroll University
Alexis Mitchell	School of Science and Medicine	Cleveland State University
Marcelita Moore	John F. Kennedy High School	Ursuline College
Janailyn Morris	Cleveland School of Science and Medicine	
Dahlia Moskowitz	Fuchs Mizrachi High School	The Ohio State University
Jaida Motley	John F. Kennedy High School	
Nathan Mu	University School	Yale
Uwela Mugabo	Facing History New Tech High School	
Patrick Murphy, Jr.	John F. Kennedy High School	Cleveland State University

Student	High School	College
Ihunanya Muruako	Cleveland School of Science and Medicine	University of Michigan Lorain County Community College
Ogechi Muruako	Cleveland School of Science and Medicine	Cleveland State The Ohio State University
George Nageeb	University School	Harvard University
Naraen Naidu	Twinsburg High School	
Mary Nazimiec	Cleveland School of Science and Medicine	Cleveland State University
Tina Nguyen	Mayfield High School	
Antoine Nichols	Cleveland School of Science and Medicine	The Ohio State University
Kiana Nicholson	Glenville High School	University of Phoenix
Sullymar Nieves	Facing History New Tech	Cuyahoga Community College
Eric Nouafo	Solon High School	University of Pennsylvania
Micha Nouafo	Solon High School	University of Pennsylvania
Fata Nyei	Cleveland School of Science and Medicine	
Gile Nzitunga	Glenville High School	University of Dayton
Ayonitemi Odukoya	Solon High School	Case Western Reserve University
Jesutomi Odukoya	Solon High School	Yale University
Oyinkansola Odukoya	Solon High School	Case Western Reserve University
Richard Ojo	Eleanor Roosevelt High School	University of Maryland
Andrea Okocha	Bedford High School	University of Rochester
Aida Omoijuanfo	Glean Academy	
Ebahi Omoijuanfo	Glean Academy	
Ese-Onosen Omoijuanfo	Glean Academy	University of Notre Dame
Jason Ong	Solon High School	University of Pittsburgh

Student	High School	College
Meredith Onnie	James F. Rhodes High School	Cuyahoga Community College Kent State University
Angel Ononogbo	Orange High School	Arizona State University
Ogechi Onyeukwu	Cleveland School of Science and Medicine	Cuyahoga Community College Cleveland State University
Kwabena Owusu	Solon High School	Cuyahoga Community College
Nana Owusu	Solon High School	Yale University
Sairam Pantham	Solon High School	
John Pape	University School	Colgate
Gabriel Papell	Shaker Heights High School	The Ohio State University
Taniya Parker	Glenville High School	University of Akron
Chantae Parsons	John F. Kennedy High School	University of Dayton
Garv Patel	Andrews Osborne Academy	
Kaitlyn Pawul	James F. Rhodes High School	Cuyahoga Community College
Rica Payne	Glenville High School	Cleveland State University
Shaquona Pearsall	Glenville High School	Kent State University
Haridu Peiris	Twinsburg High School	
Angelica Pickett	John F. Kennedy High School	Ohio State University
Eric Pieper	Shaker Heights High School	
Justin Pieper	Shaker Heights High School	
Alaina Pizarro	Hawken School	
Chad Porter	Villa Angela/St. Joseph High School	The Ohio State University
Ta'Shiyah Porter	Cleveland School of Science and Medicine	
Bre-Shay Potts	John F. Kennedy High School	Cleveland State University

Student	High School	College
Adrien Powell	New Tech East	
Trinity Pruitt	Cleveland School of Science and Medicine	
William Qu	Solon High School	Case Western Reserve University Emory University
Riley Rainey	Glenville High School	University of Phoenix John Carroll University
Keyvon Rashidi	University School	Case Western Reserve University
Gabrielle Raymont-Scott	Cleveland School of Science and Medicine	Miami University
Amaya Razmi	Hathaway Brown	Harvard University
Logan Readinger	James F. Rhodes High School	Bryant & Stratton College
Jessenia Rebello	James F. Rhodes High School	Case Western Reserve University
Anika Rede	Hathaway Brown	UC Berkeley
Shantall Reece	John F. Kennedy High School	Cuyahoga Community College
Angela Richmond	John F. Kennedy High School	American Intercontinental University
Martina Richter	Shaker Heights High School	Case Western Reserve University
Samara Rivchun	Laurel School	
Krystle Rivera	James F. Rhodes High School	John Carroll University Cleveland State University
Tai Roberts	Andrews Osborne Academy	
Kala Rodriguez	James F. Rhodes High School	
Sophia Rose	Shaker Heights High School	Carnegie Mellon University
Shira Rosenberg	Hathaway Brown	Northeastern University
Imani Rucker	Hathaway Brown	Kenyon College
Jacob Rudin-Luria	Hawken School	

Student	High School	College
Nichelle Ruffin	John Hay High School	Case Western Reserve University
Lilly Russo	Gilmour Academy	
Jonica Rutledge	John F. Kennedy High School	Lakeland Community College Western Governors University
Hamza Said	Westlake High School	
Anna Saline	Gilmour Academy	
James San	John Hay High School	Case Western Reserve University
Harsha Sanaka	Hawken Upper School	
Brittany Sanders	John F. Kennedy High School	Cleveland State University
Yaritizy Santizo	Cleveland School of Science and Medicine	
Samantha Schall	Cleveland School of Science and Medicine	Case Western Reserve University
Leo Schirokauer	Shaker Heights High School	Harvard University
Samuel Schlang	Hawken School	University of Chicago
Ariel Scott	John F. Kennedy High School	Coastal Carolina Community College
Heather Scott	James F. Rhodes High School	Ursuline College Chamberlain University
Joseph Scott	Cleveland School of Science and Medicine	
Danae Seals	St. Villa Angela-St. Joseph High School	
Khadijah Seay	John Hay High School	Bryn Mawr College Temple University
Vishal Sentilkumar	Brunswick High School	Case Western Reserve University
Aaron Sepulveda	James F. Rhodes High School	Case Western Reserve University
Cesar Sepulveda	James F. Rhodes High School	John Carroll University
Student	High School	College

Soham Shah	**St. Ignatius High School**	
Sorina Shahadeh	**James F. Rhodes High School**	**Bryant & Stratton College** **Baldwin Wallace University**
Yasmeen Shahadeh	**James F. Rhodes High School**	**Kent State University**
Kulthoom Shaheed	**Campus International High School**	**Cuyahoga Community College**
Zaynab Shaheed	**Campus International High School**	**Case Western Reserve University**
Zayne Shaheed	**Campus International High School**	
Sidney Sheppert	**Stow Munroe Falls High School**	
Sandy Shen	**Solon High School**	**University of Akron** **Swarthmore College**
Shannan Shih	**Downington STEM Academy (PA)**	
Lashaune Short	**John F. Kennedy High School**	**California College**
Channell Shoulders	**Glenville High School**	**Cuyahoga Community College**
Dylan Siegler	**University School**	**Georgia Tech**
Layce Simbeck	**Facing History New Tech**	**Cuyahoga Community College**
Jasmine Sims	**James F. Rhodes High School**	**The Ohio State University**
Tarini Singh	**Berea Midpark High School**	**Caltech**
Erica Smith	**Glenville High School**	**Lakeland Community College** **Cleveland State University**
Kayla Smith	**Cleveland School of Science and Medicine**	
Maya Smith	**Cleveland School of Science and Medicine**	**The Ohio State University**
Sherry Smith	**Glenville High School**	
She'Rise Thompson-Smith	**Glenville High School**	**Case Western Reserve University**
Asaan Snipes-Rea	**University School**	**Oberlin College**

Student	High School	College
Pranav Sompalle	Mayfield High School	
Summer Sorrell	James F. Rhodes High School	Cuyahoga Community College Cleveland State University
William Spears	James F. Rhodes High School	Cuyahoga Community College Cleveland State University
Anaya Spencer	Cleveland School of Science and Medicine	Cuyahoga Community College
Terrah Spencer	Glenville High School	Bryant & Stratton College Tuskegee University
Kristen Stash	James F. Rhodes High School	Cuyahoga Community College Ursuline College
Charnae Steward	John F. Kennedy High School	University of Toledo Tiffin University
Ryckia Sutton	Cleveland School of Science and Medicine	Xavier of Louisiana
Isabel Svec	Padua Franciscan High School	
Diya Swain	Shaker Heights High School	
Hans Swain	University School	
Ian Swain	University School	Case Western Reserve University
Eric Swander	James F. Rhodes High School	Cuyahoga Community College Hiram College
Josea Switzer	Glenville High School	Akron University
Maheera Syed	Strongsville High School	
Rubab Syed	Strongsville High School	Case Western Reserve University
Maya Tang	Hathaway Brown	
Kamar Taweel	Cleveland School of Science and Medicine	Case Western Reserve University
Aliysha Taylor	James F. Rhodes High School	Chattahoochee Technical College

Student	High School	College
Mackensie Thompson	Andrews Osborne Academy	
David Tibbitts	James F. Rhodes High School	Cleveland State University
Dashiell Tidrick	Saint Ignatius High School	
Owen Tolbert	Shaker Heights High School	
Lauren Torres	Facing History New Tech	
Giovanni Tripi	Charles F. Brush High School	
Tavaris Tucker	John F. Kennedy High School	Cuyahoga Community College Cleveland State University
Reece Turner	Shaker Heights High School	
Igor Tuteleman	Solon High School	Case Western Reserve University
Mythili Ungarala	Shaker Heights High School	
Mythreyi Ungarala	Shaker Heights High School	
Sahishnu Vallabhajoysula	Avon High School	
Zoie VanHuffel Gouldlock	Bedford High School	Case Western Reserve University
Mantas Viazmitinas	Westlake High School	University of Pennsylvania
Marcela Villegas	James F. Rhodes High School	Copper Mountain College
Damon Wallace	Nordonia High School	Walsh University
Kennon Walton	University School	Duke University
Chougyu Wang	St. Ignatius High School	
Evan Wang	Beachwood High School	
Lindsey Wang	Orange High School	
William Wang	Orange High School	
Yinyin Wang	Shaker Heights High School	
Janiece Warfield	Glenville High School	Cleveland State University

Student	High School	College
Gwen Weagraff	Avon High School	
Bianca West	Glenville High School	Baldwin Wallace University
Benjamin Weil	Charles F. Brush High School	
Isaiah Whatley	Mayfield High School	The Ohio State University
Lawrence White	Glenville High School	Akron University
Alexandria Williams	James F. Rhodes High School	Cleveland State University
Chanelle Williams	Glenville High School	Bowling Green University
Denyse Williams	Glenville High School	Lakeland Community College
Lauren Williams	John F. Kennedy High School	Cuyahoga Community College
Dianea Willis	Glenville High School	University of New Mexico
Allan Willmon, Jr	Cleveland School of Science and Medicine	Case Western Reserve University
Emily Wilson	Hathaway Brown School	
Isaiah Wilson	Cleveland School of Science and Medicine	Case Western Reserve University
Matthew Wilson	Solon High School	The Ohio State University
Gavyn Woo	Cleveland School of Science and Medicine	Case Western Reserve University
Alice Wu	Solon High School	Duke University
Daisy Wu	Solon High School	Case Western Reserve University University of Toledo
Tionna Wynn	Glenville High School	Cuyahoga Community College Akron University
Victor Xie	Solon High School	Johns Hopkins
Weixiong Xu	Cleveland School of Science and Medicine	Ohio State University
Maggie Yang	Solon High School	Washington University in St. Louis
Chasity Young	John F. Kennedy High School	Kent State University

Student	High School	College
Adam Yu	Solon High School	Vanderbilt
Kimberly Zarczynski	James F. Rhodes High School	Hiram College
Alexia Zelada	Cleveland School of Science and Medicine	
Chelsea Zheng	Beachwood High School	Case Western Reserve University
Hayley Zheng	Twinsburg High School	
Amy Zhou	Beachwood High School	
Kevin Zhou	Solon High School	Case Western Reserve University
Yong Liang Zhou	Cleveland School of Science and Medicine	John Carroll University

SEO & YES COLLEGE STUDENT ALUMNI

STUDENT	COLLEGE/GRADUATE SCHOOL
Cassidy Abdeen	Case Western Reserve University/ The Ohio State University SOM
Dylan Arnold	Case Western Reserve University
Sufia Bakshi	Case Western Reserve University/ Weill Cornell Medical College
Ramon Correa	Case Western Reserve University
Adora Ezepue	The Ohio State University
Nikita Davidenko	Case Western Reserve University
Shria Donthi	Case Western Reserve University/ Case Western Reserve University SOM
Joseph Gutbrod	University of Chicago/ Washington University St. Louis SOM
Jack Kincaid	Case Western Reserve University/ University of Cambridge
Zain Khawaja	Case Western Reserve University/ Case Western Reserve University SOM
Jesutomi Odukoya	Yale University
Richard Ojo	University of Maryland College Park
Ese Omoijuanfo	University of Notre Dame
Samantha Rodriguez	Case Western Reserve University
Heidi Schmidt	Case Western Reserve University/ University of Pittsburgh SOM
Maya Smith	The Ohio State University
Esmeralda Terrazas	Case Western Reserve University
Luis Tirado	Case Western Reserve University
Gretchen Weiss	Case Western Reserve University/ University of Buffalo SOM

YES TEACH TO BEAT CANCER TEACHER ALUMNI

TEACHER	HIGH SCHOOL
Angela Augustus	CMSD Mentor K 12 Fuel
Billy Augustus	CMSD Substitute Teacher
Gregory Archer	James F. Rhodes High School
April Archer-Bailey	Euclid Middle School
Wilmarie Busher-Betancourt	Cleveland School of Science and Medicine
William Dunn	Glenville High School
Michael Ford	Andrews Osborne Academy
Sharita Hill	Shaker Heights High School
Sergey Kolomiyets	Facing History New Tech
Deepshikha Paul	Max Hayes High School
Kim Swaggard-Svec	Cleveland School of Science and Medicine
Mike Van Kerkhove	Charles F. Brush High School
Jason Walker	Shaker Heights High School

2022 SEO/YES STUDENT RESEARCH POSTERS

Poster #	Student and High School	Title	Advisor	Department
1.	Nichele Abeyesundere Shaker Heights High School	Explaining the Cleveland African American Prostate Cancer Project to Lay People	Erika Trapl, PhD	Department of Population and Quantitative Health Sciences
2.	Amal Aboumerhi Westlake High School	COVID-19 and Transplant Patients: Mandatory Vaccine Requirements in Waitlisted Transplant Patients	Kenneth Chavin, MD, PhD	Department of Surgery
3.	Adesewa Adeweso Mayfield High School	Vitamin E and through what nuclear receptors can induce gene expression	Danny Manor, PhD	Department of Nutrition
4.	Maddy Adler Laurel School	The Effect of Hypoxia on Vascular Smooth Muscle Cell Behavior	Aaron Proweller, MD, PhD	Department of Medicine, Cardiology
5.	Nassim Aidja Mayfield High School	Quantitative MRI Assessments of Kidney Disease Progression in Patients with Autosomal Recessive Polycystic Kidney Disease (ARPKD)	Chris Flask, PhD	Department of Radiology
6.	Zain Anwar University School	Combination Therapy Promotes Increased IFN-β Production in Pediatric and AYA Sarcomas via the cGAS-STING Pathway	Alex Huang, MD, PhD	Department of Pediatrics
7.	Zaid Ashruf University School	Identification of Gene Targets by Novel Long Intergenic Non-coding RNA in Esophageal Adenocarcinoma	Kishore Guda, DVM, PhD	Case Comprehensive Cancer Center
8.	Nathan Ballman Shaker Heights High School	Potential Therapeutic Targets in Upper Gastrointestinal Malignancies Through Identification of HNF4A Target Genes	Andrew Blum, MD, PhD	Case Comprehensive Cancer Center
9.	Anusha Bangalore Westlake High School	Curcumin: A natural compound with potential benefits for renal cancer patients undergoing mTOR-targeted therapy	David Danielpour, PhD	Case Comprehensive Cancer Center
10.	Julian Berger University School	Histone H4 Y51 Nitro-Tyrosine Expression Screening	John (Zhenghe) Wang, PhD	Department of Genetics and Genome Sciences
11.	Thomas Blossom University School	The Effects of Sleep Pattern Characteristics on Aviator Diet and Fatigue	Michael Decker, PhD	Department of Physiology and Biophysics

12.	Luke Brandon University School	Pathophysiology of Prion Protein and α-Synuclein in the Effort to Treat Glaucoma	Neena Singh, MD, PhD	Department of Pathology
13.	Cara Castro Hathaway Brown	The Activity of anti-Baff receptor antibody, VAY-736, in B cell cancers	Reshmi Parameswaran, PhD	Department of Pathology
14.	Manzili Denis University School	Identify The Target Of Cancer-Targeting Compounds Using a Forward Genetic Screen	Drew Adams, PhD	Department of Genetics and Genome Sciences
15.	Claire Dunn Shaker Heights High School	Prostate cancer within the African American community and its hereditary nature	Erika Trapl, PhD	Department of Population and Quantitative Health Sciences
16.	Tommy Dunn Shaker Heights High School	Meta Analysis of Cancer Patients Living with Human Immunodeficiency Virus (HIV)	Ge Jin, PhD	Case Comprehensive Cancer Center
17.	Amy Duan Solon High School	Role of Cancer Associated Thrombosis Altered Neutrophils in Pancreatic Ductal Adenocarcinoma Progression	Lalitha Nayak, MD	Case Comprehensive Cancer Center
18.	Le'Aona Dysart Cleveland School of Science and Medicine	The roles of FABP5 inhibitors in Ovarian Cancer	John Letterio, MD	Department of Pediatrics
19.	Adam Esa St. Edward High School	Cyclodextrin-based Delivery of Tuberculosis Drugs	Horst Von Recum, PhD	Department of Biomedical Engineering
20.	Chloe Echols Hathaway Brown	The Impact of Race Concerning Deaths Due to Legal Intervention	Peter Hovmand, PhD	Center for Community Health Integration
21.	Adora Ezepue Ohio State	Repeated mild traumatic brain injury produces chronic neurodegeneration, neuroinflammation and neuropsychiatric problems	Andrew Pieper, MD, PhD	Department of Psychiatry
22.	Kaitlyn Ernst Laurel School	Using K-Nearest Neighbors Software to Assess the Host Response to an Injectable Electrode	Andrew Shoffstall, PhD	Department of Biomedical Engineering
23.	Fahness Freeman Cleveland Heights High School	Immunohistochemical localization of receptor protein tyrosine phosphatase γ and receptor protein tyrosine phosphatase ζ in mouse hippocampus	Walter Boron, MD, PhD	Department of Physiology and Biophysics
24.	Isaiah Gilbert University School	Role Hn RNP A1 in maintaining protein stability	Blanton Tolbert, PhD	Department of Chemistry

25.	Rama Al Ghalyini Westlake High School	The Role of PKNP in Cell Proliferation of CAL27 cells	Quintin Pan, PhD	Department of Otolaryngology
26.	Tarini Gowda Revere High School	The Impact of Race Concerning Deaths Due to Legal Intervention	Peter Hovmand, PhD	Center for Community Health Integration
27.	Hannah Holt Charles F. Brush High School	Determination of Normal Tau Expression in Regions of the Human Brain: Future Implications for Alzheimer's Disease Study and Prevention	Allison Kraus, PhD	Department of Pathology
28.	Jaida Hadley John F. Kennedy High School	Prostate Cancer in African American Men…Contribution of Adverse Social Conditions	Jennifer Cullen, PhD, MPH	Department of Population and Quantitative Health Sciences
29.	Isabel Hart Shaker Heights High School	Novel Insights into the Interactions Between the Gut Microbiome, Inflammasomes, and Gasdermins During Colorectal Cancer	Theresa Pizarro, PhD	Department of Pathology
30.	Asha Jha Shaker Heights High School	Knockdown of Alas-1 To Screen for Protumor Effects	Stanley Huang, PhD	Case Comprehensive Cancer Center
31.	Benjamin Jamal Shaker Heights High School	A Comparative Analysis of the Effect of Age on Specific Glial Cells in Mice	Lin Mei, MD, PhD	Department of Neurosciences
32.	Ezaiyah Jolly Shaker Heights High School	Role Hn RNP in Alternative mRNA Splicing	Blanton Tolbert, PhD	Department of Chemistry
33.	Vishwum Kapadia University School	Proximity Labeling Technique to Identify Protein Interactions Important for UPF1 Function During Nonsense-Mediated mRNA Decay	Kristian Baker, PhD	Department of Genetics and Genome Sciences
34.	Shria Kavaturu Copley High School	Analyzing Extracellular Vesicles with FACs Symphony S6 and Amnis Image Stream Cytometers	Brian Grimberg, PhD	Case Comprehensive Cancer Center
35.	Adlai Kwofie Cleveland School of Science and Medicine	Age-Dependent Differences in the Breathing Pattern in Health and Disease	Thomas E. (Ted) Dick, PhD	Department of Neurosciences
36.	Minjun Kim St. Edward High School	Targeting IDH1 enhances chemotherapy response in pancreatic cancer	Jordan Winter, MD	Department of Surgery

37.	Ishita Koppararu Hathaway Brown	3D Human Stem Cells for Neural Development	Helen Miranda, PhD	Department of Genetics and Genome Sciences
38.	Kate Lindley, Harrisburg Academy	Multimodal traumatic brain injury model induces chronic cognitive impairment with increased levels of neurodegeneration and neuroinflammation	Andrew Pieper, MD, PhD	Department of Psychiatry
39.	Cheyenne Marolt, Cleveland School of Science and Medicine	To assess the hygiene of smart watches for minimally invasive surgeries	Bryan Carroll, MD, PhD	Department of Dermatology
40.	Eleanor Meges Padua Franciscan High School	Microglial Effects on Neural Progenitor Cell Growth in Cerebral Organoid Models	Anthony Wynshaw-Boris, MD, PhD	Department of Genetics and Genome Sciences
41.	Ira Mehta Lake Ridge Academy	Direct Effect of Opioids on the Intestinal Epithelium	Alan Levine, PhD	Department of Molecular Biology and Microbiology
42.	Uwela Mugabo Facing History New Tech High School	The role of macrophages-KLF6 in the pathogenesis of arterial restenosis	Ganapati Mahabaleshwar, PhD	Department of Pathology
43.	Janailyn Morris Cleveland School of Science and Medicine	PGC-1alpha Overexpression Alleviates Neuronal Cell Death in an Alzheimer's Disease Mouse Model	Xiongwei Zhu, PhD	Department of Pathology
44.	Naraen Naidu Twinsburg High School	Imaging PSMA biomarker in a Prostate cancer tumor model with targeted PSMA-Cys-IR800 probe in athymic nude mice	James Basilion, PhD	Department of Biomedical Engineering
45.	Tina Nguyen Mayfield High School	Improving Function of DCs through Cas9/Crispr-Mediated Ex Vivo Manipulation for an Immunotherapeutic Approach to Sarcoma	John Letterio, MD	Department of Pediatrics
46.	Kwabena Owusu Solon High School	The Oxygen Permeability of Red Blood Cells Differs Significantly Across Separate Strains of Mice	Walter Boron, MD, PhD	Department of Physiology and Biophysics
47.	Angel Ononogbo Orange High School	The Role of *SLX4IP* in Tumor Cell Growth	William Schiemann, PhD	Case Comprehensive Cancer Center
48.	Eric Pieper Shaker Heights High School	The Effect of Nanobubble Shell Structure on Contrast-Enhanced Ultrasound Signal and Nanobubble Movement in Blood	Agata Exner, PhD	Department of Radiology

49.	Garv Patel Andrews Osborne Academy	Early Onset Colorectal Cancer (EOCRC) Risk Increases with Obesity Independent of Self-Reported Race	Fredrick Schumacher, PhD	Department of Population and Quantitative Health Sciences
50.	Sairam Pantham Solon High School	Understanding the Molecular Interactions Between the OC43 Nucleocapsid Protein and the 5′UTR	Blanton Tolbert, PhD	Department of Chemistry
51.	Haridu Peiris Twinsburg High School	Covid-19 Diagnosis and Evaluation with Deep Learning	Anant Madabhushi, PhD	Department of Biomedical Engineering
52.	Alaina Pizarro Hawken School	Chronic Stress Induces Protection Against Secondary Injury Through the IL-23/IL-22 Axis by Regulating Antimicrobial Peptides	Fabio Cominelli, MD, PhD	Department of Medicine
53.	Hussein Al Raheel Cleveland School of Science and Medicine	Mapping the binding sites of WD40 repeat-containing protein 5 (WDR5) and promyelocytic leukemia protein isoform 1(PML1)	Hung-Ying Kao, PhD	Department of Biochemistry
54.	Justin Pieper Shaker Heights High School	Evaluation of Accelerometer Device	Andrew Shoffstall, PhD	Department of Biomedical Engineering
55.	Lilly Russo Gilmour Academy	Impact of Gut Microbiome on Sex Differences in Experimental Crohn's Disease	Theresa Pizarro, PhD	Department of Pathology
56.	Pranav Sompalle Mayfield High School	Evaluating Associations Between Scan Quality of Prostate Bi-parametric MRI and Radiologist Performance and Agreement for Prostate Cancer Diagnosis	Satish Viswanath, PhD	Department of Biomedical Engineering
57.	Samara Rivchun Laurel School	Determining the Antifungal Activity of Miconazole Against Candida Albicans and Aspergillus Niger Isolates	Mahmoud Ghannoum, PhD	Department of Dermatology
58.	Anna Saline Gilmour Academy	Efficacy of Losartan to treat intestinal fibrosis in experimental Crohn's disease	Theresa Pizarro, PhD	Department of Pathology
59.	Sidney Sheppert Stow Munroe Falls High School	Identification of novel FABP4/5 inhibitor as potential therapeutic approach for ovarian cancer	John Letterio, MD	Department of Pediatrics
60.	Diya Swain Shaker Heights High School	The Role of MAGE-A6 in Bladder Cancer	Sanjay Gupta, PhD	Department of Urology
61.	Soham Shah St. Ignatius High School	CITED2 restrains macrophage-mediated inflammation by	Ganapati Mahabaleshwar, PhD	Department of Pathology

		elevating B Cell Leukemia / Lymphoma 6 expression		
62.	Harsha Sanaka Hawken School	Stress Increases Tumor Formation in a Murine Model of Colitis-associated Cancer	Fabio Cominelli, MD, PhD	Department of Medicine
63.	Isabel Svec Padua Franciscan High School	Empirical Comparison of Registration Approaches for Multi-Parametric MRI in Rectal Cancers	Satish Viswanath, PhD	Department of Biomedical Engineering
64.	Hamza Said Westlake High School	Racial Disparities in Healthcare	Peter Hovmand, PhD	Center for Community Health Integration
65.	Giovanni Tripi Charles F. Brush High School	Salivary Longitudinal Innate Immune Response Profiles of SARS-COV-2 Acutely Infected Breakthrough Participants	Aaron Weinberg, DMD, PhD	Department of Biological Sciences, Dental Medicine
66.	Maya Tang Hathaway Brown	Phenotype comparison of a human and murine M Opsin mutation	Paul Park, PhD	Department of Ophthalmology
67.	Owen Tolbert Shaker Heights High School	Repurposable drug discovery following single cell RNA-seq analysis in endometrial cancer	Mark Cameron, PhD	Department of Population and Quantitative Sciences
68.	Reece Turner Shaker Heights High School	Microglial Proliferation in Cerebral Organoids Formed with Early Hematopoietic Stem Cells	Anthony Wynshaw-Boris, MD, PhD	Department of Genetics and Genome Sciences
69.	Mythili Ungarala Shaker Heights High School	How the Racial Composition of a City's Police Force Affects Racial Patterns of Arrests and Violence	Peter Hovmand, PhD	Center for Community Health Integration
70.	Mythreyi Ungarala Shaker Heights High School	Genetically Modified Mice to Study Cardiac Risk Genes	Can Shi, PhD	Department of Medicine
71.	Sahishnu Vallabhajoysula Avon High School	M.gl Microbiome Prevents the Phenotypic Maturation of Immature Dendritic Cells, Enabling Cancer Malignancy	Mei Zhang, PhD	Department of Biomedical Engineering
72.	Mantas Viazmitinas Westlake High School	Investigating the Effect of Ionic Strength on GalNAc-Transferase 1 Preferences Towards Charged Substrates and Initial Mucin-Type O-Glycosylation	Thomas Gerken, PhD	Department of Biochemistry
73.	Evan Wang Beachwood High School	Using a Knowledge Graph-based Computational Framework to Identify Genes and Repositioned Drugs for Alzheimer's Disease	Rong Xu, PhD	Center for Artificial Intelligence

74.	Lindsey Wang Orange High School	12-year time trend and association of early-onset colorectal cancer with diverticulitis in the United States: 2010-2021	Nathan A. Berger, MD	Center for Science, Health and Society, Case Comprehensive Cancer Center
75.	William Wang Orange High School	Obesity and Cancer Risk in the US from 2010-2021: A revisit in a unified platform	Nathan A. Berger, MD	Center for Science, Health and Society, Case Comprehensive Cancer Center
76.	Ben Weil Charles F. Brush High School	Analyzing Potential Gene Biomarkers for Signet Ring Colon Cancer Through Exon Array Analysis in R	Sanford Markowitz, MD, PhD	Departments of Medicine, Genetics
77.	Victor Xie Solon High School	Effect of Fungal Microbiome on Maturation of Immature Dendritic Cells	Mei Zhang, PhD	Department of Biomedical Engineering
78.	Alexia Zelada Cleveland School of Science and Medicine	Determining Whether Postbiotic Supernatants Affect Keratinocyte or Monocyte Cell Response at the Level of Production of Pro- or Anti-Inflammatory Cytokines, as Assessed by PCR	Thomas McCormick, PhD	Department of Dermatology
79.	Hayley Zheng Twinsburg High School	Development of a Prostate Cancer Diagnostic Test for Barbers	Erika Trapl, PhD	Department of Population and Quantitative Health Sciences
80.	Amy Zhou Beachwood High School	Role of the SARS-CoV-2 receptor ACE2 in regulating thrombosis	Alvin Schmaier, MD	Departments of Medicine and Pathology

ABSTRACT #1

Explaining the Cleveland African American Prostate Cancer Project to Lay People

Nichele Abeyesundere, Shaker Heights High School; Rebecca Miller, MS, MPH, Case Comprehensive Cancer Center; Kristina Austin, MSEd, LSW, Case Comprehensive Cancer Center; Sydney Evans, BSPH, CHW, Case Comprehensive Cancer Center; Audrey Kinsella, MPH, Case Comprehensive Cancer Center, Sarah Frischmann, MPH, Case Western Reserve University School of Medicine; Erika Trapl, PhD, Department of Population and Quantitative Health Sciences, Case Western Reserve University School of Medicine

Background:
The incidence and mortality rate of prostate cancer in the U.S. are highest among Black or African American men. This racial disparity is significantly greater in Cuyahoga County. The Cleveland African American Prostate Cancer Project (CAAPP) aims to increase prostate cancer screening in the African American community across Cleveland, Cuyahoga County's largest city. The creation of visual aids that utilize simple language is important for informing the public about the purpose, goals and approaches of CAAPP. A better understanding of personal and familial risk may be generated by communicating health research to a lay audience.

Goal:
To develop an infographic explaining the Cleveland African American Prostate Cancer Project that can be effectively understood by a lay audience.

Methods and Materials:
A literature review on lay person health communication was conducted using Google Scholar and PubMed to inform the creation of an infographic that explains and justifies the Cleveland African American Prostate Cancer Project to the public. An infographic titled "The Cleveland African American Prostate Cancer Project (CAAPP)" was developed and further evaluated for readability by local Cleveland barbers at Urban Kutz Barbershop and Major League Barbershop.

Results:
Local barbers at Urban Kutz Barbershop and Major League Barbershop had a favorable reaction to the infographic about CAAPP. Feedback on the readability and visual aspects of the infographic was positive with barbers appreciating the infographic handout format. Our results support existing literature and resources on lay person health communication as such resources guided our successful development of a readable infographic.

Conclusions:
Plain language, visual aids, sufficient spacing and legible text are important when communicating information about health research to a lay audience. Accordingly, a readable infographic is an effective resource for helping lay people to understand the role of the Cleveland African American Prostate Cancer Project.

ABSTRACT #2

COVID-19 and Transplant Patients: Mandatory Vaccine Requirements in Waitlisted Transplant Patients

Amal Aboumerhi, Westlake High School; Kenneth Andreoni, MD, Transplant and Hepatobiliary Surgery, UH, Cleveland Medical Center; Adam Beach, UH Cleveland Medical Center; Kenneth Chavin, MD, MBA, PhD, Transplant and Hepatobiliary Surgery, UH, Cleveland Medical Center; Meelie DebRoy, MD, Transplant and Hepatobiliary Surgery, UH, Cleveland Medical Center

Background:
The global pandemic caused by the SARS Cov-2 virus has caused unprecedented, previously unthinkable changes especially in the immunosuppressed population. COVID-19 infection in transplanted patients carries an ~ 30% risk of mortality in the unvaccinated. Due to the high risk of SOT patients contracting and dying from the disease, we have mandated policies requiring COVID-19 vaccination in all patients awaiting a transplant.

Goals:
We made a decision across our Transplant Institute (including all organs - heart, liver, lung, kidney, pancreas) to mandate completed vaccination in patients waitlisted for organ transplant, in hopes that more of our patients would become vaccinated. To our knowledge, we were one of the only 9 transplant centers around the country to implement this mandatory vaccination policy at that time (September 2021) for patients on the organ transplant waiting list.

Methods and Materials:
We gathered information from our transplant database at University Hospitals, Cleveland, Ohio, specifically regarding vaccine status of adult transplant patients. All patients were directly contacted by the organ transplant coordinators and also received a letter detailing the requirement for completed vaccination. Patients who were not vaccinated by the deadline (October 15, 2021) were inactivated on the waiting list, with the option to be reactivated once completion of vaccination was documented.

Results:
Of 598 patients on the waitlist at our center, there were 465 kidney, 104 liver, 10 kidney/pancreas, 11 heart and 8 lung patients. The total number of vaccinated patients were 395 kidney, 88 liver, 5 kidney/pancreas, 11 heart and 8 lung patients. When the policy was instituted, there were 99 unvaccinated patients on the waitlist at our center. Overall, we have seen a 25% increase in vaccination rates in our patients after institution of this policy.

Conclusions:
Vaccination against COVID-19 has proven to be safe and effective in preventing severe disease, along with social distancing and masking. With the ever increasing imbalance between organ supply and demand, it behooves the transplant community to be responsible stewards of a scarce resource i.e. organs available for transplant. In addition, the increase in mortality seen in post-transplant patients infected with COVID-19 certainly poses a risk to transplant centers who are being monitored for patient and graft survival. At the current time, there are no exceptions being made in the risk adjustment modeling to exclude patient deaths post-transplant due to COVID-19. We were able to help patients overcome vaccine-hesitancy with our policy mandate and education and achieved higher vaccination rates in our waitlisted patients. Given the safety and effectiveness of the currently approved vaccines available, mandatory vaccination for waitlisted patients seems to be the most responsible and prudent course of action.

ABSTRACT #3

Vitamin E and through what nuclear receptors can induce gene expression

Adesewa Adeweso, Mayfield High School; Danny Manor, PhD, Department of Nutrition

Background:
Vitamin E is a major lipid-soluble antioxidant in most animals. The current biological functions of being an antioxidant have been well known for decades. Severe vitamin E deficiency can lead to several complications, including AVED (ataxia with vitamin E deficiency) and NAFLD (non-alcoholic fatty liver disease). More recent research has suggested that vitamin E may possess antioxidant-independent properties. Previous research in the lab indicates that these properties could play a role in modulating gene expression. One gene of interest is ENHO(energy homeostasis associated). ENHO is involved in regulating glucose homeostasis and lipid catabolism (breaking down fats). ENHO deficient individuals face mutations like non-alcoholic fatty liver disease and low adropin levels. Through Real-Time Reverse transcription polymerase chain reaction (RT-PCR), I examined vitamin E's effect on the mRNA expression levels of ENHO in IHH (immortalized Human Hepatocyte) cells.

Goal:
To find out if vitamin E's antioxidant independent functions affect the expression of the EHNO.

Methods and Materials:
IHH cells were cultured in a 6-well plate with DMEM +10% vitamin E deficient FBS. As a method of identifying modulation of ENHO expression, lHH cells were pretreated with 100 μM d-α-tocopherol in triplicate. Ethanol acts as vehicle control. After the cells had undergone 16 hours of treatment, they were lysed. RNA was harvested with Qiagen RNeasy kit and reverse transcribed using High Capacity cDNA Reverse Transcription Kit. Taqman expression assays for Fam-labeled ENHO (Hs...) and 18s (Hs00958505_m1) were used in combination with Fast Universal PCR Master Mix (Applied Biosystems) in a 96-well plate on a StepOnePlus real-time PCR machine (Applied Biosystems). The data were analyzed according to the Livak method for comparative real-time PCR.

Results:
The research is currently ongoing, and there are no definitive results. We expect the expression of ENHO to be changed; we just don't know by what circumstances.

Conclusions:
No conclusion at the moment

ABSTRACT #4

The Effect of Hypoxia on Vascular Smooth Muscle Cell Behavior

Maddy Adler, Laurel School; Sergei Merkulov, PhD; Aaron Proweller, MD, PhD, Cardiovascular Research Institute

Background:
When a tissue is injured, blood vessels in the area are disrupted and the delivery of nutrients into the tissue will be delayed. When this occurs, hypoxia (less than 7% O_2) is triggered. Hypoxia will then prompt angiogenesis (the formation of new blood vessels) in order to repair the damaged tissue, and make a new path around the injury so that necessary nutrients can continue to be delivered. Hypoxia will also activate VEGF (vascular endothelial growth factor) expression, causing endothelial cells to migrate and form a new branch. In order for the full branch to be formed, the smooth muscle cells (SMCs) must also take part and form the outer layer of the branch. This being said, there is very little known about the effects of hypoxic injury on SMCs.

Goals:
The goal of this research was to learn more about the effects of hypoxia on the growth and formation of blood vessels, specifically the outer layer formed by SMCs. We hoped to determine the effects of hypoxia on SMCs, considering how little is known. There is plenty of literature on the effects of hypoxia on endothelial cells, but very little about SMCs.

Methods and Materials:
Rat A10 embryonic smooth muscle cells were plated into 96-well tissue culture plates (4000 cells in each well used). Half of cells were treated with PDGF-BB, other were not treated; half of cells were placed under hypoxic conditions, other half were placed in normoxic (20% O_2/ambient O_2 levels) conditions. The cells were then incubated for 60 hours. After incubation, 10µl of MTT (5-diphenyltetrazolium bromide) solution was added to each well. Plates were then mixed briefly on an orbital shaker. Both plates then were incubated at 37℃ for 4 hours in normoxia. Then, 200µl of DMSO (dimethyl sulfoxide) was then added to every well, and pipetted up and down in order to dissolve the formazan salt. Lastly, plates were put into a spectrophotometer to measure the absorbance singal at 570nm. The higher the number produced, the darker the purple of the final solution, the more proliferation that has occurred.

Results:
When looking at the results from the spectrophotometer, it was evident that under hypoxia SMCs proliferate much less than under normoxia. Even when PDGF-BB was added to the cells, hypoxia still held back the speed of the SMCs growth.

Conclusion:
From these results, it was concluded that when angiogenesis is triggered by hypoxic injury, the endothelial cells begin the process of angiogenesis. With the results we obtained, it is evident that the SMCs wait for the endothelial cells to migrate before they begin to form the outer layer.

ABSTRACT #5

Quantitative MRI Assessments of Kidney Disease Progression in Patients with Autosomal Recessive Polycystic Kidney Disease (ARPKD)

Nassim Aidja, Mayfield High School; Christina MacAskill; Katherine MacRae Dell, MD; Chris Flask, PhD, Department of Radiology

Background:
Autosomal Recessive Polycystic Kidney Disease (ARPKD) is an important cause of morbidity and mortality in children with chronic kidney disease (CKD). Novel therapies have shown efficacy in ARPKD animal models, but clinical trials in ARPKD patients have not been possible due to the lack of sensitive measures of kidney disease progression. Non-invasive Magnetic Resonance Imaging (MRI) techniques, including novel MR Fingerprinting (MRF), show promise in addressing this unmet need. We previously identified MRF-based T1 and T2 mapping as potential biomarkers of ARPKD kidney disease in animal models and initial human studies. In the current study, we evaluated the relationship between these MRF-based imaging parameters with clinical assessments of renal function in ARPKD subjects.

Goals:
To compare novel quantitative MRI assessments with established clinical measures of kidney disease progression in subjects with ARPKD.

Methods:
ARPKD subjects were scanned on a Siemens 3T MRI scanner utilizing novel MRF technology to simultaneously generate kidney T1 and T2 maps in 15 secs/imaging slice with no sedation or injectable contrast agent. These two MRI metrics were compared with conventional clinical assessments of estimated glomerular filtration rate (eGFR) and renal perfusion rates as a measure of kidney function

Results:
Seven subjects with ARPKD (2M/5F, age range = 06-22; eGFR range = 52-109 ml/min/1.73m^2) were scanned. Mean kidney T2 values demonstrated a significant negative correlation with eGFR (R^2=0.59, p=0.043). Mean kidney T1 also showed a strong negative correlation (R^2=-0.51) but did not yet reach significance (p=0.07). Mean T1 and T2 values for the right and left kidneys did demonstrate a significant correlation (T1: R^2=0.99, T2: R^2=0.74). Mean kidney T1 and T2 values also demonstrated a strong negative correlation with cortical perfusion (R^2>0.72, p<0.02).

Conclusion:
This is the first study to establish a relationship between MRI-derived imaging biomarkers (T1, T2) for renal cystic burden and kidney function (eGFR and perfusion) in ARPKD subjects. Despite the small cohort, data clearly demonstrate that mean T1 and T2 both increase with declining eGFR and perfusion. These important findings suggest that MRF-based T1 and T2 mapping may provide a safe, non-invasive, quantitative, and reproducible measure of kidney disease severity to support future clinical trials to identify subjects at high risk for disease progression and monitor response to treatment.

ABSTRACT #6

Combination Therapy Promotes Increased IFN-β Production in Pediatric and AYA Sarcomas via the cGAS-STING Pathway Read

Zain Anwar, University School; Suzanne L. Tomchuck, PhD; Alex Y.C. Huang, MD, PhD, Department of Pediatrics

Osteosarcoma (OS) and rhabdomyosarcoma (RMS) are the most common malignant bone and soft-tissue sarcomas in children and adolescent young adults (AYA). Despite standard of care including surgery, chemotherapy, and radiation therapy, the 5-year survival rate for localized sarcomas is about 70% but drops to a mere 30% upon metastasis. Additional treatments are required to increase these patients' overall survival time. Cryoablation, an alternative treatment using freeze-thaw cycles on tumors, has the potential to help these patients. Primarily, cryoablation leads to the tumor's cold-induced necrosis, which releases many immune activation molecules into the microenvironment. The cyclic GMP-AMP synthase-stimulator of interferon genes (cGAS-STING) pathway, a potential pivotal part in cryoablation's ability to improve tumor immunogenicity, is activated by the factors released following cryoablation. Previous studies in the Huang lab have shown that cryoablation reduces tumor size and metastases in murine models of RMS. However, using human OS and RMS models treated with STING agonists, the lab was unable to elicit complete activation of the cGAS-STING pathway *in vitro*. Although *IFN-β* mRNA was transcribed, the protein itself was never secreted. Recent studies have shown that combination therapy using a STING agonist and a chemotherapeutic agent significantly enhanced IFN-β production in models of triple-negative breast cancer. To determine if a similar result would happen in sarcoma, human RMS cell lines were treated using combinations of next-generation STING agonists, MSA-2 and diABZI, along with a microtubule destabilizer, vinorelbine. Treatment with vinorelbine alone was able to increase IFN-β expression. However, when the sarcoma was treated with a combination of vinorelbine and a STING agonist, the resulting IFN-β expression was more than double in one of the sarcoma cell lines. As expected, healthy non-cancerous PBMCs didn't respond to vinorelbine as the chemotherapeutic is only supposed to target fast-dividing cells. These findings provide insight into how combined therapy using chemotherapeutics and STING agonists promotes increased IFN-β production to combat sarcoma. Future studies plan to test additional combination therapies to increase the effectiveness of cryoablation.

ABSTRACT #7

Identification of Gene Targets by Novel Long Intergenic Non-coding RNA in Esophageal Adenocarcinoma

Zaid Ashruf, University School; Durgadevi Ravillah PhD; Komal Keerthy; Kishore Guda, DVM, PhD, Case Comprehensive Cancer Center

Background:

Esophageal Adenocarcinoma (EAC) is a type of esophageal cancer that starts at the cellular level of the mucus-secreting glands and is preceded by Barrett's Esophagus (BE), a precursor lesion of esophageal cancer typically caused by gastroesophageal reflux disease. The drastic rise in obesity in the United States paired with a lack of preventive strategies has resulted in the National Cancer Institute labeling EAC as the fastest growing cancer in the United States. Poor BE prognosis is also causing the rise in EAC's incidence rate; however, a potential solution to this could be the analysis of long intergenic non-coding RNA (lincRNA), a 200-nucleotide long RNA molecule located between two genes that is unable to code for proteins. Despite the use of LincRNA as prognostic biomarkers for other cancers, it has not been done with EAC.

Goals:

Our primary objective will be to evaluate the expression of potential gene targets regulated by two novel lincRNAs in EACs. Based on our preliminary findings, our hypothesis is that our two lincRNAs will positively regulate the genes involved in EAC pathogenesis. By identifying these gene targets, possibilities of earlier diagnosis or new drug pathways to treat EAC could open up for the growing number of patients

Materials and Methods:

The two lincRNA candidates were identified through analysis of 105 patient biopsies and by identifying which lincRNAs were present in the cancerous EAC cell lines and absent in the others. This resulted in the use of linc1 and linc2. Seven EAC cell lines were tested for which linc they expressed at baseline. A list of 18 genes was generated for the first criterion testing, two for linc1 and 16 for linc2. Linc1 and linc2 have been tested in two separate experiments. Both experiments had five conditions, a negative control, two gapmer knockdowns, a stuffer overexpression, and a linc overexpression. A revised criterion was used to test another set of 18 genes in four conditions, a negative control, two gapmer knockdowns, and a parental line. Gene expression was monitored using a two-step reverse transcription-quantitative polymerase chain reaction (RT-qPCR) which was run in triplicate.

Results:

One gene (SCHM1) and four genes (GPR61, NDUFA4L2, AGAP4, and C4A) followed the predetermined first criterion for linc1 and linc2, respectively, by being knocked down in the gapmer conditions and overexpressed in the OE condition. For the second criteria, results are yet to be validated.

Conclusion:

The data suggests that these five genes are the gene targets that are driving the EAC. However, it cannot be ruled out that these genes are passenger genes being driven by a separate mutation. Additional research is needed to confirm this research in preclinical trials so it can be applied to EAC therapy.

ABSTRACT #8

Potential Therapeutic Targets in Upper Gastrointestinal Malignancies Through Identification of HNF4A Target Genes

Nathan Ballman, Shaker Heights High School; Andrew Blum, MD, PhD, Case Comprehensive Cancer Center

Background:
Gastrointestinal cancers are some of the deadliest and common maladies around the world. Their lethality stems from the fact that these diseases are often not detected until an advanced and inoperable stage with few or no effective treatment options. Previous work done in this lab, and others, demonstrate that the transcription factor HNF4A sustains cancer cell growth in upper GI cancers that express high levels of HNF4A. Treatments targeting HNF4A directly may result in serious side effects due to the central role of HNF4A in organ maintenance. This work therefore addresses the critical unmet clinical need for effective therapeutic targets for upper GI cancers through identification of an HNF4A gene signature in GI cancers.

Goals:
The identification of genes that are most strongly impacted by HNF4A expression *in vivo*, and the tumor and molecular contexts that might influence this association.

Materials and Methods:
We identified the genes most strongly correlated with HNF4A expression (Pearson correlation coefficient >0.7) using the Cancer Cell Line Encyclopedia. We tested the hypothesis that these genes would correlate *in vivo* using TCGA samples. Subsequently, tumor cohorts were sorted based on tumor type, and further by carriage of specific genetic variants in oncogenes and tumor suppressors, and the strength of correlations and differences among sub groups were tested using a Fisher z transformation on Pearson correlation coefficients and a Welch t-test.

Results:
HNF4A expression is aberrant in many cancers compared to normal control samples, typically elevated in cancer samples. However, differences in HNF4A expression do not result in consistent upregulation of all HNF4A target genes across cancer types. The correlation of HNF4A gene targets are stronger in upper GI malignancies (Esophagus, Stomach, Pancreas) compared to other GI malignancies (Bile duct, Colon), while an additional tumor control (Breast) showed no correlation of HNF4A with the GI cancer HNF4A gene signature. Additionally, though the impacts of many oncogenic mutations were significant, we did not see a clear impact of oncogenic mutations on this signature

Conclusion:
We have identified a panel of HNF4A associated genes in upper GI cancers that may serve as biomarkers or potential therapeutic targets.

ABSTRACT #9

Curcumin: A natural compound with potential benefits for renal cancer patients undergoing mTOR-targeted therapy

Anusha Bangalore, Westlake High School; David Danielpour, PhD, Case Comprehensive Cancer Center

Background:
Renal cell carcinoma (RCC) is one of the 10 most commonly occurring cancers in the world, with approximately 400,000 individuals being diagnosed with RCC in 2018 alone. Several cancers, including RCC, are often associated with the deregulation of a protein kinase called mammalian target of rapamycin (mTOR). Because mTOR regulates a plethora of cellular activities, it is predicted to be a powerful therapeutic target. In clinical trials, however, mTOR inhibitors have demonstrated disappointing outcomes against treating cancers because they induce cell survival pathways, such as the Notch signaling pathway. Our lab has shown that Jagged-1 (JAG1), a ligand of the Notch signaling pathway, is linked to the ineffectiveness of mTOR inhibitors. JAG1 is also upregulated by TGF-β, a known driver of the invasiveness of many cancers. Studies have shown that curcumin, a natural product found in turmeric, affects several aspects of cancer, including survival pathways. Thus, we speculate that curcumin may improve the potency of mTOR inhibitors by affecting the JAG1-Notch signaling pathway.

Goals:
Our first goal is to determine the effect of mTOR inhibitors on Notch signaling. Our second goal is to analyze the effect of curcumin on TGF-β1-JAG1-Notch signaling and its subsequent effect on RCC growth and invasion. We hypothesize that curcumin enhances the effectiveness of mTOR inhibitors by inhibiting JAG1-Notch-TGF-β signaling, thus suppressing tumor cell survival and motility.

Materials and Methods:
To conduct this experiment, we used two RCC cell lines: RCC4 and 786-O. To determine the effect of mTOR inhibitors on the Notch signaling pathway, we conducted western blots on both cell lines with four treatment groups of various mTOR inhibitors: control, rapamycin, BEZ235, and KU-0063794. We also conducted MTT assays on both cell lines to measure cell viability against various doses of curcumin. To analyze the effects of curcumin on the Notch signaling pathway, we conducted further western blots on both cell lines with the following four treatment groups: control, TGF-β only, curcumin only, and a combination of TGF-β and curcumin.

Results:
By analyzing western blots, we determined that JAG1 is induced by mTOR inhibitors, and that TGF-β1-induced JAG1 is inhibited by curcumin. By analyzing the MTT assay results, we determined that the viability of both RCC4 and 786-O cells decreases as the dosage of curcumin increases.

Conclusions:
Because curcumin inhibits JAG1 and reduces the survivability of RCC cells, future research could investigate the impact of curcumin on the effectiveness of mTOR inhibitors in treating RCC. Further pre-clinical research could also test the effects of incorporating curcumin into the diets of RCC patients.

ABSTRACT #10

Histone H4 Y51 Nitro-Tyrosine Expression Screening

Julian Berger, University School; John (Zhenghe) Wang, PhD, Department of Genetics and Genome Sciences; Xuan Zhao, PhD, Department of Genetics and Genome Sciences

Background:
Tyrosine nitration is a post translational protein modification that can result in a change in protein structure and function. Through a proteomic mass spectrum analysis, our lab recently found that in Histone H4, a protein important in chromatin structure and function, tyrosine can be nitrated at the Y51 site. This opens research possibilities to further study a modified Histone H4 protein. The first step of researching this modified protein would be to generate it, so it can be readily available for further research.

Goals:
This project aims to screen a colony of bacteria that contains high expression of nitro-tyrosine modified version of Histone H4 at the Y51 site. These bacteria would ideally be available for further research on the synthesis-modified protein.

Methods:
We first generated a plasmid that contains Histone H4, then we did mutagenesis to mutate UAC to UAG at Y-51 site to introduce the Amber codon. This plasmid was transformed to E.Coli C321 bacteria for further protein purification. We then used glutathione-S-transferase (GST) protein purification to express the nitro-tyrosine modification. The bacteria with the highest expression of modification will be cultured into a stock for further use in the lab.

Results:
We did three cycles of screenings. Of the colonies in the first screening, we found two with high expression. We took the colony with the highest expression, labeled 2-1, re-streaked the LB plate, and inoculated 8 single colonies for a second screening. In the second screening, we found five colonies with high expression, indicating that 2-1 was consistent in its expression. Of the eight colonies that came from 2-1, we selected the two with the highest modified protein expression to culture into our stock for further use.

Conclusion:
We successfully found a colony that has high expressions of the modified Histone H4 protein.

ABSTRACT #11

The Effects of Sleep Pattern Characteristics on Aviator Diet and Fatigue

Thomas Blossom, University School; Elizabeth Damato, PhD; Michael Decker, PhD, Department of Physiology and Biophysics

Background:
Aviators who are exposed to multiple long duration, high altitude flights ("sorties") often experience cognitive fatigue post-sortie. Fatigue could be connected to sleep and diet. A lack of sleep has been shown to increase hormones that regulate hunger the next day which could lead to a proinflammatory diet. Recent studies show a relationship between unhealthier diets and inflammatory responses in the human body. The Decker Lab has been examining the physiological response of the body in extreme aviation conditions.

Goals:
The goal of this analysis is to observe the effects of sleep on aviator diet and biomarker concentrations and determine if there is a relationship between fatigue levels and sleep.

Methods:
Data from a previously executed study in the Decker Lab was analyzed. In that study, aviators (n = 22) were assessed over a week (Baseline = Sunday, Midweek = Tuesday, Final = Thursday). The assessment included a sleep report, 24-hour diet recall, a self-administered five-category multidimensional fatigue index (MFI) test, and blood collection for subsequent serum biomarker analysis. Aspects of the sleep report (duration, sleep quality, feeling rested, night awakenings, daytime sleepiness) and fatigue levels were examined to look for relationships with diet and serum biomarkers.

Results:
Aviators were separated into groups based on sleep pattern characteristics. Pilots who reported feeling rested had significantly lower concentrations of the serum markers VEGF-D and Flt-1 and a significantly higher concentration of the serum marker PlGF than pilots who did not feel rested after a night's sleep. Pilots who woke up frequently during the night had significantly lower concentrations of the serum markers Leptin and MCP-4. Pilots who reported good quality sleep had a significantly higher concentration of the serum marker IL-17. No significant differences in inflammatory diet scores or serum biomarkers were found when comparing pilots who reported sleeping < 7 hours or those who reported feeling sleepy the next day. Inflammatory diet scores did not differ based on frequency of night awakenings, self-rated sleep quality, or feeling rested. Finally, the aviators were grouped based on if they became more fatigued from baseline to final. Those two groups did not differ in terms of their sleep pattern characteristics.

Conclusions:
The analysis found no direct relationship between sleep and diet inflammation scores or fatigue and sleep characteristics. However, aviators with better sleep characteristics had significantly higher concentrations of the biomarkers PlGF, Leptin, MCP-4 and IL-17 at final. Aviators with worse sleep characteristics had significantly higher concentrations of the biomarkers VEGF-D and Flt-1. This suggests that the aviators with better sleep pattern characteristics experienced increased inflammation and white blood cell count in addition to the increased Leptin levels. Aviators with worse sleep characteristics had higher levels of angiogenic promoters suggesting increased vascular growth.

ABSTRACT #12

Pathophysiology of Prion Protein and α-Synuclein in the Effort to Treat Glaucoma

Luke Brandon, University School; Anika Adulla, Department of Pathology; Urvi Patel, MD; Neena Singh, MD, PhD, Department of Pathology

Background:
The inner structure of the eye is split up between the anterior and posterior segment. The anterior segment is before the lens, and includes the iris, cornea, trabecular meshwork (TM), ciliary body (CB), aqueous humor (AH), and more. The posterior segment houses the lens, vitreous humor (VH), retina, choroid, and the optic nerve. The AH and VH are fluids that maintain the shape of the eye. The anterior segment is further divided into anterior and posterior chambers by the iris, and communicate through the pupil. AH is secreted by the CB in the posterior chamber, travels through the pupil into the anterior chamber, and is drained from the TM into the blood stream. Impairment of the drainage pathway increases intraocular pressure (IOP), resulting in glaucoma. Chronic increase in IOP causes death of the retinal ganglion cells in the inner retina, resulting in permanent blindness. TM cells are surrounded by the extracellular matrix (ECM), which plays an important role in xmaintaining the flow of AH across these cells to the Schlemm's canal, that ultimately drains it in the venous circulation. Excess deposition of ECM proteins in the TM is a common cause of elevated IOP by impairing the ability of TM cells to respond to physiological changes in IOP. Recently, we discovered that the prion protein (PrPC) and α-Synclein (α-Syn), proteins implicated in prion disorders (or Mad Cow disease) and Parkinson's disease (PD) respectively, are expressed in TM cells, and modulate ECM protein synthesis.

Goal:
The goal of this project was to better understand the pathophysiology of PrP and α-Syn in the regulation of IOP and its connection to the pathogenesis of glaucoma.

Materials and Methods:
We cultured neuroblastoma cells, M17 (human cell line) and N2A (mouse cell line). Then, we lysed our cultured cells, fractionated the lysates on SDS-PAGE, and performed Western blot to detect the proteins of interest, including α-Syn, PrP^C, alpha-smooth muscle actin (SMA), fibronectin, and Gapdh. Additionally, to try to understand whether PrP^C functions as a receptor for α-Syn, we used cells expressing GFP-tagged PrP^C, and exposed them to different concentrations of purified α-Syn, and imaged them at different time points.

Results:
Preliminary data suggests that α-Syn is endocytosed by PrP^C, and leads to up regulation of some ECM proteins.

Conclusions:
Further research of the role of α-Syn and PrPC in the modulation of IOP can aid in the development of effective therapies for glaucoma.

ABSTRACT #13

The Activity of anti-Baff receptor antibody, VAY-736, in B cell cancers

Cara Castro, Hathaway Brown; Claire Fritz, BA; Akshaya Radhakrishnan; Dan Feinberg, Department of Pathology; Derek Wong, Department of Pathology; Reshmi Parameswaran, PhD, Department of Pathology

Background:
Non-Hodgkin's Lymphomas (NHL) has the sixth highest mortality rate in cancers in the United States and killed around 248,700 people globally in 2018. Currently, the treatment includes chemotherapy, radiotherapy, immunotherapy, and stem cell transplantation, which all comes with various side effects. Long term effects in survivors of NHL consist of fatigue and a higher risk of developing a second malignancy or abnormalities. Working on new therapies could improve some of these effects and decrease the chances of relapse. We are targeting a protein named B-cell activating factor receptor (BAFF-R) expressed on these cancer cells. BAFF signaling provides survival signals to these cancer cells. When BAFF ligand binds to the BAFF receptor, it activates several downstream signaling pathways including non-canonical NF-κB pathway, providing survival signals to these NHL cells.

Goal:
The goal of the project is to test whether a BAFF-R antibody named VAY-736 is able to bind to NHL cells, inhibit BAFF signaling and thus inhibit cell proliferation and viability of these NHL cells.

Materials and Methods:
The two lymphoma cell lines Jeko and Mino cells were used. These cells were cultured in media, containing RPMI with 10% FBS and 1% P/S. Every 2 days, the cells were passaged in the ratio of 1:5 with the cells and media. They were kept in an incubator at 37ºC. Jeko or Mino cells were plated in triplicates in a 12-well plate with 100,000 cells per well. VAY-736 antibody was added every 24 hours and the cells were stained using trypan blue and counted by the Countess machine. The cell number and viability were recorded and entered into the GraphPad Prism Software for analysis. Alternate NF-κB signaling was analyzed using western blot technique using anti-p52 antibodies. VAY-736 binding to NHL cells was analyzed using flow cytometry.

Results:
The data shows that VAY-736 antibody binds to NHL cells at different concentrations of the antibody. VAY-736 binding inhibited BAFF induced alternate NF-κB signaling in NHL cells. Addition of BAFF causes nuclear translocation of NF-κB p52, while VAY-736 antibody inhibited this process. We did not see any significant changes in NHL cell viability or proliferation after incubation with VAY-736.

Conclusion:
Although the VAY-736 antibody binds to NHL cells and inhibits BAFF signaling, further experiments are needed to determine whether it has any effects in cell proliferation and viability of NHL cells.

ABSTRACT #14

Identify The Target Of Cancer-Targeting Compounds Using a Forward Genetic Screen

Manzili Denis, University School; Matthew Pleshinger, Department of Pharmacology; Anna Zinsser, Department of Genetics; Ralston Goldfarb, Department of Genetics; Drew Adams, PhD, Department of Genetics and Genome Sciences

Understanding the intracellular target of a compound can allow for a better understanding of the compound's mechanism of action. This is done through target identification. There are many types of target identification but in certain situations, one form will be the most effective depending on the compound. One method of target validation is the Forward Genetic Screen (FGS). In short, the Forward Genetic Screen is an unbiased approach in which a compound is added to a hypermutated cancer cell line in hopes that cells develop resistance to the compound. Though there will be many mutations, the remaining cells may share a limited amount of mutations which could lead to the discovery of the target. This approach is relatively new. By testing the FGS on a cell line that hasn't been tested on, it will aid the credibility of the approach. DU-145 is a type of prostate cancer with a high mutation rate, making it an exceptional candidate for the Forward Genetic Screen. The DU-145 cell line will be tested with several different compounds such as bortezomib and SPOX. This project aims to identify the targets of new compounds and expand this approach to new cell lines.

ABSTRACT #15

Prostate cancer within the African American community and its hereditary nature

Claire Dunn, Shaker Heights High School; Erika Trapl, PhD, Department of Population and Quantitative Health Sciences; Rebecca Miller, MS; Kristina Austin, MSEd, LSW, Case Comprehensive Cancer Center

Background:
The American Cancer Society states, that prostate cancer is the second most dangerous cancer for men but for African American/Black men it is the most dangerous cancer. According to Zerocancer.org Black men are twice as likely to get prostate cancer and to die from it than white men. There are a lot of factors that play into why African Americans are more likely to get prostate cancer. Genetics can play a role in one of the reasons why African Americans suffer more from prostate cancer. This could depend on hereditary, lifestyle, and environmental factors. However, it is not clear how big of rate genetics play. African Americans have low participation in clinical trials. In addition, another factor is how accessible care is to African Americans. Studies have shown that African Americans with prostates are less likely to get recommended care. Reasons could include a lack of trust in the healthcare system, prejudice in the community, or just lack of access to health centers. In addition, these all play a big role in their health. Prostate cancer is hereditary, meaning it seems to run in families. There may be a genetic factor or people just inherited it. However, men can still develop prostate cancer regardless of their family history. The sooner a man detects prostate cancer the better his chance of survival.

Goals:
My goal is to inform the African American community about prostate cancer. By informing them how serious it is, how they are at a higher risk of getting it, and where to get help. African Americans have low attendance when it comes to regular pharmacy care appointments. A goal of mine is to see the attendance to pharmacy care appointments get better. I seek to educate/spread awareness. I want African Americans to know when to get tested, the signs, who they can trust, and where they should go.

Materials and Methods:
In this research, I focused on prostate cancer within the African American community and the hereditary nature of prostate cancer. Furthermore, I did a literature review where I read a lot of articles on what puts explicitly African Americans at a higher risk to get prostate cancer.

Results:
After completing my literature review I found the contributing factors to why African Americans get prostate cancer.

Conclusions:
African Americans are at a higher risk of getting prostate cancer and dying from it. Also, prostate cancer is hereditary but it does not exclude anyone even if someone does not don't have a family history of it they may still be likely to get it. Furthermore, I want to make a change, make sure people are informed about this topic, and help the African American community. In addition, I want to bring more awareness to this topic to save lives.

ABSTRACT #16

Meta Analysis of Cancer Patients Living with Human Immunodeficiency Virus (HIV)

Tommy Dunn, Shaker Heights High School; Ge Jin, PhD, Case Comprehensive Cancer Center

Background:
HIV (*human immunodeficiency virus*) is a virus that attacks cells that help the body fight infection, making a person more vulnerable to other infections and diseases. It is spread by contact with certain bodily fluids of a person with HIV, most commonly during unprotected sex, or through sharing injection drug equipment. If left untreated, HIV can lead to the disease AIDS (*acquired immunodeficiency syndrome*). There is presently no known cure, only treatments to delay regression. People infected with HIV have a substantially higher risk of some types of cancer compared with uninfected people of the same age. The general term for these cancers is "HIV-associated cancers." Three of these cancers are known as "acquired immunodeficiency syndrome (AIDs)-defining cancers" or "AIDS-defining malignancies": Kaposi sarcoma, aggressive B-cell non-Hodgkin lymphoma, and cervical cancer. A diagnosis of any of these cancers in someone infected with HIV confirms a diagnosis of AIDS.

Goals:
To gather Information pertaining to HIV+ patients who have also developed cancer.

Methods:
Meta analysis among data connecting the two.

Results:
Experiments in progress, results to be reported.

Conclusions:
Experiments in progress, results to be reported.

ABSTRACT #17

Role of Cancer Associated Thrombosis Altered Neutrophils in Pancreatic Ductal Adenocarcinoma Progression

Amy Duan, Solon High School; Kenneth Kalikasingh, MS; Asha Thomas, PhD; Lalitha Nayak, MD, Case Comprehensive Cancer Center

Background:
The development of thromboembolism is a major complication in pancreatic cancer patients. Previous studies show that the occurrence of a thrombotic event is a marker of poor prognosis in pancreatic cancer patients. To study the role of thrombosis in the growth and progression of pancreatic adenocarcinoma (PDAC), we developed a unique animal model that combines both PDAC and venous thrombosis. Recently, the role of neutrophils within the tumor microenvironment has increasingly become an area of interest, as neutrophils have exhibited both a correlation to thromboembolism and cancer. Cancer cells generate cytokines that can alter the antitumor nature of neutrophils, leading to a conversion to immunosuppressive cells that promote tumor cell growth. However, whether this is affected by the presence of venous thrombosis is not understood. It is important to develop a better understanding of the cells and mechanisms that are involved within the tumor microenvironment in the setting of thromboembolism, as the knowledge has potential to help develop new strategies for the management of pancreatic cancer in the future.

Goals:
The goal of this study was to determine the role of the neutrophils in tumor progression under the setting of thromboembolism.

Materials and Methods:
C57B1/6 mice were injected with the mouse pancreatic cancer cell line PANO2 (stably transfected with luciferase) into the flank to monitor for tumor growth. A week later, an inferior vena cava ligation procedure was performed to induce thromboembolism in half of the mice. Tumor growth was monitored by bioluminescence. Tumors were harvested 3 weeks after injection of PAN02 cells and processed for either flow cytometry or immunohistochemistry to determine the number of crucial white blood cell populations and CD8 cytotoxic T-cells present in the tumor. To examine the importance of neutrophils, tumor growth was examined in the presence of neutropenia, which was generated with a Ly6G antibody injection for two weeks.

Results:
Mice with tumors that had undergone IVC ligation developed larger tumors than tumor-only mice. Generation of neutropenia was associated with decrease in tumor growth in mice with the IVC ligation, suggesting that neutrophils are important regulators of tumor growth in the setting of venous thrombosis. Though the number of neutrophils and macrophages in the tumor in both groups were similar, tumor + IVC mice had smaller CD8+ T-cell populations as compared to PANO2 only mice. This result was confirmed by both flow cytometry and immunohistochemistry. Apoptotic assays after coculturing tumor-associated neutrophils (TANs) and T cells isolated from the spleen of the same mice indicated that neutrophils isolated from tumors of mice with a thrombotic incidence induced higher apoptotic rates of CD8 T-cells as compared to tumor-only mice T cells.

Conclusion:
Venous thromboembolism contributes to the second leading cause of mortality among cancer patients. In our study, we find that VTE associated with pancreatic cancer increases the growth of PDAC, which is neutrophil-dependent. Further, our studies show that tumor growth may be altered through the apoptosis of cytotoxic T-cells by TANs. These results highlight the importance of understanding the mechanisms that are involved in tumor progression in the setting of thrombosis. Current studies are examining specific pathways utilized by neutrophils to induce CD8 cytotoxic T-cell apoptosis.

ABSTRACT #18

The roles of FABP5 inhibitors in Ovarian Cancer

Le'Aona Dysart, Cleveland School of Science and Medicine; Jinkyu Choi, PhD; Liraz Levi, PhD; John Letterio, MD, Department of Pediatrics

Background:

Ovarian cancer is the fifth leading cause of cancer deaths in women. Approximately 140,000 women die globally per year of ovarian cancer. This weakening disease presents subtly, and when someone is diagnosed treatment options vary and are often limited. Despite there being a variety of subtypes, these subtypes are treated as a single disease. Efforts are being put forth to characterize the subtypes and identify potential biomarkers for therapeutic strategies. Tumor heterogeneity appears to be high across subtypes and in single tumors, causing treatment failure. Ovarian cancer can occur at any age, but it is more common in patients older than fifty. Patients will often have pelvic or abdominal symptoms. Initially, transvaginal ultrasonography and serum cancer antigen 125 measurements will be done. A CA 125 test measures the amount of the protein CA 125 (cancer antigen 125) in the blood. Standard treatment involves debulking followed by chemotherapy. This allows for as much cancerous tissue presented in the patient to be eliminated. Prognosis varies depending on the stage of cancer in the patient and treatment depends on tumor genetic composition. Epithelial ovarian cancer is the most common type of ovarian cancer since 70 percent of cases are diagnosed at stage III or IV, it is associated with a poor prognosis. Fatty acid binding proteins 4 and 5 (FABP4 and FABP5) are members of the intracellular lipid-binding protein family. They bind lipids such as long-chain fatty acids and vitamins and protect them from the hydrophilic environment in the cytoplasm and therefore have an important role in lipid metabolism. FABP4/5 were also shown to transport lipid ligands to the nuclear receptors PPARδ and PPARγ and activate transcription of genes. FABP4 is mainly expressed in adipocytes and macrophages while FABP5 is expressed in many epithelial tissues. Both FABP4 and FABP5 were found to be highly regulated in multiple types of cancer and specifically in breast and prostate cancers there were shown to promote tumor growth and metastasis.

Goal:

The purpose of our research is to evaluate if the FABP4/5 are valid targets for treatment in patients with ovarian cancer. We also would like to identify novel FABP4 and FABP5 inhibitors using a two-step screening: 1) having high binding affinity to FABP4/5, and 2) not activating PPARδ that was shown to activate cancer-promoting genes.

Materials and Methods:

During our study we produced the proteins FABP5, FABP4 on bacteria. We then purified the proteins, then tested the protein. An inhibitor was then placed in the cell to see if it would activate the carcinogenic genes. We transfected cells with PPARδ, β-gal, and PPRE. PPRE represents luciferase which causes a cell to become luminous. The reporter gene then reads the luminous cells. We transfect and create three cells with those three genes. We then used the Kaplan Meier Plotter to assess the correlation between the expression of genes in healthy patients and those who have ovarian cancer. We performed a statistical analysis, also known as a T-test, for our survival analysis we used Kaplan-Meier plotter, and for the end of our studies we used a plate reader that read floressence, FABP's 3,4,5, and 7, and ANS which gave the FABP's their fluorescents. A competition binding was also performed. During our binding essay we looked at FABP3 and FABP7 to ensure that our inhibitors were specific to FABP4 and FABP5.

Results:

Results are forthcoming

ABSTRACT #19

Cyclodextrin-based Delivery of Tuberculosis Drugs

Adam Esa, St. Edward High School; Emmanuel Opolot, Department of Biomedical Engineering; Horst Von Recum, PhD, Department of Biomedical Engineering

Background:
Tuberculosis (TB) is a lung disease that causes more than two million deaths per year worldwide. TB is typically treated by using antibiotics such as Piperacillin, Novobiocin, and Kanamycin; however, many of these antibiotics have a quick drug release that last for a short period of time. A short drug release can be dangerous for patients prescribed these antibiotics because irregular consumption of them can lead to the bacteria growing resistant to the treatment. Such situations increase not only the duration of the disease, but chances of death. Cyclodextrin, a toroidal-shaped glucose polymer, may be able to increase the duration of the drug release because of its ability to use affinity-based drug delivery instead of diffusion.

Goals:
This study was performed to investigate the delivery of tuberculosis drugs; Piperacillin, Novobiocin, and Kanamycin using the cyclodextrin polymer, as well as assess the bactericidal effect of these drugs in vitro.

Materials and Methods:
To conduct this experiment, we created gamma, alpha, and beta cyclodextrin gels and dextran gels to be used for the drug loading and drug delivery. We then made a key to determine the concentration of each of the antibiotics in phosphate-buffered saline (PBS) during drug release by finding the absorbance value of a known concentration of antibiotics using the Plate Reader Machine. This was followed by the drug loading of the antibiotics into the cyclodextrin gels and dextran (which is used as the control) by adding 1 ml of PBS, with a concentration of 25 mg/ml of each of the antibiotics, into each of microcentrifuge tubes which have one cyclodextrin or dextran gel in them. To complete the drug loading, the microcentrifuge tubes were put on an end to end mixer for four days. Daily drug release was then done by putting the cyclodextrin gels and dextran gels into a new microcentrifuge tube with fresh PBS which were still placed on the end to end mixer. The PBS was removed and replenished daily. The PBS that was removed was stored in the fridge until it was used to determine the concentration of released drug via absorbance readings on the Plate Reader Machine. The concentration of the drugs was then determined by conversion of the absorbance value using the already determined key. Simultaneously, bactericidal assays were done by preparing agar plates and culturing them with *Staphylococcus aureus* (S.Aureus). The cyclodextrin and dextran gels were placed in these agar plates containing the bacteria in order to assess the effect of the drug release on the bacteria.

Results:
This research remains ongoing and results are not currently available; however, based on pre-existing journals on cyclodextrin and affinity-based drug delivery, we believe that the cyclodextrin will result in a longer drug release compared to dextrin. We also expect that the drug released by the cyclodextrin gels will inhibit more bacteria growth compared to the dextran gels.

Conclusions:
This study demonstrates that cyclodextrin provides a platform that can be optimized for loading and release of antibiotics and could be explored further for application in treatment of an infectious disease like tuberculosis caused by *Mycobacterium tuberculosis* that requires antibiotic therapy.

ABSTRACT #20

The Impact of Race Concerning Deaths Due to Legal Intervention

Chloe Echols, Hathaway Brown; Braveheart Gillani, MSW; Peter Hovmand, PhD, Center for Community Health Integration

Background:
Gun violence within the United States has been a dividing and minacious issue throughout the past few decades. With mass shootings increasing, about 100 people die a day due to gun violence. Although Caucasians make up 75.8 percent of the population and African Americans (AA) make up 13.6, AA are disproportionately killed by legal intervention and gun violence. Why? AA face a greater likelihood of being killed by police than their white counterparts. Being killed by police has to do with more than just race, but a multitude of factors, like age, gender, socioeconomic background, physical location, mental health disorders, and other contact with the police (like being pulled over for speeding), etc.. In the age range of 20 years to 35 years old, AA men face a 2.5 times greater chance of being killed than Caucasian men by police intervention. Specifically between 25 and 29 years of age, black men are killed "at a rate between 2.8 and 4.1 per 100,000." AA women face a 1.4 times greater chance of being killed than white women. As it has been shown, gun violence has a negative impact on communities, health of the individual, and the nation as a whole. More research is needed to find and understand why there are racial biases and other ways to prevent them from causing a negative impact on communities.

Goals:
The goal of the literature review was to create a basic understanding of information surrounding the subject and to collect it for the purpose of creating a basis of information to then input into the Causal Loop Diagram (CLD) and S&F. The goal of the CLD is to map out the information collected and to also help create a basis of variables and information for the Stock and Flow Diagram (S&F), which has the purpose of running a simulation in order to prove if a feedback loop is accurate in its prediction of action. The S&F is then used as a basis to create an interface which is used as an interactive tool to model the data and present it to communities. However, the overarching goal is to learn more about this issue and to create solutions that will hopefully have a positive, lasting impact on communities.

Methods:
A literature review was conducted using peer reviewed sources from PubMed, Pew Research Center, Harvard School of Public Health, Plos One, PNAS, The CDC, and the U.S. Census Bureau. Gun violence within the U.S. was researched, in addition to factors contributing to deaths due to legal intervention, and information about racial disparities concerning deaths due to police officers, statistics on risk of being killed after being pulled over according to race and sex, along with using the key words/phrases of: racial disparities, gun violence, trends in gun violence, and racism, and "risk of being killed as a minority." Information was collected to identify the critical variables needed for the simulation modeling done in the S&F. System Dynamics, a method of identifying and displaying factors of multifaceted and multivariable dynamic problems using non-linear equations and feedback loops, was used to make a CLD. The CLD went through a critique and edit phase, and was changed to a final format in order to make the S&F. S&F will be made to run a simulation and test race's impact on death due to legal intervention.

Results:
Within the literature review, more information was discovered that led to the conclusion that race does have an impact on deaths due to legal intervention. Results from the CLD, and S&F, will be determined in the coming week.

ABSTRACT #21

Repeated mild traumatic brain injury produces chronic neurodegeneration, neuroinflammation and neuropsychiatric problems

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Background:
Around 1.7 million patients are diagnosed with traumatic brain injury (TBI) every year in the US. The majority of these cases are classified as mild TBI, and patients recover relatively quickly. However, repeated concussive events, which are common with contact sports or military operations, are associated with greater complications. Repeated mild TBI (rmTBI) has been associated with more severe sensorimotor, cognitive, and behavioral deficits, compared to single TBI events, including progressive neurodegenerative changes leading to severe functional decline. Neuropathological changes associated with rmTBI progress over time and increase the risk of developing other neurodegenerative conditions, including Parkinson's disease, vascular dementia, chronic traumatic encephalopathy, and Alzheimer's disease. Because of the large number of patients with a remote history of rmTBI, we have investigated the chronic consequences of rmTBI using the electromagnetic controlled cranial impact (CCI) model. We hypothesized that rmTBI would cause cognitive impairment associated with neurodegeneration and neuroinflammation.

Goals:
The goal of this project is to characterized the electromagnetic CCI model chronically, with respect to repeated mild TBI in people.

Materials and Methods:
Ten-week-old C57/Bl6J mice were subjected to single, repeated and sham impacts delivered to the scalp of the mice by the electromagnetically controlled device garnished with a rubber-tipped probe and housed under standard conditions for 6 months. After 6 months, cognitive function was evaluated through Morris Water Maze (MWM) while anxiety-like behaviors were evaluated by the Elevated Zero Maze. After behavior tests, mice were anesthetized with ketamine (100 mg/kg) and xylazine (10 mg/kg) via IP injection and transcardially perfused with phosphate-buffered saline (PBS) followed by 4% paraformaldehyde in PBS at pH 7.4. Brains were collected and post-fixed in 4% paraformaldehyde in PBS at pH 7.4 overnight at 4 °C and then transferred to 30% sucrose for 72 h. Brains were cut coronally (40-µm sections), preserved in cryoprotectant, and stored at −20° before staining. Brain sections were stained using the TUNEL assay for measuring neurodegeneration and Iba1 combined with BODIPY to assess neuroinflammation. Images of stained brain tissue were taken using a fluorescent microscope. Positive signals in the hippocampus and cortex were quantified-using ImageJ. GraphPad Prism was used to analyze the data and determine statistical significance.

Results:
Our results demonstrate that repeated mild TBI causes cognitive impairment and anxiety-like behavior, as tested by Morris Water Maze and elevated zero maze, respectively. TUNEL assay, in combination with NeuN, demonstrates a significant increase in neurodegeneration in the injured cortex (CTX) and hippocampus (HPC). Both areas show dysfunctional and proinflammatory microglia, as indicated by the accumulation of lipid droplets (LD).

Conclusion;
Our results provide insights into the chronic cognitive and neuropathophysiological consequences of the repeated mild TBI CCI model. This is the first time that the accumulation of LD has been shown in this model. Further studies are necessary to understand the specific roles of LDs in the brain damage caused by TBI, and whether this represents a potential therapeutic target.

ABSTRACT #22

Using K-Nearest Neighbors Software to Assess the Host Response to an Injectable Electrode

Kaitlyn Ernst, Laurel School; Kevin Yang, School of Engineering; Andrew Shoffstall, PhD, Department of Biomedical Engineering

Background:
Implanted electrodes represent a new potential for neuromodulation to treat severe illnesses, including chronic pain, epilepsy, migraines, and more, without the use of opioids. An injectable model mitigates the excess costs and invasiveness of current neuromodulation therapy. However, inflammation that occurs as a result of implantation may limit clinical success and suggest that the electrodes are not biocompatible if inflammation does not stabilize at an acceptable level. Macrophage recruitment is vital in the initiation, maintenance, and resolution of inflammation; moreover, matrix metalloproteinase (MMP)-9 regulates the pathological remodeling processes of the extracellular matrix (ECM). In our study, we investigate the host response to injectable electrodes through macrophage recruitment and MMP-9 expression by utilizing image analysis of immunohistochemistry slides.

Goals:
The objectives of the project are twofold: 1) design and confirm the accuracy of Matlab software to provide an objective and easily accessible method for analyzing immunohistochemistry images, and 2) assess macrophage recruitment, macrophage differentiation, and ECM remodeling in response to varying samples of injectable electrodes.

Materials and Methods:
Rat tissue samples were collected at one, two, and six months for two formulations of injectable electrodes: one made only of gold wire and one made of gold wire and a coseal polymer (n=40). DAB staining was used with CD68 for macrophage recruitment, CD86 for M2 macrophage polarization, MMP-9 for ECM remodeling, and a control stain. Images were taken at 100x magnification and batch-processed using the Matlab software. The script included DAB segmentation based on trained centers and a k-nearest neighbors (KNN) algorithm to determine the intensity of stained tissue.

Results:
Matlab software successfully indicated the intensity of stained tissue. Macrophage recruitment steadily increased over time for wire-only samples and decreased for wire and coseal samples. Interestingly, as time progressed, wire and coseal samples appear to have a larger proportion of M2 macrophages. MMP-9 expression increased over time for wire-only samples and decreased for wire and coseal.

Conclusions:
Due to the increased presence of M2 macrophages and decreased inflammation, injectable electrodes with coseal appear to promote a stable immune response, indicating biocompatibility. This lays the groundwork for future research and clinical applications of injectable electrodes, especially for patients for whom current technologies are inaccessible. Moreover, the KNN software holds exciting potential in promoting accessibility and efficiency for those in the field seeking to perform similar research.

ABSTRACT #23

Immunohistochemical localization of receptor protein tyrosine phosphatase γ and receptor protein tyrosine phosphatase ζ in mouse hippocampus

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The Protein Tyrosine Phosphatase Receptor Type G (*ptprg*) gene encodes the Receptor Protein Tyrosine Phosphatase Protein γ (RPTPγ), a member of the protein tyrosine phosphatase (PTP) family. PTP's are signaling molecules that regulate a variety of cellular processes including cell growth, differentiation, mitosis, and oncogenic transformation. We hypothesize that in the central nervous system (CNS), RPTPγ is expressed mainly in neurons. Similarly in the CNS, we hypothesize that another member of the PTP family, RPTPζ, encoded by the Protein Tyrosine Phosphatase Receptor Type Z1 (*ptprz1*) gene, is expressed mainly in glia. Both proteins are single pass transmembrane proteins with important functional domains on both the extracellular and intracellular side of the plasma membrane. On the extracellular side, the proteins possess carbonic anhydrase-like domains (CALD) that are similar in structure to the α-type carbonic anhydrases that catalyze the interconversion of CO2 and H_2O to HCO_3^- and H^+; however, the CALDs have lost the necessary amino acids needed to catalyze this reaction and are therefore enzymatically inactive. However, because neither RPTPγ nor RPTPζ can catalyze CO2 hydration, we hypothesize that both can act as CO_2/HCO_3^- sensors. RPTPγ and RPTPζ also both possess extracellular fibronectin type III domains. On the intracellular side, both proteins have two phosphatase domains. Regulation of the intracellular phosphatases has downstream implications on the activity of other proteins that control the transport of HCO3− into or out of the cell, thereby controlling the intracellular pH (pH_i). The regulation of pH is a vital homeostatic function shared by all tissues. Mechanisms that govern $[H^+]$ in the intra- and extracellular fluid are especially important in the brain. Neuronal activity can elicit rapid pH changes in both compartments. Maintenance of physiological pH is extremely important in the CNS and can affect neuronal excitability. We are investigating the differential expression of RPTPγ and RPTPζ in neurons and astrocytes of the mouse hippocampus. We hypothesize RPTPγ is exclusively expressed in hippocampal neurons, while RPTPζ is exclusively expressed in hippocampal astrocytes in adult mice. To test our hypothesis we are staining mouse brain cryosections to investigate in which hippocampal regions and cell types RPTPγ and RPTPζ are expressed. We will use a primary antibody against RPTPγ that was raised against the fibronectin III domain of RPTPγ. We will detect where the RPTPγ binds using a secondary antibody conjugated to a green fluorescent probe. We will use a novel rabbit polyclonal primary antibody developed in the Boron lab and a goat anti-rabbit IgG conjugated to a red fluorophore to detect RPTPζ expression. We will measure the colocalization of RPTPγ and RPTPζ in mouse hippocampal neurons and glia; the percent colocalization has not been previously determined. These data will show the extent of colocalization of these two hypothesized CO_2/HCO_3^- sensors, specifically in the mouse hippocampus, which will help us understand the role of RPTPγ and RPTPζ in modulating acid-base transport in neurons and astrocytes. In the future, we plan to further classify whether the neurons in which we observe RPTPγ or RPTPζ expression are excitatory or inhibitory. We will also expand the scope of our study to brain regions, including the cerebellum and cerebral cortex.

ABSTRACT #24

Role Hn RNP A1 in maintaining protein stability

Isaiah Gilbert, University School; Blanton Tolbert, PhD, Department of Chemistry

Background:
hnRNP A1 is made up of a UP1 that features two RRM domains; RRM1 and RRM2. Together, these make up one fully functioning protein. Efficient and accurate communication between these two domains in order for proper functioning, RNA binding, and stability.

Goal:
The overall aim of this project is to successfully create clones of E. Coli that feature the missense mutations that can be present within hnRNP A1. This will help as we will be making naturally occurring mutations to assess and observe the overall effects on protein stability and function of hnRNP A1. The mutations in particular that this project focuses on are T61A, V84L, V109I, and V159L. It also must be noted that all mutations that are focused on in this project are within the hydrophobic pocket of the RRM domain.

Materials and Methods:

Results:
Forthcoming

Conclusions:
In conclusion, hnRNP A1's role in cancer still remains not fully explored. Thus, this work's importance must be emphasized. Cancer is one of the top leading causes of death as of right now and any more knowledge that we are able to cultivate regarding it is a step in the right direction. This work will allow for us to continue the exploration of the role that hnRNP A1 plays in cancer, thus providing knowledge for the future.

ABSTRACT #25

The Role of PKNP in Cell Proliferation of CAL27 cells

Rama Al Ghalyini, Westlake High School; Katherine Chatfield-Reed, PhD, Department of Otolaryngology; Quintin Pan, PhD, Department of Otolaryngology

Background:
Head and neck cancer (HNC) is the sixth most common cancer worldwide with an annual incidence of ~800,000 new cases. Despite clinical advances in the multi-disciplinary care of these patients, the 5-year survival for HNC has been static at ~50% over the past number of decades. Therefore, there is a critical need to identify and push forward novel therapeutic concepts to optimally manage HNC patients. Our research group performed a state of the art gene editing strategy, CRISPR/Cas9 kinome screen, and identified several kinases that impact HNC cell fitness. In this study, we decided to focus on polynucleotide kinase-phosphatase (PNKP) for two key reasons: PNKP biology in cancer is largely unknown and a PNKP inhibitor, A12B4C3, is commercially available.

Goal:
Our goal is to validate our CRISPR/Cas9 kinome screen by determining the effect of PNKP inhibition on the survival of CAL27 cells, an HNSCC cell line.

Materials and Methods:
CAL27 HNC cells were cultured on 96-well plates, treated with vehicle or A12B4C3, and cell proliferation was measured over 5 days using the Incucyte Live-Cell Imaging Systems. For clonogenic survival, CAL27 HNC cells were 6-well plates and allowed to attach overnight. Subsequently, cells were treated with vehicle or A12B4C3 for 10 days. Colonies were stained with crystal violet and counted.

Results:
A12B4C3 reduced the proliferation of CAL27 HNC cells in a dose-dependent manner with an EC50 of 16.86 μM. Similarly, clonogenic survival was suppressed in response to A12B4C3 treatment.

Conclusions:
Our results showed that PNKP is a druggable fitness gene in HNC and the continued development of PNKP inhibitors should be prioritized.

ABSTRACT #26

The Impact of Race Concerning Deaths Due to Legal Intervention

Tarini Gowda, Revere High School; Braveheart Gillani, MSW; Robinson Salazaar, PhD; Peter Hovmand, PhD, Center for Community Health Integration

Background:
Lung cancer is one of the most common types of cancers in men and women. There are many different variables that play a role in causing this specific type of cancer. Some variables include age, the amount of radiation a person has been exposed to, their work environment, living conditions and family health history.

Goals:
The goal of the research project is to see how age, the amount of radiation a person has been exposed to, their work environment, living conditions and family health history are affecting lung cancer.

Materials and Methods:
System dynamics are used to solve dynamic problems. System dynamics is a mode of modeling that simplifies complex systems into models that can be understood easily and interacted with. These models simulate the nonlinear behavior of systems using stocks, flows, feedback loops, and much more. I will identify whether or not the feedback loops are being reinforced, as in the same outcome is being selected over a chosen period of time, or if they are being balanced, or counteracted, by some other variable. This will be accomplished by first creating a causal loop diagram (CLD), to identify possible variables that could cause discrimination, whether purposely or systemically. The CLD will take into account time restraints as well as help me identify feedback loops. Next, I will transfer that data, into a stock and flow simulation where secondary data will also be input to see if there is a correlation between certain variables. The reason I am using Stella is because the problem I am researching is a dynamic problem.

Results:
Experiments in progress, results to be reported.

Conclusions:
Experiments in progress, results to be reported.

ABSTRACT #27

Determination of Normal Tau Expression in Regions of the Human Brain: Future Implications for Alzheimer's Disease Study and Prevention

Hannah Holt, Charles F. Brush High School; Matteo Manca, Department of Pathology; Mikayla Huntley, Department of Pathology; Heidi Standke, Department of Pathology; Allison Kraus, PhD, Department of Pathology; Danielle Browne, Department of Pathology

Background:
Dementias are considered ambiguous in terms of diagnosis and general classification. For example, Alzheimer's is a neurodegenerative disease that is characterized by the depletion of one's brain cells, resulting in a central nervous system (CNS) that gradually loses proficiency in skills such as memory, cognitive and critical thinking, and the overall ability to execute tasks in an orderly and timely manner. The symptoms that patients develop are similar to other dementias, like Lewy body and vascular types. The main risk factor for developing Alzheimer's disease (AD) is age, however, there are cases of people developing AD in their 30s and 40s. Although there is no definitive cause of AD, risk factors that increase a person's chances of contracting AD (e.g. lifestyle, genetics, etc.) are influential. Scientists have now determined that the generation of neurofibrillary tangles (NFTs) in neurons precedes the onset of AD. As these NFTs grow in complexity and size, they eventually destroy the neuron, subsequently deforming brain tissue as cell destruction elevates. NFTs are primarily made of corrupted versions of tau proteins, a microtubule-supporting unit. Tau protein by itself is coded by the gene MAPT (microtubule-associated protein tau). Splicing MAPT results in six isoforms of tau. Both 3-repeat (3R) and 4-repeat (4R) tau isoforms are misfolded and prominent in Alzheimer's disease. "3R" implies that the tau variation has three microtubule-binding repeats, while "4R" implies that four repeats are present.

Goals:
Through our research, we have tried to determine the normal tau protein expression levels in specific regions of the brain to see if higher initial expression of specific tau isoforms accounts for increased corrupted tau output. Data is limited as to what is currently known about where in the human brain and what isoform of normal tau is expressed. However, rat brains have been found to express more 4R-tau in the entorhinal cortex rather than in the cerebellum. Corrupted forms of tau protein have been found in other regions of the human AD brain, but not in the cerebellum. There might be a connection here.

Materials and Methods:
We plan to use gel and immunoblot analysis with antibodies specific to tau isoforms, and quantitative immunoblot readouts to determine expression levels. With this approach, we can identify the tau proteins in brain regions and quantify their amounts according to their CNS locations.

Results:
Our experimentation is still in progress. Our prediction is that tau expression levels may be lower in areas of the brain known to accumulate less corrupted tau (e.g. cerebellum). Alternatively, expression of specific tau isoforms may differ by brain region.

Conclusions:
By exploring brain regions and their normal tau isoform expression, we could help future scientists by giving them a solid foundation of experiments that determine what forms of normal tau may be corrupted in specific brain regions and further indicate which brain regions need to be monitored the most for disease progression. By using gel analysis and antibodies, we can identify and quantify tau according to their locations. Our results can also be compared to specific readouts to assess how much corrupted tau protein is present by using the same samples for each specified location in an immunoblot and real-time quaking-induced conversion (RT-QuIC) experiment.

ABSTRACT #28

The roles of social factors, neighborhood, poverty on the higher incidence of prostate cancer African American/Black Males

Jaida Hadley, John F. Kennedy High School; Jennifer Cullen, PhD, MPH, Department of Population and Quantitative Health Sciences

Background:
The mortality rate for Black men from prostate cancer is more than twice as high as for all other races. Overall US prostate cancer mortality, from 2015 to 2019, among black men, was the highest in the world (1). (2) The rate was 38.3 per 100,000 Black men; 8.8 per 100,000 Asian/Pacific Islanders, 4 times greater rates than non-Hispanics, and 88.6 per 100,000 Hispanic. (3) In terms of the risk factors associated with newly diagnosed prostate cancer, older age, Black race/African descent, family history of prostate cancer, and taller height are considered to be significant. In addition to obesity, smoking, physical activity, vitamin D levels, statin medications, and some dietary factors, including dairy/calcium intake. Hereditary factors play an important role in developing prostate cancer. (5) There have been 269 single nucleotide polymorphisms (SNPs) replicated to date in multiethnic populations. (6) A significantly higher mortality rate in Black men among men with prostate cancer during this period. Black men have experienced a higher prostate cancer mortality rate during this period.

Goals:
The goal of this literature review is to explain why African Americans/Black men are more likely to develop prostate cancer compared to other races. This review will focus on prostate cancer in African American/Black men and the social factors like housing, transportation, neighborhoods, racism and discrimination, violence, education, job opportunities, income, access to healthy foods, access and ability to exercise, pollution, education, language, and literacy (7). Most African American/Black men have to deal with neighborhood disadvantages because they are more likely than other racial groups to lack access to social resources and economic opportunities (8). This review will help give others a better understanding of prostate cancer causes and why African American/Black men have a greater risk of getting prostate cancer than other races.

Materials and Methods:
This literature review was performed using PubMed. PubMed is a free resource supporting the search for biomedical and life sciences literature. The PubMed database contains more than 34 million citations and abstracts of biomedical literature (9). While using PubMed, this review used the following combination of search words: (10) Black men, prostate cancer, and poverty; (11) Black men, prostate cancer, and neighborhood; and (12) Black men, prostate cancer, and social factors.

Results:
There were 40 articles found in PubMed when using the search for "prostate cancer, and Black men and neighborhood"; for the years 1978-2022, 40 articles under prostate cancer, and Black men, and poverty for the years 1989-2022; and 153 articles when searching for prostate cancer, Black men and social factors for the years 1978-2022.
The most interesting papers from the first search (13, 14, 15). that were most interesting was called "Prostate cancer severity among low-income, uninsured men". It was interesting to read about the proportions of men with non-metastatic tumors diagnosed with cancers showing low-, intermediate, or high-risk characteristics (13).
Another interesting article was about prostate cancer and black men and social factors; it was called "Social and clinical determinants of physical activity in prostate cancer survivors" (14). It was interesting to read about the proportion of patients with metastatic disease at enrollment and the

distribution of non-metastatic cases by D'Amico risk group classification did not differ significantly by race/ethnicity.
The last article was about prostate cancer and black men and neighborhood was called "Racial and Ethnic Disparities in Cancer Survival: The Contribution of Tumor, Sociodemographic, Institutional, and Neighborhood Characteristics" (15). It was interesting to read about how Black patients had the lowest survival for all cancer sites, and Asian American and Pacific Islander patients had the highest, compared with whites.

Conclusion:
Future studies should look into why African American/Black Men have a more chance of getting prostate cancer than other races. It might also be valuable to look at African men from other countries than the United States who have much lower prostate cancer incidence and mortality compared to African American men (16). For example, compared to Nigerian men, African American men are more than 10 times as likely to develop prostate cancer and 3.5 times more likely to die from the disease (17). However, contrary to the global ranking, there is documented evidence in the literature indicating that prostate cancer in at least one West African country is similar to rates found in the United States and Caribbean Islands.

The point of the review was to identify why prostate cancer is so common in African American Black men.

ABSTRACT #29

Novel Insights into the Interactions Between the Gut Microbiome, Inflammasomes, and Gasdermins During Colorectal Cancer

Isabel Hart, Shaker Heights High School; Hannah L. Wargo, Department of Pathology; Joseph Williams, MPA; Carlo De Salvo, PhD, Department of Pathology; Theresa T. Pizarro, PhD, Department of Pathology

Background:
Colorectal cancer (CRC) is one of the most prevalent and fatal forms of cancer among Western countries. Inflammation, a well-known driver of colonic carcinogenesis, plays a role in CRC that extends far beyond colitis-associated cancer (CAC). Gasdermins (GSDMs) are a family of pore-forming effector proteins that cause pyroptosis, an inflammatory form of cell death. There are 5 members of the GSDM protein family, GSDME, GSDMC, GSDMB, GSDMD, and GSDMA. Gasdermins have been linked to different types of cancers, including CRC; however, their role in inflammation-driven CRC, or CAC, has not been investigated.

Goals:
The aim of this research project is to determine the expression of GSDM family members in an experimental murine model of CAC and to evaluate the impact of interleukin-33 (IL-33) on GSDMs, which our group previously reported is involved in the pathogenesis of CAC.

Material and Methods:
To induce colitis-associated polyposis, the AOM/DSS protocol was conducted on wild type and IL-33 deficient mice (*Il33*$^{-/-}$). Firstly, the carcinogen azoxymethane (AOM) was injected intraperitoneally on day 0 of the protocol, then, after two weeks, 3% dextran sodium sulfate (DSS) was added to the mice's drinking water for one week. The next two weeks were a recovery period, and the mice were fed normal water. This was repeated once more before euthanizing mice for tissue collection and analysis. Two groups of mice were compared, BL6 mice and *Il33*$^{-/-}$ mice. Mice were sacrificed and the last 10 cm of colons were collected and processed for histological evaluation by H&E staining and for GSDM transcripts by RT-qPCR.

Results:
WT mice developed severe CAC after treatment with AOM/DSS compared to *Il33*$^{-/-}$ mice, which lacked colon polyps. No significant differences were observed in *Gsdmc1*, *Gsdmd Gsdme* from colon tissues of WT compared to *Il33*$^{-/-}$ mice. However, there was a trend towards increased expression of colonic *Gsdma* in *Il33*$^{-/-}$ compared to WT mice.

Conclusions:
Through our experiment, we have concluded that IL-33 plays a pathogenic role in CAC. However, while IL-33 does not appear to affect the mRNA expression of most GSDM family members, *Gsdma* could potentially serve as a protective factor in IL-33-dependent CAC. Further research is required to determine whether GSDMs contribute to the pathogenesis of CAC, particularly at the protein and/or post-translational level.

ABSTRACT #30

Knockdown of Alas-1 To Screen for Protumor Effects

Asha Jha, Shaker Heights High School; Lydia Raines; Cao Wei; Stanley Huang, PhD, Case Comprehensive Cancer Center

Background:
White blood cells are seen as fighters against the harmful bacteria and viruses invading our body. One kind of white blood cells are macrophages, the first line of defense against pathogenic microbes. However, macrophages are largely ineffective against cancer cells, as when faced with them, they turn traitor and become Tumor Associated Macrophages (TAMs) that support cancer growth. Recent studies suggest that rate-limiting mitochondrial enzymes in heme biosynthesis, 5-aminolevulinate synthase (ALAS-1) and Ferrochelatase (FeCH) may be a factor in TAMs that blunt its antitumor effector function.

Goal:
To test if the ALAS-1 expression and activity is responsible for the pro-tumor effect of TAMs we will utilize genetic knockdown of ALAS-1 using short hairpin RNA (shRNA). Effect of ALAS-1 knockdown will be functionally analyzed in macrophages and in cancer cells. We hypothesize that removing Alas-1 may reduce the cancer cells' survival, resulting in ALAS-1 as a vulnerability in Cancer.

Materials & Methods:
We utilized a software to design specific shRNA to knockdown a specific area of ALAS-1. The designed RNA will be synthesized and procured. The shRNA will be delivered to the cells via transfection. The effect of shRNA will be confirmed by quantitative PCR (qPCR) and western blot analysis. Then set up the mix with the RNA solution, sequencing primer and DMSO to sequence the shRNA.

Results:
We have successfully designed shRNA targeting ALAS-1. Unfortunately, as of this date, the experiment is still pending. However, based on previous findings with the knockdown of Alas-1, positive results have been shown that inhibition of Alas-1 works as an anti-inflammatory agent, working well against affected macrophages meant to kill microbes. We also used a western blot prior to the experiment, if Alas-1 is affiliated with macrophages, and have shown. This shows that the gene is more effective against cancer, and more applicable considerably, so I expect the shRNA to show a high percentage of effectiveness against tumor promoting TAMs and cancer growth.

Conclusion:
As cancer continues to dominate the realm of medicine with its variations and claiming many lives, these results show that treatment is possible, and can pioneer more pathways of medicine. Even if we see the gene suppression fail, we gain more knowledge to apply for other trials.

ABSTRACT #31

A Comparative Analysis of the Effect of Age on Specific Glial Cells in Mice

Benjamin Jamal, Shaker Heights High School; Raquel Lopez de Boer; Lin Mei, MD, PhD, Department of Neurosciences

Background:
Although astrocytes and microglia are very structurally different, they function together to fulfill homeostatic and immune functions in the central nervous system (CNS). They promote developmental synapse formation and pruning, with astrocytes releasing multiple molecules that promote neuronal synapse formation, while microglia's primary developmental role is phagocytic. Astrocytes surround and contact most neuronal synapses as well as form the borders of the brain and vasculature. Together, the molecules released by astrocytes have been shown to promote both presynaptic assembly as well as postsynaptic maturation. Microglia engulf apoptotic neuronal corpses, phagocytose synapses and other components of the neuropil. Aging is the largest risk factor for neurodegenerative diseases such as Parkinson's disease (PD), Alzheimer's disease (AD), and dementia. Increasing evidence suggests that glial cells, such as astrocytes and microglia, play a major role in brain aging and in several disease processes.

Goals:
To develop a protocol for a spinal cord staining of a mouse and do a comparison of the motor neurons/inflammation markers of a 3 month old vs 12 month old mouse. Our goal is to see how aging contributes to changes in microglia and astrocytes and make connections to neural development and decline in aging mice.

Materials and Methods:
Immunofluorescence Spinal Cord Staining
Primary Antibodies:
- **Chicken GFAP (astrocytes)**
- **Goat ChAT (Motor Neurons)**
- **Rabbit TMEM (Microglia)**

Secondary Antibodies:
- **Anti Rabbit 594**
- **Anti Goat 488**
- **Anti Chicken 647**

Conjugated Antibody
- **DAPI**

Results:
The results are still to be determined, but based on the changes in astrocytes and microglia in the brain with age, we expect to see a decrease in the number of glial cells or see more damage in glial cells in the spinal cord. With age, glial cells are known to become worse at responding to neural injury because their inflammatory regulation capabilities diminish.

Conclusions:
With age, there is no significant neuronal loss as physiological aging is not associated with neurodegeneration. Glial cell loss or damage would result in the progression from physiological to pathological aging, meaning greater risk for neurodegenerative diseases. This could expand into further research in determining the specific differences in the glial cells of healthy vs neurodegenerative mice.

ABSTRACT #32

Role Hn RNP in Alternative mRNA Splicing

Ezaiyah Jolly, Shaker Heights High School; Blanton Tolbert, PhD, Department of Chemistry

Heterogeneous Nuclear Ribonucleoproteins (hnRNPs) are a family of RNA binding proteins (RBPs) that play a role in alternative splicing, mRNA stabilization, and transcriptional and translational regulation. The hnRNP A1 protein is composed of three domains; two RNA recognition motifs (RRMs) that form one functional protein known as unwinding protein one (UP1), and a disordered C-terminal domain (LCD) responsible for protein-protein interactions. Communication between the two RRMs is required for RNA binding and stability in UP1. This manuscript is investigating how changes in one domain affect overall protein function. This is done by cloning naturally occurring mutations through PCR, digests, and ligation reactions. All of the mutations have been associated with cancer. The mutations are T61A, V84L, V109J, and V159L. Because all of the mutations are in the hydrophobic pockets of the RRM domains we theorize that they play a significant role in the stability of the protein. We hope to gain insights into how these mutations affect structure in the protein as well as their role in cancer.

ABSTRACT #33

Proximity Labeling Technique to Identify Protein Interactions Important for UPF1 Function During Nonsense-Mediated mRNA Decay

Vishwum Kapadia, University School; Sarah Nock; Kristian Baker, PhD, Department of Genetics and Genome Sciences

Nonsense-mediated mRNA decay (NMD) is a cellular mechanism that identifies and removes flawed mRNA transcripts harboring premature stop codons. If these mRNA transcripts are not removed, they translate to nonfunctional proteins or proteins with deleterious function. NMD contributes to several diseases, including beta thalassemia, cystic fibrosis, and polycystic kidney disease. Three proteins are required for NMD: UPF1, UPF2, and UPF3. The core factor is UPF1, but its interactions with other proteins to mediate NMD is unclear. The objective of this study was to use the new method of proximity labeling to identify UPF1's interactions during NMD. Proximity labeling is a method of labeling proteins that neighbor a protein of interest (UPF1). TurboID enzyme was fused to UPF1 in yeast such that when UPF1 interacted with other proteins, the TurboID enzyme labeled these proteins with biotin. Since UPF1 interacts with several proteins during NMD in a rapid process, mutant UPF1s were used to stall the NMD process at specific stages. This allowed for the identification of interactions of UPF1 during different steps of NMD. Western blot was carried out to detect proteins that were labeled with biotin. Mass spectrometry was then performed to identify these biotinylated proteins. Western blot identified different proteins interacting with different UPF1 mutants, suggesting that UPF1 has various protein interactions at different stages of its function. This also proves that proximity labeling can identify proteins interacting with UPF1.

ABSTRACT #34

Analyzing Extracellular Vesicles with FACs Symphony S6 and Amnis Image Stream Cytometers

Shria Kavaturu, Copley High School; Karina Inacio Carvalho, PhD; Brian Grimberg, PhD, Case Comprehensive Cancer Center

Background:
Flow cytometry is a method used to identify the phenotype and characteristics of a cell. After a cell's initial detection by the cytometer they can be organized based on varying sizes, granularities, and presence of fluorophores. Recently, researchers have begun to explore smaller particles such as extracellular vesicles (EVs). EVs are small particles that play an important role in cell communication and may even play an important role in cancer growth.

Goals:
This experiment has two primary aims. One of the aims of this experiment is to understand and follow the process necessary to obtain EVs from a cell line. The second aim is to understand how effectively the FACs Symphony S6 and Amnis Image Stream machines are able to analyze small particles such as EVs.

Materials & Methods:
In order to conduct this experiment it is necessary to first obtain EVs from a cell line. We will be using the H1299 lung cancer cell line in this experiment. These cells must undergo four centrifugations. One centrifugation at 300 g for 10 minutes, another at 2000 g for 10 minutes, a third at 10,000 g for 30 minutes and a final centrifugation at 100,000 g for 70 minutes. After the centrifugations vFRed membrane stain must be added to the EVs. After staining the EVs are ready to be analyzed by the aforementioned machines.

Results:
Our research is ongoing and definitive results are not yet available. However, based on preliminary analysis we expect both machines to be able to effectively analyze the EVs with the FACs Symphony S6 being the more sensitive analyzer of the two.

Conclusion:
As diseases such as HIV and cancers become more pressing concerns, these results could be key in furthering current research. By opening up a new avenue for analysis of these diseases researchers can analyze small particles, such as EVs, and identify key information about the diseases they are studying from them.

ABSTRACT #35

Age-Dependent Differences in the Breathing Pattern in Health and Disease

Adlai Kwofie, Cleveland School of Science and Medicine; Gina Kola, Division of Pulmonary, Critical Care and Sleep; David Nethery, Division of Pulmonary, Critical Care and Sleep; Thomas E. (Ted) Dick, PhD, Department of Neurosciences

Background:
The respiratory pattern is produced by a central pattern generator (CPG), which is located in the brainstem. The motor output of the respiratory CPG is breathing. We visualize and record breathing using a technique called plethysmography, which involves animals (rats) breathing spontaneously in chambers where pressure transducers measure the small change in pressure across a high impedance screen due to the rats heating and humidifying the air they breathe. Last year, I analyzed the occurrence of sighs in adult rats that received intraperitoneal injections of either lipopolysaccharide (LPS) or phosphate-buffered saline (PBS). LPS-treatment induces systemic inflammation and increases respiratory frequency (fR) and sighing. In contrast to adult rats, adolescent rats have a much higher baseline fR, so we hypothesized that LPS ip injection would evoke smaller increases in breathing and sighing frequencies compared to adult rats.

Goals:
The goal of this research was to analyze sighs before and 12h after injecting LPS ip in rats at postnatal day age (P)22-P27. Specifically, we analyzed the frequencies of breathing and sighing. Sighing during illness increases oxygenation.

Methods:
I followed the same analysis protocol utilized last year. Briefly, my colleagues placed adolescent rats in the plethysmography chamber, unanesthetized, for their baseline recording using the Spike2 software. Then after baseline recordings, they administered an LPS or PBS injection to the rats and then 24h later placed the rat back into the plethysmograph, unanesthetized, for recording. Then, I analyzed the data for the number of sighs that occurred during these sessions and divided that number by the duration of the session for sighs per min. I display the analyzed data in a table to compare the differences.

Results:
Rats that received LPS had more sighs in their recording than rats received PBS. One possibility is that LPS induces a proinflammatory state systemically but can also induce central neural inflammation.

Conclusion:
We interpret that the increase in sighing is due to direct activation of respiratory nuclei is important for the timing and generation of inspiration. Thus, sighing is produced in the brainstem and complements a constellation of other behaviors referred to sickness behaviors.

ABSTRACT #36

Targeting IDH1 enhances chemotherapy response in pancreatic cancer

Minjun Kim, St. Edward High School; Arian Hajihassani, Department of Surgery; Mehrdad Zarei, PhD, Department of Surgery; Jordan Winter, MD, Department of Surgery

Background:
Pancreatic ductal adenocarcinoma (PDAC) is one of the most aggressive types of cancer. The five-year survival rate for patients with PDAC in the United States is less than 10%. Current therapeutic options include chemotherapy, immunotherapy, targeted therapy, radiation therapy, and surgery. The current standard care therapy for patients with PDAC is 5-fluorouracil, leucovorin, irinotecan, and oxaliplatin (FOLFIRINOX) and the combination of gemcitabine and nab-paclitaxel. Despite this achievement in past decades for treating cancers, pancreatic cancer patients are still limited to clinical efficacy. Our work has previously shown that AG-120 (ivosidenib), an FDA-approved drug, is a potent wild-type isocitrate dehydrogenase 1 (IDH1) inhibitor. IDH1 is a cytosolic enzyme that is protective of cancer cells under chemotherapy-induced oxidative stress by producing nicotinamide adenine dinucleotide phosphate (NADPH) to maintain redox balance by lowering the reactive oxygen species (ROS) level and alpha-ketoglutarate to maintain mitochondrial function which results in resistance to the chemotherapy drugs.

Goals:
This study aims to see if IDHI inhibitor (AG-120) enhances the chemotherapy (FOLFIRINOX) response in the pre-clinical pancreatic cancer mouse model.

Materials and Methods:
To pursue the effects of IDH1 inhibition in combination with FOLFIRINOX, the suspension of 1x106 MIA PaCa-2 cells were injected subcutaneously in 6-8 weeks old athymic nude mice. Treatment started after two weeks after tumors were palpable and tumor volume reached around 100mm^3-120mm^3. The mice were randomly assigned for treatment in four groups: Vehicle, AG-120, FOLFIRINOX, and a combination of AG-120 and FOLFIRINOX. AG-120 (75 mg/kg) was administered orally twice a day, and FOLFIRINOX (5FU 12.5 mg/kg, oxaliplatin 2.5 mg/kg, and irinotecan 25 mg/kg) was administered through Intraperitoneal (i.p) injection once weekly. Body weight and tumor volume were measured weekly.

Results:
Summarizing the data collected from the tumor-bearing mice treated with vehicle, AG-120, FOLFIRINOX, and a combination of AG-120 with FOLFIRINOX. The combination group receiving the AG120 and FOLFIRINOX had significantly smaller tumors than the other treatment groups. Importantly the body weight of all groups of the mice was stable, and mice did not show any signs of toxicity, resulting in no change in the body weight of the mice, meaning the drug was not toxic to the mice.

Conclusions:
The combination therapy of AG-120 and FOLFIRINOX showed a tremendous decrease in the tumor size compared to the control group and monotherapy groups of AG-120 and FOLFIRINOX. This has proven that combination therapy of AG-120 and FOLFIRINOX strongly inhibited the tumor growth and provided a novel explanation why chemotherapy may be ineffective in pancreatic cancer patients that combination therapy with AG-120 works more effectively than monotherapy of AG-120.

ABSTRACT #37

3D Human Stem Cells for Neural Development

Ishita Koppararu, Hathaway Brown; James Costanzo; Helen Miranda, PhD, Department of Genetics and Genome Sciences

Organoids are a 3D stem cell model which recapitulate the physiology of the human organs and are derived from induced pluripotent stem cells (iPSCs). The purpose of this project was to optimize cortical organoid differentiation protocol to be implemented in neurodevelopment and disease progression studies. Animal models such as mice have limitations such as inaccurate representation of the human brain development, and 2D models such as iPSCs have limitations with regard to being able to explore development through cell to cell interactions. However, organoids present a unique model as they are more effective and much closer to that of a human organ's physiology. iPSCs were cultured until completely confluent and later differentiated into cortical organoids in order to study neurodevelopment. When observing the organoids, morphology and electrophysiology were deeply studied. Results showed that at specific time points, the cell types within the organoid began to migrate. With the specific protocol used, neural rosettes formed later compared to other protocols, however, rosettes indicate neural development as they are known to be representative of the neural tube. The objective of optimizing the protocol was to shorten the process and increase the effectiveness of the differentiation process.

ABSTRACT #38

Multimodal traumatic brain injury model induces chronic cognitive impairment with increased levels of neurodegeneration and neuroinflammation

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Background:
Traumatic brain injury (TBI) annually affects upwards of 70 million people worldwide. In the United States alone, there are almost 3 million annual emergency department visits for TBI, and approximately 5 million people living with TBI-related disabilities. TBI survivors frequently experience chronic diffuse axonal degradation and nerve cell death associated with sensorimotor impairment, cognitive dysfunction, and emotional dysregulation, as well as an increased risk of developing other neurodegenerative conditions like Parkinson's disease, vascular dementia, chronic traumatic encephalopathy, and Alzheimer's disease. We have developed a mouse model of multimodal TBI (mmTBI) that entails jet-flow exposure in an overpressure chamber to produce a global concussion along with acceleration-deceleration and early blast wave exposure. Because of the large number of patients currently living with a remote history of TBI, we have used our model to investigate the chronic consequences of TBI. We hypothesized that the mmTBI model would cause chronic cognitive impairment associated with neurodegeneration and neuroinflammation, similar to what is seen in people after TBI.

Goal:
The goal of this project was to characterize chronic injury 6 months after mmTBI in mice.

Materials and Methods:
Two-month-old C57/Bl6J mice were subjected to TBI or sham-TBI and housed under standard conditions for 6 months. After 6 months, cognitive function was evaluated through Morris water maze (MWM) and anxiety-like behavior by elevated zero maze. After finished with the behavior tests, mice were anesthetized with ketamine (100 mg/kg) and xylazine (10 mg/kg) via IP injection and transcardially perfused with phosphate-buffered saline (PBS) followed by 4% paraformaldehyde in PBS at pH 7.4. Brains were collected and postfixed in 4% paraformaldehyde in PBS at pH 7.4 overnight at 4 °C and then transferred to 30% sucrose for 72 h. Brains were cut coronally (40-µm sections), preserved in cryoprotectant, and stored at −20° before staining. Brain sections were stained using the TUNEL assay to measure neurodegeneration and Iba1 combined with BODIPY to assess neuroinflammation. Images of stained brain tissue were taken using a fluorescent microscope and positive signal in the hippocampus and cortex was quantified using ImageJ. GraphPad Prism was used to analyze the data and determine statistical significance.

Results:
We found that mmTBI caused chronic learning and memory problems with no anxiety-like behavior, as tested by Morris water maze and elevated zero maze, respectively. TUNEL assay, in combination with NeuN, demonstrated significantly increased neurodegeneration in the cortex (CTX) and hippocampus (HPC) 6 months after mmTBI. Both areas also showed more microglia with lipid droplet (LD) accumulation, which is characteristic of a dysfunctional and proinflammatory state of microglia.

Conclusions:

Collectively, our results provide insights into the chronic cognitive and neuropathophysiological consequences of the mmTBI model. This is the first time that DNA damage in neurons and lipid droplet accumulation in microglia has been reported in a mouse model of chronic TBI. Further studies are necessary to understand the specific roles of lipid droplets in chronic brain pathology after TBI, including whether this represents a new therapeutic target.

ABSTRACT #39

To assess the hygiene of smart watches for minimally invasive surgeries

Cheyenne Marolt, Cleveland School of Science and Medicine; Kelsey Ouyang, BS, Department of Dermatology; Bryan T. Carroll, MD, PhD, Department of Dermatology; Scott Mahlberg, DO, Department of Dermatology

Background:
Wearable technology is a key element in our ability to advance our understanding of surgeries and advance our surgical education. Over the past few decades, we have witnessed a revolution in technological advancement in the field of surgery with the introduction of many different technologies. Some of these technologies include smartwatches, virtual reality, and sensors. In particular, smartwatches have allowed us to assess the work status of surgeons, which can improve the quality of surgical performance and the outcome of minimally invasive surgeries. However, few, if any, researchers have determined whether the use of surgical tools violates safety measures, such as surgical hand-washing procedures.

Goal:
Our goals included quantifying the colony-forming units on smartwatches frequently worn by healthcare workers, and to investigate whether there is bacterial transfer from the watch during the hand washing procedure before surgery or not.

Materials and Methods:
To prepare for our experiment we needed to make Blood Heart Infusion plates (BHI) and we needed to buy Brucella Blood Agar with Hemin and vitamin K (BRU). The process in making the BHI plates was to take 52.0 grams of the BHI powder and dissolve it in 1000 ml of distilled water and then heat it to a boil to make sure it was incorporated completely. Once we had it all combined we put it in the autoclave for 15 minutes at 121° C and then let it cool. After we had our plates done we were able to collect our samples. We will ask random participants to allow us to swab their watches. We will let them know that everything is optional and that they do not have to allow us to swab their watches. When we have consensus to swab their watches, we will first swab the sample without any cleaning done to it. Our next step will be to clean the same surface that we swabbed with an alcohol swab and then take another sample from the same surface of the watch. Once we have collected all of our samples we will send them to the pathology group for them to analyze the watches. Once we get our results from the watch samples we took, we will look at all the data and see what the results were from the watches before and after they were cleaned. We did this by counting the colonies on the BHI and BRU plates and then putting that data into a chart so that we could compare the numbers. To test our protocol we took some samples from different objects in the lab and plated them on the BHI and BRU plates to ensure the success of our plating and collection methods. We also counted the colonies of these samples for us to test for our protocol.

Results:
To figure out what grew on the BHI and BRU plates we took a little sample from the plate and put it on a microscope slide. We determined that the samples mostly had a bacteria or yeast on them.
Conclusions:
From learning whether or not smartwatches or any other piece of jewelry can carry different bacterias and yeast that can be harmful to the patient, we can learn more about this. We can alter what we are doing now to provide the best care for our patients and staff.

ABSTRACT #40

Microglial Effects on Neural Progenitor Cell Growth in Cerebral Organoid Models

Eleanor Meges, Padua Franciscan High School; Jaejin Eum; Anthony Wynshaw-Boris, MD, PhD, Department of Genetics and Genome Sciences

Background:
Numerous neurological conditions such as autism spectrum disorder develop during embryonic cortical development and can be difficult to model for research. Cerebral organoid systems can recapitulate neurodevelopment by modeling neural progenitor cell (NPC) growth and differentiation. However, in reality, an array of other cells contribute to this process such as microglial cells - macrophages that comprise 5-6% of cells in the cerebral cortex. Because of their presence in neural development, we incorporated microglia (MG) with NPCs in cerebral organoid systems so that they can more holistically represent this development and be used to model diseases more accurately in the future.

Goals:
We incorporated NPCs and MG into cerebral organoid models to study how interactions between them contribute to cortical growth. The organoid models were generated with a combination of either NPCs and MG (NPC:MG) or NPCs and CD34+ hematopoietic stem cells (HSC) that differentiate into MG (NPC:CD34). By contrasting these organoid samples at different stages of growth, we aim to determine how NPC development is influenced by MG maturity.

Materials and Methods:
Cerebral organoid samples were stained via immunohistochemistry for different NPC markers at three time points (3 weeks, 5 weeks, and 7 weeks). NPC:MG organoids were generated with mature microglia while the NPC:CD34 organoids were generated with HSCs. SOX1 was the marker used for general NPC identification, PAX6 was the marker used for radial glial cell identification, CTIP2 was the marker used to identify early born neurons, MAP2 was the marker used to identify mature neurons, and DAPI was used to identify cell nuclei. Epifluorescent microscopy and qualitative analyses were completed.

Results:
At around 7 weeks, SOX1 markers in the NPC:CD34 organoids appeared more strongly around the perimeter compared to the NPC:MG organoids, in which SOX1 was more ubiquitously distributed. Previous research indicates organoids model realistic cerebral growth around a ventricular zone, where NPCs move away from a central ventricle as they differentiate. This observation indicates that CD34 NPCs were differentiating sooner as they migrated away from the center and that these organoids may exhibit faster development. In comparison, the NPC:MG organoids' even distribution of SOX1 markers indicates NPCs were still undergoing initial neurogenesis. No other markers differed between the two organoid conditions.

Conclusions:
Growing NPCs with HSCs appeared to contribute to different NPC distribution and potentially accelerated growth of NPCs. This could be representative of the effect HSCs have on actual neurogenesis or simply a byproduct of organoid-specific growth with that protocol. These results give us insight about the specific role microglial cells play in cortical development and help contribute to the development of more realistic models for neurological research. This provides a baseline for microglial influences on neurogenesis so we can identify abnormalities in embryonic cortical development and better understand neurological conditions and diseases.

ABSTRACT #41

Direct Effect of Opioids on the Intestinal Epithelium

Ira Mehta, Lake Ridge Academy; Alan Levine, PhD, Department of Molecular Biology and Microbiology

Background:
The United States is experiencing a tragic opioid epidemic with increasing rates of morbidity and mortality. The risk of death is 6 to 20 times greater for those with opioid use disorder (OUD) than the general population, and overdose deaths in the past two years have risen dramatically; In 2020, during the coronavirus pandemic, US drug-related deaths significantly increased to over 93,000 deaths, nearly 30% higher than in 2019. Chronic opioid use is also associated with severe constipation, gastrointestinal (GI) distress, and decreased gut motility. Our research team has demonstrated that opioid use also leads to dysbiosis of the gut microbiome, in which balance in the population of bacteria is severely disrupted.

Goals:
In order to address the GI distress in patients with OUD, the goal of this project is to investigate the direct effects of opioids on the epithelial cells that line the gastrointestinal tract. If the barrier function provided by these cells is damaged by opioids, this is likely to contribute to disease pathogenesis.

Materials and Methods:
Human colorectal adenocarcinoma Caco-2 BBE cells were used as a model of the human intestinal epithelial barrier. The cells were maintained in Eagle's minimal essential medium (EMEM) with 10% fetal bovine serum (FBS.) Intestinal epithelial cell monolayers were established by seeding a semi-permeable transwell membrane with 6,000 to 60,000 cells. The permeability of the barrier was tested using the EVOM2 Epithelial Voltohmmeter, which measures TransEpithelial Electrical Resistance (TEER) across the monolayer.

Results:
When the monolayer was established using 6,000 cells the change in electrical resistance over time is shown in blue in Figure 1. When the monolayer was seeded at 60,000 cells the resistance increased much more rapidly. These findings enabled us- to define the optimal conditions for our experimental approach when the monolayer is exposed directly to opioids and opioid antagonists.

Conclusions:
Having optimized the experimental design, we are now positioned to evaluate the effects of synthetic opioids on intestinal barrier integrity.

ABSTRACT #42

The role of macrophages-KLF6 in the pathogenesis of arterial restenosis

Uwela Mugabo, Facing History New Tech High School; Soda Guisse, The University of Cincinnati; Atif Zafar, MD, Department of Pathology; Hang Pong Ng, Department of Pathology; Ganapati Mahabaleshwar, PhD, Department of Pathology

Background:
Cardiovascular diseases (CVDs) are a group of diseases of the heart and the blood vessels. Cardiovascular diseases are one of the most common causes of death in the world. An estimated 17.9 million people died from CVDs in 2019, representing 32% of all global deaths. The majority of cardiovascular events are caused by the occlusion of arteries that supply blood to major organs. These arterial occlusions are either caused by the buildup of lipid-rich plaques or narrowing of arterial lumen due to endovascular injuries. Most commonly, vascular injury promotes vascular smooth muscle cell proliferation as well as attracts immune cells as an injury response. Here, we analyzed the role of macrophage-kruppel-like factor 6 (KLF6) in the pathogenesis of arterial restenosis.

Goals:
The goal of this project is to determine the impact of macrophage-KLF6 deficiency on inflammatory gene expression and injury-induced carotid artery restenosis.

Materials and Methods:
The left common carotid artery of macrophage-KLF6 deficient and control mice was exposed and ligated to induce arterial injury response. The sham surgery on the right carotid served as a control. The elastin structures within the carotid arteries were visualized and detected by using a modified Verhoeff Van Gieson elastic stain kit. The circumferences of the lumen, internal elastic lamina (IEL), and external elastic lamina (EEL) were measured by tracing along the luminal surface, IEL, and EEL, respectively, using ImageJ software. These measurements were used to calculate luminal area, IEL area, and EEL area. The total neointimal growth area was calculated by subtracting the luminal area from the area defined by IEL. The total vessel area was calculated by tracings obtained by the external perimeter of the artery.

Results:
The wild-type mice that macrophage- KLF6 showed a significant increase in neointima formation in the lumen of the carotid arteries following 28 days after the injury. Interestingly, the mice with macrophage-KLF6 deficiency showed significantly decreased neointimal growth in the lumen of the carotid arteries 28 days after the injury.

Conclusions:
Our studies provide evidence that macrophage-KLF6 promotes injury-induced arterial restenosis *in vivo*.

ABSTRACT #43

PGC-1alpha Overexpression Alleviates Neuronal Cell Death in an Alzheimer's Disease Mouse Model

Janailyn Morris, Cleveland School of Science and Medicine; Fengqin Wu, Department of Pathology; Yubing Lu, PhD, Department of Pathology; Xiongwei Zhu, PhD, Department of Pathology

Background:
Alzheimer's disease (AD) is a neurodegenerative disease that progressively impairs cognitive and memory abilities, which is caused by a hallmark of AD, neuronal cell death in the hippocampus and cortex. By 2050, AD is projected to affect nearly 100 million people worldwide, therefore exerting a tremendous burden on society. Mitochondrial dysfunction is an early and prominent feature during the progression of AD, which is likely a critical role in the pathogenesis of AD. Mitochondria constantly undergo a process that is necessary for its function and distribution. This process is called fusion and fission and can cause neurological disorders if ineffective. Mitochondria fusion/fission impairment is a prominent factor of mitochondrial dysfunction. PGC-1alpha is a key component of regulatory pathways of mitochondria biogenesis, which also impacts mitochondrial fission/fusion. Since mitochondria are a major source of ATP, PGC-1alpha is found profusely in tissues with high energy demand, such as the brain. Importantly, the expression of PGC-1alpha is reduced in the brain of AD patients, which may contribute to mitochondrial dysfunction in AD. We hypothesized that PGC-1alpha overexpression should serve as a mechanism for rescuing neuronal cell death.

Goals:
The objective is to rescue neuronal cell death within an AD mouse model brain by overexpressing PGC-1alpha.

Materials and Methods:
A widely used AD mouse model, 5xFAD mice, was crossed with mice overexpressing PGC-1alpha in neurons in the forebrain. We characterized neuronal number and pathology in the brains of WT mice and 5xFAD mice to compare with 5xFAD x PGC-1alpha mice at 10 months of age by immunocytochemistry (IHC) study. Primary antibodies 82E1, NeuN, GFAP, and Iba1 were used in the IHC study. 82E1 stained for amyloid plaques, NeuN stained for neuronal nuclei, GFAP stained for astrocytes, and Iba1 stained for microglia. Imaging was completed with an upright fluorescent microscope using 5x1.25 magnification of the hippocampus and cerebral cortex. Layer 5 of the cerebral cortex was quantified. Quantification will demonstrate the effectiveness of PGC-1alpha on alleviating neuronal cell death and also the effects on other AD-related pathological changes associated with AD.

Results:
Research is still ongoing, but overexpression of PGC-1alpha is hypothesized to rescue neuronal cell death in 5xFAD mice along with microgliosis and astrocytosis. However, it appears that there are not many effects on plaque loads.

Conclusion:
PGC1alpha overexpression plays a neuroprotective role in an AD mouse model and alleviates neuroinflammation. PGC1alpha and mitochondrial biogenesis pathway is likely a good target for future therapeutic development for AD.

ABSTRACT #44

Imaging PSMA biomarker in a Prostate cancer tumor model with targeted PSMA-Cys-IR800 probe in athymic nude mice

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Background:

Prostate cancer is a specific type of cancer that develops in the prostate gland of the male reproductive system and ranks second in cancer mortality among men. These cancer cells express many proteins/biomarkers, among them is the Prostate-Specific Membrane Antigen (PSMA), which is almost exclusively overexpressed in prostate cancers and its expression levels are related to the extent of disease progression. Different human prostate cancer cell lines expressing PSMA to varying degrees have been isolated to model this disease in mice. The extent to which PSMA is expressed in a cell line or a tumor on an animal can be measured by molecular imaging. Using fluorescent imaging probes that are selectively targeted to the PSMA biomarker, the level of PSMA can be measured fluoroscopically both in vitro and in vivo. Here we propose to develop two different tumor models in mice, high and low-expressing PSMA tumors, to demonstrate that the PSMA-targeted molecular imaging probes can measure PSMA expression non-invasively.

Goal:

Determine the selectivity and sensitivity of the PSMA targeted probe for imaging PSMA expression in vivo. For these studies, we will use immuno-compromised (nu/nu) mice implanted with PSMA-expressing human prostate PC3pip tumors or PSMA-non-expressing PC3flu tumors. A PSMA non-binding control probe will also be included.

Materials and Methods:

Probe Synthesis: **For this study, a PSMA binding peptide, PSMA-Cys, and a PSMA non-binding peptide, PSMA-CysNA, were synthesized in the lab via peptide synthesis reactions and were purified by HPLC. PSMA-Cys or PSMA-CysNA were then reacted with IRdye800 maleimide to obtain the probes PSMA-Cys-IR800 and PSMA-CysNA-IR800. The IR800 probes were then administered through the tail vein to the mice and were imaged at various time intervals using different imaging modalities to see the binding capacity to the PSMA biomarker.**

Animal Studies: **Two prostate cancer cell lines, PC3pip (PSMA+) and PC3flu (PSMA-) were cultured, and then approximately 1 million cells from each cell line were mixed with matrigel and subcutaneously injected into the flank of mice (n=3). When the tumors reached the appropriate size (~1cm) the animals were injected with 1 nmol of PSMA-targeted imaging probe PSMA-Cys-IR800 or PSMA non-targeting probe PSMA-CysNA-IR800. The animals were then imaged at different time points after injection for 24-48 hours. Based on previous studies, we will measure probe uptake at 1, 4, 8, 16, 24, and 48 hours after injection.**

Results:

These studies are still in progress. Currently, the tumors are growing in the flank of the animals at a rate of 0.8 cubic mm per day. Based on this rate, the tumor reached a suitable size for imaging on the 13th of July. Currently, imaging and data collection are still in progress. The anticipated results are that the PSMA-expressing cells will take up more of the PSMA-Cys-IR800 probe than the PSMA negative cells. Additionally, it will be interesting to determine if the rate of uptake between the two cell lines will also vary in accordance with the different levels of PSMA expression, as there is a possibility that non-PSMA-related uptake of the probe can occur.

Conclusion:

One of the major treatments for prostate cancer is radical prostatectomy. This is a procedure in which the entire prostate gland, where the tumor develops, is removed. There is currently no way to visualize prostate cancer during surgery resulting in cancer remaining in the patient 10-15% of the time. The development of fluorescent imaging probes that can be visualized during surgery could significantly impact surgical outcomes.

ABSTRACT #45

Improving Function of DCs through Cas9/Crispr-Mediated Ex Vivo Manipulation for an Immunotherapeutic Approach to Sarcoma

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Background:
Dendritic cells (DCs) are phagocytic antigen-presenting cells (APCs) that play a pivotal function in initiating the body's adaptive immune responses. Because of their capacity to present tumor-specific antigens, DCs have become an attractive prospect within the research of cancer immunotherapy. DCs have a unique ability to elicit an immune response within inactive naive T lymphocytes through the process of capturing antigens from invading pathogens or tumors, subsequently presenting these antigens on their cellular surfaces. T cells, like CD4 and CD8, both possess abilities that are detrimental to the survival of cancerous growths. When CD4 T cells come into contact with DCs, they generate a signal to recruit CD8 T cells, which are responsible for fighting off malignancies.

Goals:
The goal of this experimentation is to develop a modality improving APC function using CRISPR knockout technology for mouse bone marrow-derived dendritic cells (BMDCs).

Materials and Methods:
BMDCs were differentiated from the cells of the femurs and tibia of mice. The BMDC differentiation is verified by flow cytometry analysis measuring the level of expression of DC surface markers including CD11c, CD80, CD86, and MHC-II. These cells will be manipulated in an ex-vivo environment with the utilization of Cas9/RNA-based CRISPR knockout procedures with the aim of eliminating a proprietary genetic sequence via induction of non- homologs end joining (NHEJ)-indel events. Next-generation sequencing (NGS) will subsequently be used to analyze cells treated with the CRISPR knockout. Indel discrepancies and the knockout ratio will be determined using ICE analytic algorithm (Synthego Co.) by comparing the edited genetic sequence with a wild-type sequence used as the control.

Results:
Due to the ongoing nature of the experiments, results are not available at this time.

Conclusion:
Although the estimated 5-year survival rate of sarcoma is roughly 65%, patient survival largely relies on individual factors associated with metastasis to the secondary organ, which sharply drops the 5-year survival rate to 16%. While the relationship between CD4 and CD8 T cells, as well as DCs, has provided a promising avenue for the future of cancer immunotherapy, DC vaccination methods still maintain their limitations in terms of efficacy, thus warranting a need for DC vaccines to be further functionally improved for effective tumor-specific antigen presentations via genetic modifications of inhibitory molecules

ABSTRACT #46

The Oxygen Permeability of Red Blood Cells Differs Significantly Across Separate Strains of Mice

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Background:
Gas exchange is essential for the survival of living organisms as it is the process in which O_2 and CO_2 are exchanged between the atmosphere and the blood. Many believed that O_2 crossed the red blood cell (RBC) membrane only by dissolving in and diffusing through membrane lipids, but later studies with mouse RBCs indicate that O_2 can also cross the RBC membrane through channel proteins. It has been observed that proteins aquaporin-1 (AQP1) and the Rhesus complex (RhAG) contribute to the majority of mouse red blood cell O_2 permeability. However, many aspects of gas exchange are still unclear, and these are only two of many possible O_2 channels. Studies using an inhibitor p-chloro mercuri benzenesulfonate (pCMBS) with RBCs from mice genetically deficient in both AQP1 and RhAG indicate the existence of other unknown protein channels that may contribute to O_2 permeability of mouse RBC membrane. The identification of additional O_2 channels and greater command over the physiological mechanisms of gas exchange present great promise in the treatment of a multitude of diseases.

Goals:
Find differences in the release rate of oxygen from the hemoglobin in multiple strains of mice that could be attributed to the presence of additional O_2 channel proteins in the red blood cell membrane.

Materials and Methods:
We utilized stopped-flow spectroscopy to monitor the rate constant of oxygen off-loading from hemoglobin (we defined it as k_{HbO2}) in the red blood cells of two strains of mice, adult C57BL/6 case wild type mice from Case Western Reserve University (CASEWT) and adult C57BL/6J wild type mice from the Jackson Laboratory (JWT). Rate constants for the off-loading of O_2 from hemoglobin in both strains of mice were recorded for blood samples of both intact red blood cells and completely lysed red blood cells.

Results:
The average rate constant for the off-loading of O2 from the RBC lysates of C57BL/6 case was 11.494 (s^{-1}) while the average rate constant from the lysates of C57BL/6J mice was almost the same at 11.409(s^{-1}) (N=4). However, the average rate constant for the off-loading of O_2 from intact RBCs of C57BL/6 case mice was 4.359(s^{-1}), while the average rate constant for the intact RBCs of C57BL/6J mice increased significantly to 5.070(s^{-1})(N=3). Hematological analyses show that the average values for mean corpuscular volume (MCV) are 50.1(fl) for C57BL/6 case mice and 45(fl) for C57BL/6J mice (N=3), meanwhile, the average values for mean corpuscular hemoglobin concentration (MCHC) are 28.4(g/dl) for C57BL/6 case mice and 31.7(g/dl) for C57BL/6J mice (N=3).

Conclusion:
We observed that k_{HbO2} of intact RBCs from C57BL/6J mice significantly increase by 16.3% compared to that of C57BL/6 case mice. There are several factors that may contribute to this different k_{HbO2} between the two strains of mice, such as numbers of membrane proteins that may function as oxygen channels, different RBC geometry, difference of RBC membrane lipid components et al. While the greater mean corpuscular volume (MCV) of RBCs of C57BL/6J mice would lead to a decreased rate constant, this diminution is offset by an increased mean corpuscular hemoglobin concentration (MCHC), so one would assume any difference in the rate constants between the two strains of mice would be statistically insignificant. Further studies based on proteomics and lipidomics by analyzing RBC ghosts should be conducted to further verify whether this increased k_{HbO2} of intact RBCs from C57BL/6J mice is contributed either by membrane proteins like AQP1/RhAG and/or additional protein channels or by some specific lipids or by both.

ABSTRACT #47

The Role of *SLX4IP* in Tumor Cell Growth

Angel Ononogbo, Orange High School; Deepak Babu, Department of Biochemistry; William Schiemann, PhD, Case Comprehensive Cancer Center

Background:
Breast Cancer is among the deadliest cancers in the world and often poses ample clinical burden and resistance to therapy. One leading cause of this is its uncontrolled growth and metastatic behavior, also known as tumor progression. Previous studies have identified the overexpression of the *SlX4IP* gene in Breast Cancer and its relationship with the Hedgehog Signaling Pathway. While we know that the hedgehog signaling pathway is responsible for the maintenance of cell renewal of both normal and tumor cells, we do not know how the expression of *SLX4IP* influences tumor cell growth.

Goals:
This study aims to determine the role of *SLX4IP* in cancer cell growth and how it is possibly associated with hedgehog signaling in breast cancer tumorigenicity.

Methods:
We first investigated the expression levels of *SLX4IP* in two distinct human breast cancer cell lines: MDA-MB-468 and HCC1954. To test how *SLX4IP* affects cell growth, we genetically modified these cell lines using shRNA against *SLX4IP*, which depletes cellular expression of *SLX4IP*. We also engineered these cells to express a non-targeting shSCRAM, which does not impact *SLX4IP* expression and serves as a vector control in our experiments. Breast cancer cells expressing shRNA against *SLX4IP* are referred to as "shSLX4IP," while those expressing non-targeting shSCRAM are referred to "shSCRAM."
We extracted total RNA from the cell lines (shSCRAM and shSLX4IP) and performed a real-time Polymerase Chain Reaction to monitor the expression levels of *SLX4IP* in shScram and shSLX4IP breast cancer cell lines. We also extracted protein from both cell lines to use for a Western blot analysis, which would confirm the extent of knockdown in SLX4IP protein expression.
Currently, we are preparing a cell growth assessment using a colony forming assay and IncuCyte cell proliferation assay for both cell lines to see how *SLX4IP* influences cell growth. Additionally, we will also treat these lines with Hedgehog signaling inhibitor and activator to verify *SLX4IP* influence on the Hedgehog signaling pathway and its role in regulating breast cancer growth.

Results:
Both the real-time Polymerase Chain Reaction and Western blot assays confirmed knockdown of *SLX4IP* expression in MDA-MB-468 and HCC1954 cell lines. We are still in the planning stages for the Colony growth assay; thus, we are still awaiting these results to confirm the role of *SLX4IP* in breast cancer growth.

Conclusions:
Considering the results we have gathered so far, we believe we are well-equipped to test our hypothesis that *SLX4IP* induces cancer stem cell phenotypes and enhances tumor burden. Should this prove to be the case, future studies will investigate the influence of *SLX4IP* in regulating drug resistance and disease recurrence in metastatic breast cancers.

ABSTRACT #48

The Effect of Nanobubble Shell Structure on Contrast-Enhanced Ultrasound Signal and Nanobubble Movement in Blood

Eric Pieper, Shaker Heights High School; Michaela Cooley, Department of Biomedical Engineering; Eric Abenojar, Department of Biomedical Engineering; Agata Exner, PhD, Department of Radiology

Background:
Microbubbles (MBs) and nanobubbles (NBs) are ultrasound contrast agents. They can be used for diagnostic imaging and for therapeutic purposes (e.g. triggered drug delivery). Bubble shells are made from polymer, lipid, or proteins. NB stability under ultrasound of lipid formulations with a C3F8 gas core with varying shell stiffness and surface markers have been studied before. These studies were conducted *in vitro* with PBS or *in vivo* in mouse tumors. However, beyond shell stiffness, there may be other explanations for their reported stability. NB interactions with RBCs in whole blood have been shown to improve stability and cause a delay to peak ultrasound enhancement *in vitro*. However, the mechanism for these interactions has not been fully elucidated. Other groups have studied nanoparticles interactions with RBCs according to ζ-potential, but ζ-potentials close to zero were not studied.4 Further, nanoparticle shell stiffness was not studied and none of the examined particles were as flexible as NBs (liposomes being the most similar). In this study, we examine the effect of shell stiffness and ζ-potential on NB- generated contrast enhancement and decorrelation time under ultrasound.

Goals:
Analyze how NB shell structure and ζ-potential affect contrast enhancement and decorrelation time under ultrasound in human whole blood versus PBS.

Materials and Methods:
An agarose tissue-mimicking phantom was made by dissolving 1.5g of agarose into 100mL of deionized water and pouring it into a mold. Lipid shell stabilized C_3F_8 NBs were prepared as previously described with four formulations. All shells included DBPC, DPPA, DPPE, and DSPE-mPEG2K. Propylene-glycol (PG) and glycerol (G) concentrations were varied in different formulations: 1. PG, 2. G, and 3. PG + G (PG-G). The final formulation included group with a targeting agent, prostate specific membrane antigen (PSMA), to the PG-G formulation. NBs were activated with mechanical agitation and filtered through centrifugation. 4.07×10^9 NBs/mL were mixed with PBS or human whole blood (WB), obtained the day of the experiment, and imaged under a Toshiba contrast-enhanced ultrasound with a 12MHz transducer for 500 s at 1 fps (0.1 MI, 65 DR, 70 2DG). Decorrelation time analysis is ongoing.

Results:
All four NB types showed similar decreases in enhancement over time in PBS. PG, PG-G, and PSMA-NBs exhibited a delay in time to peak enhancement and greater final enhancement than G-NBs in WB. G-NBs had a steady signal in WB that did not increase or decrease. There were differences in time-intensity curves when different donor blood was used. The delay in time to peak enhancement was always present for the PG, PG-G, and PSMA NBs, but depending on the blood used, time to peak and peak enhancement changed. Further, one donor blood showed a quick sedimentation rate and the NBs stayed within the RBC layer for the entire the experiment.

Conclusions:
The delay in time to peak enhancement observed in WB with PG-G, PG, and PSMA NBs may be due to their lower shell stiffness compared to G-NBs. Other possible explanations include interaction of the NB phospholipid head with the RBC membrane, which is more sterically hindered in G-NBs. The ζ potential of these NBs do not seem to play a significant role in the results. When RBCs separate from plasma, NBs only stay within the RBC layer, giving additional evidence for NB-RBC associations. Blood donor is an important component to these studies and future studies should be conducted with biological replicates to account for this.

ABSTRACT #49

Early Onset Colorectal Cancer (EOCRC) Risk Increases with Obesity Independent of Self-Reported Race

Garv Patel, Andrews Osborne Academy; Fredrick Schumacher, PhD, Department of Population and Quantitative Health Sciences

Background:
Colorectal cancer (CRC) is the third most common cancer for men and women and one of the leading causes of cancer mortality. CRC is uncommon in young individuals (<45), however, the incidence of early-age onset CRC (EOCRC) has been steadily increasing over the past few decades. Suspected EOCRC risk factors include physical activity, diabetes, smoking/alcohol use, forms of medications and obesity. The impact of obesity on EOCRC may differ by self-reported race, thus contributing to racial health disparities.

Goals:
We hypothesize the association of obesity on EOCRC risk may differ by self-reported race.

Materials and Methods:
The National Health Interview Survey, a prospective cohort study, was used to assess the association between EOCRC (<45 years old at diagnosis) and obesity using body mass index as a proxy. All CRC cases were categorized based on their age at diagnosis,<45, 45-55, and >55, and controls were cancer free. BMI was categorized as healthy (18-25), overweight (25-30) and obese (>30). We applied chi-square tests for univariate associations with CRC age of onset. A multivariable logistic regression framework was employed to assess adjusted effects and effect modification. All statistical tests were two-sided with statistical significance defined at the alpha level of 0.05, and completed in either Excel or the R computing environment.

Results:
In total, we had CRC status on 48,085 participants with age of disease onset. The frequency of obesity among EOCRC (<45 years old) cases was 31%, 38.5% and 30.3% for healthy, overweight and obese BMI categories, respectively. The obesity distribution was similar among those 45-55, but significantly less among older CRC cases (>55). Furthermore, the racial distribution was significantly associated with age of CRC onset. Individuals who self-reported as Black and Asian were frequent among EOCRC cases, compared to other age of onset groups. In a multivariable model, a statistically significant association was observed between BMI obese and <45 (OR=1.30) and 45-55 (OR= 1.70), but not for CRC >55, as compared to controls adjusting for several factors. Although the effect estimates for BMI obese and CRC age of onset was consistent across the self-reported race strata, statistical significance was only detected among White participants (OR=1.37). The statistical interaction between BMI*race was not statistically significant.

Conclusions:
These findings suggest that obesity is significantly associated with CRC age of onset, and additional research is needed to determine effect modification by self-reported race. These results provide support for the recent screening guidelines changes from age 50 to age 45 and may warrant a lower age of screening based on obesity status.

ABSTRACT #50

Understanding the Molecular Interactions Between the OC43 Nucleocapsid Protein and the 5'UTR

Sairam Pantham, Solon High School; Matthew MacKeown; Blanton Tolbert, PhD, Department of Chemistry

Background:
HCoV-OC43, a virus serving as a model for SARS-CoV-2, is part of a group of coronaviruses known as Betacoronaviruses (Beta-CoVs), which regulate viral processes through a leader sequence known as the 5' UTR. We will study the interactions between the second stem-loop (SL2) and third stem-loop (SL3) of the OC43 5' UTR and the nucleocapsid protein, which packs the RNA genome within the viral capsid. Specifically, while N protein-SL3 interactions are well known, this study investigates whether SL2 promotes interactions between the N protein and SL3.

Goals:
Our hypothesis is that the presence of SL2 promotes the binding of the N protein to the 5' UTR. The data gathered will provide understanding that may be utilized to design methods to block N protein-RNA interactions, creating life-saving treatments that can mitigate Beta-CoV infections.

Materials and Methods:
N protein (purified through E. coli transformation/translation) was combined with RNA (purified through transcription reactions), with data collected using nuclear magnetic resonance (NMR), isothermal titration calorimetry (ITC), and small angle x-ray scattering (SAXS), giving information on the binding affinity and structure of N protein-RNA interactions.

Results:
As calculated from ITC data, the dissociation constant (KD) between the N protein and SL3 (430 nM) was more than 4 times greater than that between the N protein and SL1-4 (2000 nM), suggesting that the N protein has a much tighter bond with SL1-4 than with SL3. However, at the time of writing this abstract, NMR data and SAXS data has not been made available, but we predict that they will show amino acid residues from SL2 binding to the N protein SL3 residues.

Conclusions:
Currently, the data strongly supports the conclusion that SL2 is a significant promoter in the interactions between the OC43 N protein and the 5' UTR. Such activity from SL2 could prove to be invaluable in understanding how to block N protein-RNA interactions and potentially develop new therapeutics for Beta-CoV and SARS-CoV-2 infections.

ABSTRACT #51

Covid-19 Diagnosis and Evaluation with Deep Learning

Haridu Peiris, Twinsburg High School; Pushkar Mutha; Mohammadhadi Khorrami; Anant Madabhushi, PhD, Department of Biomedical Engineering

Background:
Lung cancer is the leading cause of cancer death worldwide. About 85% of lung cancer cases can be classified as non-small cell lung cancer (NSCLC), with adenocarcinoma as the main subtype. Due to their visual similarities on CT scans, benign granulomas are often confused with malignant adenocarcinomas, leading to invasive biopsies for diagnosis. Radiomics, referring to the analysis of medical images using high throughput extraction of quantitative image features, has shown promising results in complex clinical decision making tasks such as diagnosis, prognosis, and treatment evaluation. Through extracting quantitative features that describe the nodular and peri-nodular (tumor surrounding region) shape and texture, the distinction between adenocarcinoma and granuloma can be made, noninvasively. However, this analysis hinges entirely on the quality of the extracted features, which are susceptible to many sources of variation due to differing image acquisition parameters, image preprocessing, and analysis pipelines. It is imperative to study these sources of variation and limit their possible impact, in order to develop reproducible and generalizable models for clinical adoption. Thus, a stress testing process for the features must be implemented

Goals:
The goal of this study is to determine the impact of Slice Thickness (ST), CT Reconstruction Kernel (RK) and Test-Retest (TR) stability on intra and peri-tumoral radiomic features in patients with adenocarcinoma and granuloma.

Materials and Methods:
Non-contrast CT scans from 289 patients (146 Adenocarcinomas) were acquired from two institutions. We extracted 579 texture and shape features within the nodule (intra-tumoral features) and 555 texture features immediately surrounding the nodule (peri-tumoral features), using an in-house pipeline on MATLAB R2022a. The texture features include Gabor, Law, Laplace, and Haralick feature families. To study the impact of ST, we selected 172 scans (146 adenocarcinomas) with acquisition ST<=1mm. These scans and their associated manually labeled nodule segmentations were resampled to 5 different ST from 1mm to 5mm. Pixel size was unchanged. Features were then extracted from each resampled scan, and the feature variability was measured using average pairwise concordance correlation coefficient (CCC). For the RK experiment, features were extracted from 68 scans that were acquired using both a smooth kernel (less noise, lower resolution) and a sharp kernel (more noise, higher resolution). CT scans of 31 patients from the RIDER dataset, who were scanned twice in one sitting, 15 minutes apart were used to evaluate the test-retest variability of the radiomic features. CCC was used to assess the feature stability, with a value greater than 0.8 considered as a stable feature.

Results:
The features were affected to a varying degree by the different parameters implemented over the experiments. Overall, varying slice thickness seemed to have the least impact on extracted features, resulting in a total of 446 intratumoral and 516 peritumoral features with a CCC over 0.8. On the other hand, the different kernels (sharp v.s. smooth) had a much larger impact on the features, with only 250 intratumoral and 290 peritumoral features having a CCC over 0.8. The test retest experiment yielded 443 intratumoral and 458 peritumoral features with a CCC over 0.8, putting it in between varying slice thickness and varying reconstruction kernel. The Gabor feature family remained the most stable throughout all experiments, having 70-100% of features with a CCC over 0.8.

ABSTRACT #51 CONTINUED

Conclusions:

Overall, the features showed strong stability when slice thickness was varied, and with a test retest scan format. However, the robustness of the features was slightly lower when it came to varied reconstruction kernel, meaning the features will change due to change in the acquisition parameters of scanners. This means that, when using said features to distinguish between adenocarcinoma and granuloma, or make other prognostic/diagnostic decisions, varied reconstruction kernels may have an impact on said analyses. Our results also showed that peritumoral texture features were less affected by different parameters than intratumoral texture features. Moreover, the experiments run were univariate, testing only the impact of one variable on extracted features. Next, we must run multivariate analyses, to determine the combined impact of various parameters. In addition, we must determine what impact prior harmonization methods (such as resampling, denoising, etc.) may have on the feature stability as well. The impact of acquisition parameters on model predictions should also be studied. Overall, we believe our findings could allow for the creation of more generalizable models for distinguishing granulomas from adenocarcinomas.

ABSTRACT #52

Chronic Stress Induces Protection Against Secondary Injury Through the IL-23/IL-22 Axis by Regulating Antimicrobial Peptides

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Background:
Inflammatory bowel diseases (IBD), including Crohn's disease and ulcerative colitis, are chronic inflammatory disorders of the gastrointestinal tract. Psychological stress has been identified as a triggering environmental factor for IBD patients and is known to adversely affect the course of disease. After studying the effects of chronic stress on experimental Crohn's disease using the ileitis-prone SAMP1/YitFc (SAMP) mouse model, we surprisingly found that stressed mice did not develop worse disease nor did they develop colitis induced by secondary injury through DSS administration, but developed tertiary lymphoid organs (TLOs), with increased expression of IL-23 and IL-22.

Goals:
We will investigate whether the increased IL-23/IL-22 production in SAMP TLOs following chronic stress induces expression of antimicrobial peptides (AMP), such as defensins, that protect against DSS-induced colitis. We hypothesize that stressed SAMP mice with increased IL-23 (and therefore IL-22) will produce increased levels of AMPs, which protects stressed SAMP mice against DSS-induced colitis. By comparison, stressed SAMP mice lacking IL-23 (and therefore IL-22) will produce decreased levels of AMPs, and will be less protected compared to native SAMP mice.

Materials & Methods:
We first analyzed the transcriptome profiles (mRNA levels) of tertiary lymphoid organs (TLOs) in stressed SAMP mice compared to control (unstressed) SAMP mice using Nanostring GeoMx spatial transcriptome profiler technology. Based on these results, we evaluated AMP expression by RT-qPCR in the colons of stressed and unstressed SAMP compared to SAMP lacking IL-23 (SAMP x Il23-/-).

Results:
Our results showed that the AMPs, Defb1, Lyz2 and Reg3g, were the most upregulated genes in the TLOs of stressed compared to unstressed SAMP mice before DSS challenge as analyzed by spatial transcriptomics. Interestingly, the expression of Defb1, Lyz2 and Reg3g was not significantly changed in full-thickness colon tissues of stressed and unstressed SAMP mice, suggesting that they may have specificity according to organs (TLOs vs. colon) that are producing them. SAMP x Il23-/- did not express intestinal colonic antimicrobial peptides as expected.

Conclusions:
We conclude that a certain level of chronic stress could protect against worsening of intestinal inflammation through the production of antimicrobial peptides that are differentially regulated by the IL-23/IL-22 axis and differentially expressed in TLOs vs. colons, and may be beneficial to limit the development of chronic intestinal inflammation, such as that observed in IBD.

ABSTRACT #53

Mapping the binding sites of WD40 repeat-containing protein 5 (WDR5) and promyelocytic leukemia protein isoform 1(PML1)

Hussein Al Raheel, Cleveland School of Science and Medicine; Zhenghao Liu, Department of Biochemistry; Hung-Ying Kao, PhD, Department of Biochemistry

Background:
endocrine therapy resistant breast cancer. This type of breast cancer can not be treated using endocrine therapy, Which is breast cancer treatment with the estrogen hormone to increase the amount of estrogen in the body of the patient. In ERT breast cancer there is a protein called PML 1promyelocytic leukemia protein isoform 1) which is oncogenethat suppresses tumors by using its ability to regulate transcription, DNA repair, and apoptosis (Controlled death of cells). There is also WDR5 (WD Repeat Domain 5) which plays a huge role in the invasion and metastasis of cancer.

Promyelocytic leukemia protein (PML) was originally thought to be a tumor suppressor, but our recent studies have shown that PML1 is an oncogene and that its isoform 1 (PML1) can promote breast cancer cell progression, migration, invasion, and endocrine therapy resistance. The WD40 repeat-containing protein 5 (WDR5) plays a key role in the regulation of multiple cellular processes. From our preliminary GST pulldown data, we know that PML1 interacts with WDR5 in MCF7 breast cancer cells. However, the specific binding site is still unclear. This study was conducted to figure out what specific motif WDR5 binds to PML1.

Goal:
The goal of this project was to map the WDR5 and PML1 binding sites.

Materials and Methods:
GST Pulldown Assay
GST-WDR5 proteins bound to Glutathione-Sepharose 4B were incubated with Hek293T cell lysates which were separately transfected with HA-PML1 fragments 2-180, 181-350, 351-565, 500-633, 621-883 in a 4 ℃ cold room for 2 hours. After centrifugation and wash, proteins bound to GST-WDR5 beads were separated by 10% SDS-PAGE followed by immunoblot analysis using anti-HA monoclonal antibodies.

Results:
The results clearly show that purified GST-WDR5 binds with HA-PML1 2-180, but not with the HA-PML1 181-350, 351-565, 500-633, 621-883.

Conclusions:
Through GST fusion pulldown assays, PML1 2-180 was identified as WDR5 and PML1 binding sites.

ABSTRACT #54

Evaluation of Accelerometer Device

Justin Pieper, Shaker Heights High School; Andrew Shoffstall, PhD, Department of Biomedical Engineering

Background:
Neural modulation can be used to help regulate the autonomic system, block chronic pain, and regain bladder control. Cuff electrodes are widely used to perform these functions, however, these types of electrodes are very invasive within the body. Invasiveness poses risks as inserting and removing the cuff electrode can damage surrounding tissue and the nerve itself. To overcome this, the Injectrode, an injectable electrode, has been designed to replace the need for cuff electrodes within the peripheral nervous system. Unlike the cuff electrode, the Injectrode is minimally invasive, mitigating the risk of injury to the patient. The Injectrode, however, utilizes transcutaneous electrical nerve stimulation (TENS) which relies on subcutaneous stimulation. As a result, off-target stimulation can occur leading to muscle fibrillations. Because of this, two devices were constructed to test for off-target stimulation when TENS is applied to pig models.

Goals:
The goals of this project are to construct a device capable of measuring off-target subcutaneous muscle activation and test the efficacy of the constructed device.

Materials:
- **Double sided tape**
- **Timer**
- **Components for device:**
  - **Accelerometer (ADXL335)**
  - **Arduino**
  - **0.1 capacitor**
  - **Excel Data Streamer**

Methods:
The two devices constructed were calibrated prior to conducting the experiment. One device was then taped to an arm and the other device was taped to the other arm. Data were then recorded for ten seconds using Excel Data Streamer for three conditions: 1) moving up and down while remaining still; 2) using a surrogate method of off-target stimulation to replicate muscle fibrillations; 3) remaining still. Throughout each condition, only one arm was manipulated while the other was kept still. Each of these conditions were compared through a one way ANOVA test which evaluated if the data gathered could accurately distinguish off-target stimulation from other movements.

Results:
Experiments in progress, results to be reported.

Conclusions:
Experiments in progress, results to be reported.

ABSTRACT #55

Impact of Gut Microbiome on Sex Differences in Experimental Crohn's Disease

Lilly Russo, Gilmour Academy; Anna Saline, Department of Pathology; Hannah L. Wargo, Department of Pathology; Joseph Williams, MPA; Theresa Pizarro, PhD, Department of Pathology

Background:
Inflammatory Bowel Disease (IBD), is a chronic inflammatory disorder affecting the gastrointestinal tract. IBD is organ specific, and presents itself in two major forms, Crohn's disease (CD) most commonly present in the Ileum, and Ulcerative colitis (UC) which develops in the Colon. Epidemiology studies in Western cohorts indicate that Crohn's Disease develops most commonly in adult women and pediatric men, and least commonly in adult men. At puberty, the risk of developing CD increases substantially for women and drops dramatically for men. The risk for developing Crohn's disease continually has a female sex bias thought adult life. Although it is well established that environmental factors, including the gut microbiome, play an important role in the pathogenesis of IBD, it is currently unknown whether the gut microbiome differentially affects male versus female patients with IBD. To further study this, the mouse strain, SAMP1/YitFc (SAMP) is used as a spontaneous model for CD inflammation of the ilium. Without chemical, genetic or immunological manipulation, it replicates human Chrone's disease in both the location of disease and histology or microscopic anatomy.
Goals:
Using the SAMP1/YitFc (SAMP) mouse model of CD-like ileitis, we will determine if the gut microbiome impacts the severity of intestinal inflammation differently in males compared to females with IBD, and whether potential sex-based differences are caused by specific immunophenotypes in male vs. female SAMP mice.

Materials and Methods:
Both male and female SAMP mice (SAMP-M and -F, respectively) were raised under either specific pathogen-free (SPF) or germ-free (GF) conditions and sacrificed at 20 weeks of age. Ilea were harvested and processed for histological evaluation by H&E staining, and for immunophenotyping. RNA has been isolated from the GF and SPF groups, cDNA has been generated through Reverse Transcription (RT) and will be used for Quantitative PCR (qPCR). qPCR will detect and amplify specific target genes through the analysis of TH1, TH2, and TH7 cytokine profiles. ACS analysis was also performed on freshly isolated MLN to determine differences in immune cell subsets between SAMP-Ms and -Fs, and the impact of the microbiome by comparing SPF- vs. GF-SAMP mice.

Results:
Preliminary data using SPF SAMP mice show a clear female sex bias, in terms of an earlier onset, and increase in serverity over thier male counterparts. SAMP mice bread in germ-free (GF) conditions however, show no sex based differnces. Despite being raised under germ free conditions, GF SAMP mice still display gut inflammation, but both the severity and age of onset are drastically reduced. This indicates that the microbes in the gut may have signifigant impact on the femine sex bias in the development and severity of CD. Currently, RNA has been extracted from ileal tissues of all experimental groups, and quality controls performed. cDNA has been generated from total RNA and RT-qPCR will be performed for a panel of Th1, Th2, and Th17 cytokines. FACS analysis for MLN are also in progress.
Conclusions:
Overall, there is a distinct prevalence in early onset, the likelihood of onset, and severity of intestinal inflammation in females compared to males that ceases to exist under GF conditions lacking microbial bacteria. However, it has yet to be determined by what specific mechanism this occurs and whether disease is impacted by sex-based differences in the immunoprofiles of male vs. female SAMP mice. These differences can have important implications for the pathogenesis and treatment for IBD patients based on sex, and lays the foundation for sex-based precision medicine approaches.

ABSTRACT #56

Evaluating Associations Between Scan Quality of Prostate Bi-parametric MRI and Radiologist Performance and Agreement for Prostate Cancer Diagnosis

Pranav Sompalle, Mayfield High School; Satish Viswanath, PhD, Department of Biomedical Engineering; Rakesh Shiradkar, PhD, Emory University

Background:
Prostate Cancer (PCa) is the most common cancer and third deadliest cancer among men in the United States. Improving the identification of PCa, thus, has recently received a greater focus. A Gleason Grade Group (GGG), the current gold standard for PCa diagnosis, can be determined using a prostate biopsy. However, biopsies are invasive and not always accurate; imaging-based diagnosis offers several advantages over its biopsy-based counterpart. Bi-parametric Magnetic Resonance Imaging (bpMRI) is being increasingly explored to diagnose PCa and consists of two sequences: T2-Weighted (T2W) and Apparent Diffusion Coefficient (ADC). T2W images provide an anatomical view of the prostate, while ADC maps quantify water diffusivity in the prostate. Prostate Imaging Reporting And Data System (PI-RADS) guidelines in conjunction with bpMRI are used by radiologists to assign a probability score (1-5) for the presence of clinically-significant PCa (csPCa). Quality is a factor that can affect the PCa diagnostic pipeline. Batch effects arising from scanner and site specific variations influence MRI quality, potentially affecting diagnosis. Thus, recent efforts have been devoted to studying quality and its role within PCa diagnosis.

Goals:
To evaluate the associations between scan quality of prostate bpMRI and the diagnostic performance and inter-rater agreement among four radiologists in characterizing/diagnosing PCa.

Materials and Methods:
The ProstateX dataset (112 scans of patient lesions) was used in this study. A bounding box dataset highlighting the volume occupied by the prostate mask within both sequences was then generated. MRQy, an image-analysis software that quantifies a scan's quality, was run on all sequences. 15 quality metrics' data were collected for each sequence. A given quality metric (QM) was compared against four readers' diagnostic performance, which was evaluated using the Area Under the Curve (AUC) of the Receiver Operating Characteristic (ROC) curve, sensitivity, and specificity (calculated using GGG and PI-RADS scores). The association between a QM and inter-rater agreement, which was measured using Fleiss' Kappa (κ), was then determined. Python was the primary language used.

Results:
The QMs of Range of the Foreground (RNG) and Peak Signal-to-Noise Ratio (PSNR) of both sequences or ADC maps were negatively associated with the readers' AUC; RNG of T2W images, Mean of the Foreground (MEAN) of both sequences, and Variance of the Foreground (VAR) of ADC maps were positively associated with AUC. As both or only ADC sequences' RNG and PSNR increased, AUC (≥2 readers) decreased for both datasets ($\mu_{AUC,\ Bin\ 1} = 0.612$, $\mu_{AUC,\ Bin\ 3} = 0.322$). In contrast, as the ADC maps' VAR increased in value, AUC increased for both datasets ($\mu_{AUC,\ Bin\ 1} = 0.496$, $\mu_{AUC,\ Bin\ 3} = 0.792$). Similarly, AUC (3 readers) increased as the RNG of the T2W images and MEAN data of both sequences increased for the bounding box dataset ($\mu_{AUC,\ Bin\ 1} = 0.442$, $\mu_{AUC,\ Bin\ 3} = 0.633$). As both whole sequences' PSNR increased, inter-rater agreement increased; as PSNR increased for only one sequence, agreement decreased ($\kappa_{Bin1\ ADC,\ Bin1\ T2W} = 0.224$, $\kappa_{Bin2\ ADC,\ Bin2\ T2W} = 0.439$, $\kappa_{Bin2\ ADC,\ Bin1\ T2W} = 0.186$, $\kappa_{Bin1\ ADC,\ Bin2\ T2W} = 0.175$).

Conclusions:
For ADC, T2W, or both whole sequences and bounding boxes, positive and negative associations between four QMs and classification performance were found. However, no clear trends were observed between bpMRI quality and reader performance for most other QMs. Inter-rater agreement was found to be positively associated with diagnostic quality (PSNR) of ADC and T2W. These results highlight how imaging quality can impact aspects of the PCa diagnostic pipeline, specifically classification performance and agreement between radiologists.

ABSTRACT #57

Determining the Antifungal Activity of Miconazole Against Candida Albicans and Aspergillus Niger Isolates

Samara Rivchun, Laurel School; Ahmed Gamal; Mahmoud Ghannoum, PhD, Department of Dermatology

Background:
Otomycosis is a condition classified as a fungal outer-ear infection, which has been previously treated by the drugs fluconazole and clotrimazole. These drugs come from a class of antifungals categorized as azole derivatives. Miconazole is a similar drug to fluconazole and clotrimazole that has been previously approved to treat tinea pedis, tinea corporis, and tinea cruris. Over the course of this research study, the goal is to determine if Miconazole has antifungal activity against 100 strains of *Candida albicans*, *Candida parapsilosis*, *Aspergillus niger*, and *Aspergillus flavus*. These fungal strains are the most common causes of Otomycosis. This discussion will focus specifically on the antifungal activity of Miconazole for approximately 82 isolates of *Candida albicans* and 35 isolates of *Aspergillus niger*.

Goal:
The goal of this research study is to determine if Miconazole has consistent antifungal activity. This will continue the process of gaining FDA approval for Miconazole in treating Otomycosis.

Materials and Methods:
This research study is conducted using the method of Minimum Inhibitory Concentrations (MICs). Ten different Miconazole concentrations are added into a 96-well plate with RPMI 1640 media and either *Candida albicans* or *Aspergillus niger*. After inoculation, the plates are placed into an incubator to sit for 24H or 48H respectively. The plates are then checked to look for 50% fungal growth inhibition relative to the growth control, which determines Miconazole's antifungal activity against each isolate.

Results:
My results suggest that Miconazole is effective in inhibiting the growth of Candida albicans and Aspergillus niger. With the current results, *Candida albicans* has an MIC 50 value of 0.063 ug/mL and an MIC 90 of 0.5 ug/mL. The data also implies that *Aspergillus niger* has an MIC 50 of 2 ug/mL and an MIC 90 of 4 ug/mL.

Conclusions:
To prevent 90% of fungal growth for *Candida albicans*, 0.5 ug/mL is suggested to be the proper concentration. To prevent 50% of fungal growth, 0.063 ug/mL is suggested. For *Aspergillus niger*, 2 ug/mL should inhibit 50% growth and 4 ug/mL should inhibit 90% growth. Therefore, it is implied that Miconazole will be promising in treating Otomycosis and a strong candidate for FDA approval.

ABSTRACT #58

Efficacy of Losartan to treat intestinal fibrosis in experimental Crohn's disease

Anna Saline, Gilmour Academy; Joseph Williams, MPA; Hannah L. Wargo; Shuvra Ray, PhD, Department of Electrical Engineering and Computer Science; Theresa Pizarro, PhD, Department of Pathology

Background:
Intestinal fibrosis and stricture formation are common occurrences in Crohn's disease that are generally not responsive to medical treatment, with surgical resection as the only therapeutic option. Angiotensin II is best known to be involved in systemic fluid and blood pressure homeostasis as part of the renin-angiotensin system (RAS) but has also been shown to be important during inflammation, cancer, and fibrogenesis in multiple organs. Losartan is a specific inhibitor of the angiotensin II receptor 1 (AT1) and has been shown to be efficacious in treating fibrosis in various mouse models.

Goal:
The aim of this study is to investigate the effects of Losartan on intestinal inflammation and fibrosis in the SAMP1/YitFc (SAMP) mouse model of Crohn's disease-like ileitis and to determine specific profibrogenic genes that Losartan may regulate.

Materials and Methods:
30-wk-old SAMP mice with the established disease received Losartan at 0.6 g/L (high dose) or 0.2 g/L (low dose) in drinking water and compared to untreated (placebo) controls. Mice were treated for 10 weeks (from 30-40 weeks of age), after which they were sacrificed. Ileal tissues were harvested for histological evaluation for inflammation and fibrosis by H&E and Mason's Tri-Chrome staining, respectively. Losartan-treated and placebo groups were also evaluated for ileal expression of pro-fibrotic genes by RT-qPCR.

Results:
Losartan has been observed to reduce fibrosis but not inflammation after treatments in previous experimenting. Currently, RNA has been extracted from Ileal tissues of all experimental groups, and quality controls performed. cDNA has been generated from total RNA and RT-qPCR will be performed for a panel of profibrogenic genes.

Conclusions:
It has yet to be determined whether the administration of Losartan has the ability to regulate molecules responsible for fibrogenesis. As such, targeting the RAS system by inhibiting AT1 may represent a novel therapeutic strategy to target inflammation-associated intestinal fibrosis, such as that observed in Crohn's disease patients.

ABSTRACT #59

Identification of novel FABP4/5 inhibitor as potential therapeutic approach for ovarian cancer

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Background:
Cancer has made a tremendous effect worldwide on each person's life. Ovarian cancer in particular is the fifth leading cause of death among women with cancer with approoximatley 14,000 deaths per year. Ovarian cancer mortality rates have continued to increase throughout the years. It is very important to learn more about ovarian cancer due to the inefficient treatments and high mortality rates. Fatty Acid Binding Proteins (FABPs) function as lipid carriers that bind hydrophobic ligands in the cytoplasm and shuttle them in the cell to different organelles. Among them, FABP4 and FABP5 were implicated in multiple cancers to promote tumor initiation, growth and metastasis through their role as mediators of fatty acids (FAs) metabolism and their ability to deliver ligands to, and activate transcription by the nuclear receptors PPARδ and PPARγ. Hence, FABP4/5 inhibitor has the potential to serve as a novel therapeutic approach for cancers that express high levels of these proteins. In this project I will evaluate the potential of using FABP4/5 inhibitors to suppress growth of ovarian tumors.

Goals:
The two main goals of the project are:

1. **Identify novel FABP4/5 inhibitors by screening compounds that bind the proteins in high affinity and do not activate transcription of carc77inogenic pathways by PPARδ and PPARγ.**
2. **Evaluate whether FABP4 and FABP5 are good therapeutic targets in ovarian cancer.**

Materials and Methods:
The materials I used for the binding essay consisted of FABP3, FABP4, FABP5 and FABP7 recombinant proteins that were purified from E. coli. I also used the fluorescent compound ANS and the tested compounds. I read the results in a plate reader that can read the fluorescence. Correlation between levels of FABP4 and FABP5 with poor survival of ovarian cancer patients, was done using the Kaplan-Meier plotter. To assess whether FABP4 and FABP5 are highly regulated in ovarian cancers I used publicly available databases for ovarian cancer patients and healthy individuals. For the statistical analysis I used a t-test to determine whether differences between levels of FABP4/5 in normal samples is significantly different from the levels in patients with ovarian cancer.

Results:
No results can be made at this point.

Conclusions:
Experiments in progress, results to be reported.

ABSTRACT #60

The Role of MAGE-A6 in Bladder Cancer

Diya Swain, Shaker Heights High School; Shiv Verma; Prem Kushwaha; Sanjay Gupta, PhD, Department of Urology

Background:
Bladder cancer (BC) is when the cells in the bladder start to grow abnormally. BC prognosis and diagnosis remain poor because there is a lack of ideal biological markers and treatment options in BC. Identifying these biological markers is important, so they can help BC prognosis and create cancer therapeutics to treat BC. Previous research has found biological markers, such as CA 15-3, that may serve as either prognostic markers or therapeutic targets in BC. Among those, the gene MAGE-A6 is a part of the larger MAGE protein family which studies have shown could potentially promote tumorigenesis in cancers. The TCGA cancer database and previous research shows that the expression of MAGE-A6 is higher in BC. There is very limited information available on the molecular mechanisms of MAGE-A6 in BC, however, MAGE-A6 may promote tumorigenesis in BC. Therefore, understanding the molecular mechanism of MAGE-A6 in BC as a possible oncogene or as a therapeutic target is important to treating BC. Regarding its oncogenic nature, MAGEA6 may interact with other regulating genes and influence cancer progression. Furthermore, preliminary data have shown interactions between MAGE-A6 and Androgen receptors (AR) that could also promote tumorigenesis in BC. ARs are expressed in several cancers, including BC, and studies have shown that its aberrant expression may promote tumor growth. Moreover, the possible interaction between AR and MAGE-A6 together may modulate cancer progression in BC which could impact the overall survival of BC patients.

Goals:
To investigate the molecular mechanisms of MAGE-A6 in Bladder cancer

Materials and Methods:
Bladder cancer cells (J82 and UMUC3) were grown in cell culture media under optimum conditions. The cell lines were treated with Enzalutamide (Enzu) and dihydrotestosterone (DHT) to see changes in the expression of AR and MAGE-A6. MAGE-A6 was knocked down in the cells grown using CRISPR-Cas9. CRISPR is a genetic engineering tool that can silence or inhibit certain genes, such as MAGE-A6, to observe its effects. The expression of MAGEA6, AR, and other related genes were quantified using the quantitative real-time PCR (qRT-PCR) and Western Blot Analysis.

Results:
The TCGA database and other preliminary studies showed that the expression of MAGE-A6 is significantly higher in BC patients. The expression of MAGE-A6 also changes between different stages of BC. The J82 cell line had a lower expression of MAGE-A6 than the UMUC3 cell line at RNA level. This correlates with the difference in cancer aggression between the 2 cell lines. The UMUC3 cell line showed a higher level expression of MAGE-A6 than the J82 cell line at the protein level.

Conclusions:
The expression of MAGE-A6 could promote the growth of tumors in BC. The expression of MAGE-A6 is lower in the J82 cell line than in the UMUC3 cell line. This correlates with J82 being a less aggressive cancer than UMUC3, showing how MAGE-A6 may promote tumor aggressiveness. As an expression of MAGE-A6 relates to different

ABSTRACT #61

CITED2 restrains macrophage-mediated inflammation by elevating B Cell Leukemia / Lymphoma 6 expression

Soham Shah, St. Ignatius High School; Vedant Shinde, Solon High School; Atif Zafar, Department of Pathology; Ganapati Mahabaleshwar, PhD, Department of Pathology

Background:
Macrophages are the principal component of the innate immune system. They play a critical role in eliminating foreign agents, tissue repair, and preventing excessive inflammatory responses to subtle environmental changes. Macrophages recognize foreign agents by utilizing pattern recognition receptors, including Toll-like receptors (TLRs). The TLRs relay extracellular cues inside the cytoplasm and nucleus utilizing adapter proteins and transcriptional factors (NFκB, STAT1, and IRFs) for robust pro-inflammatory macrophage activation. However, uncontrolled macrophage inflammatory response leads to many chronic and acute inflammatory disease conditions. Thus, probing the cell-intrinsic negative regulatory mechanisms will help us to better understand the pro-and anti-inflammatory signaling dynamics in disease pathogenesis.

Goals:
The goal of this project is to understand the role of Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal domain 2 (CITED2), a cell-intrinsic negative regulator of inflammation, on pro-inflammatory signaling in macrophages.

Materials and Methods:
Real-time quantitative PCR and western blotting were performed to determine the mRNA and protein expression of BCL6 in bone marrow-derived macrophages (BMDMs) from $Lyz2^{cre/cre}$ and $Cited2^{fl/fl}$:$Lyz2^{cre/cre}$ mice after exposure with lipopolysaccharides (LPS). Real-time quantitative PCR was also performed to determine the expression of BCL6 repressive target genes in BMDMs after the LPS challenge.

Results:
Real-time-PCR and western blot analyses confirmed a substantial reduction in BCL6 mRNA and protein expression, respectively in $Cited2^{fl/fl}$:$Lyz2^{cre/cre}$ mice BMDMs after exposure to LPS. LPS stimulation also robustly induced BCL6 repressive target gene expression (*Mx1*, *Cxcl9*, *Cish*, *Ccl7*, *Cd40*, *Ccnd2*, and *Oasl1*) in $Cited2^{fl/fl}$:$Lyz2^{cre/cre}$ mice BMDMs.

Conclusions:
Our results provide evidence that CITED2 augments BCL6 expression in macrophages following the LPS challenge.

ABSTRACT #62

Stress Increases Tumor Formation in a Murine Model of Colitis-associated Cancer

Harsha Sanaka, Hawken School; Giulio Verna, MD, PhD, Department of Medicine; Fabio Cominelli, MD, PhD, Department of Medicine

Background:
Psychological stress is a known risk factor for inflammatory bowel disease (IBD), a set of chronic inflammatory conditions of the gastrointestinal tract whose global prevalence is steadily increasing. There is a well-established association between ulcerative colitis, a subtype of IBD, and carcinogenesis; however, the exact mechanisms behind it remain enigmatic. The Winnie mouse is a spontaneous model of colitis-associated cancer (CAC) due to a missense mutation in the *Muc2* gene, which leads to a looser, thinner mucus layer and intestinal dysbiosis. Here, we investigated the effects of psychological stress on the Winnie mouse.

Goals:
To determine whether stress exacerbates the phenotype in CAC, considering it is a risk factor for colitis.

Materials and Methods:
Restraint stress was performed on mice for 3 hours a day over 14 days. Stool was collected before and after the stress trial to quantify levels of lipocalin-2, a known marker of inflammation which inhibits bacterial growth. Mouse weight and disease activity index (DAI) were also periodically measured. Colonoscopies were performed on day 15, followed by explant of the colon. Colon weight, length, and tumor area were measured. Wild type Bl/6 mice were used as a control for all experiments.

Results:
Stressed Winnie featured higher DAI scores and lost more weight than their unstressed counterparts ($p < 0.05$ and 0.001, respectively). Colonoscopy scores and colon weight were higher in stressed mice, indicating a more severe disease state ($p < 0.05$ and 0.01, respectively). There was a trend towards greater tumor area and higher lipocalin-2 stool concentration in stressed Winnie mice ($p = 0.07$ and 0.09, respectively).

Conclusions:
Stress leads to increased tumor formation in the Winnie CAC model and worsens the cancer phenotype. The varying levels of lipocalin-2 provide insight into future directions; next steps include analyzing the impact of stress on the Winnie microbiome, as this may elucidate CAC mechanisms.

ABSTRACT #63

Empirical Comparison of Registration Approaches for Multi-Parametric MRI in Rectal Cancers

Isabel Svec, Padua Franciscan High School; Satish Viswanath, PhD, Department of Biomedical Engineering

Background:
Rectal Cancer can be defined as a tumor in the region of the large intestines after the colon and before the anus, or the rectum. Rectal cancer can be diagnosed using MRI scans, as diagnosis happens through the relationship of a tumor and the surrounding organs. MRI scans can be categorized into different types of subclasses, these subclasses are based on how the MRI scan appears. The most common one of these subclasses used is T2-weighted MRI scans, where structures on the image appear with different contrasts based on their T2 relaxation times. However, there are other MRI scans that can be used that aren't T2-weighted, such as, T1-weighted MRI scans and ADC scans. ADC, however, visualizes water diffusion by highlighting areas of restriction vs area of healthy normal tissue, via diffusion weighted imaging.

Goals:
One goal of this experiment is to register ADC scans to T2-weighted MRI scans, so that the ADC scans can be similar to the T2-weighted, allowing for the ADC to be analyzed for further analysis. Another of the goals of this experiment is to see the difference in data between ADC registered using Rigid Registration versus Affine Registration. This will allow for better understanding of which process of registration yields better spatial correlation between modalities.

Methods:

- Converting ADC DICOM to MHA Files

The DICOM files that were first converted to MHA Files were pre-treatment MRI, then post-treatment MRI scans. The same was done for pre-treatment and post-treatment files for VA and CCF files. The rectal cancer data used was obtained from the database on the server. Once the files were downloaded, ITK Snap was used to convert the DICOM files to MHA. Once converted on ITK Snap the MHA file was renamed to have the pre-processing for resampling, resizing, and renaming, the patient id, and whether the scan was pre-treatment or post-treatment. The MHA files were then checked on a separate software called 3D Slicer that the files were converted and could be viewed.

- Registering ADC Files to T2 weighted files using Rigid Registration

Once the ADC DICOM files are converted to ADC MHA files then the ADC files can be registered using general registration to the same patients T2-weighted MHA files. Rigid Registration is where the files are sized and fitted to T2-weighted MHA files, but constrained to only translation and rotation parameters. The results can be visualized byADC files being super- imposed to a T2-weighted file. The registration process is done by going on 3D slicer, and registering the ADC files using Rigid techniques.

Results:
The experiment is still ongoing and there are not yet concrete results. Data from this Rigid registration process will be used to compare it to Affine Registration, which has yet to be done. Evaluation will include root mean squared error as well as similarity metrics to compare which registration process is more accurate.

Conclusions:
The next steps after this will be to begin the registration process using Affine registration and then compare rigidly registered ADC to affinely registered ADC.

ABSTRACT #64

Racial Disparities in Healthcare

Hamza Said, Westlake High School; Braveheart Gillani, MSW; Robinson Salazar, PhD, Center for Community Health Integration; Peter Hovmand, PhD, Center for Community Health Integration

Background:
Racial minorities in America are much more likely to receive worse quality healthcare than white people, due to their inability to access care and learn about healthcare. Based on data, Black, Asian, and Hispanic people all receive worse quality healthcare than white people and are less likely to visit a dentist once over the course of a year. They are also less likely to receive preventative healthcare or have health insurance. Using Stella, a model building software that specializes in system dynamics, multiple variables, such as "ability to access care", and "ability to learn about care" will be tested to try and understand where discrimination arises, and to find solutions to them.

Goals:
The goal of this project is to identify possible sources of discrimination in healthcare and whether the quality of healthcare for minorities is significantly worse in America than those of white people. If true, then possible solutions will be proposed based on the data to try and counteract the problems.

Methods:
System dynamics is a mode of modeling that looks to simplify complex systems into models that can be understood easily and interacted with. These models simulate the nonlinear behavior of systems using stocks, flows, feedback loops, and causal loop diagrams. Using Stella, a model building software that specializes in system dynamics, feedback loops will be identified from multiple variables to see where the discrmination in healthcare originates from. In addition, I will identify whether or not the feedback loops are being reinforced, as in the same outcome is being selected over a chosen period of time, or if they are being balanced, or counteracted, by some other variable. This will be accomplished by first creating a causal loop diagram (CLD), to identify possible variables that could cause discrimination, whether purposely or systemically. The CLD will take into account time restraints as well as help me identify feedback loops. Then, I will transfer that data, into a stock and flow simulation where secondary data will also be input to see if there is a correlation between certain variables. The data will show me if there is a discrepancy between the quality of care minorities receive compared to that of white people.

Results:
Experiments in progress, results to be reported.

Conclusion:
Based on secondary data, I believe the discrepancies will arise because minorities in America make less money than white people on average, and have less access to healthcare and preventative care. Minorities also seem to trust healthcare organizations less because there aren't as many minority doctors and nurses, and so do not follow the guidelines healthcare organizations make for them. However, this could prove false as the system dynamics model might disprove this theory and draw blame to other variables.

ABSTRACT #65

Salivary Longitudinal Innate Immune Response Profiles of SARS-COV-2 Acutely Infected Breakthrough Participants

Giovanni Tripi, Charles F. Brush High School; Santosh K. Ghosh, PhD, Dept. of Biological Sciences; Christopher King, MD, School of Medicine; Jeffrey Jacobson, MD; Aaron Weinberg, DMD, PhD, Dept. of Biological Sciences, Dental Medicine

Background:
The COVID-19 pandemic is the result of infection by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2; CoV-2) virus. Along with the nasal mucosa, the oral cavity serves as a primary infection site of CoV-2. While longitudinal studies have previously reported innate responses in the blood of mild to severe COVID-19 patients, they do not capture the early responses at the primary sites of infection during the acute phase of the infection. An ongoing longitudinal study of innate responses from saliva samples of participants who are recruited within 7 days of testing positive is currently underway at CWRU SODM and SOM.

Goals:
The main goal of this study is to document innate immune responses of the oral cavity during an acute CoV-2 infection and correlate it with the vaccination status of the participant. Longer term, by recruiting CoV-2 uninfected participants undergoing mRNA booster protocols and comparing their salivary innate immune responses with results obtained from acute breakthrough participants, we will be able to test how well vaccines elicit oral innate targets that are correlated with reduced viral load in breakthrough infections.

Materials & Methods:
A longitudinal study is ongoing in which saliva samples from acutely infected breakthrough participants are being collected over a 21 day period. The present study represents the first subset of seven participants who had been vaccinated at least once and whose infection was reported at various times post-vaccination (AV). Additionally, four participants who also underwent a vaccination protocol were household contacts (HHC) of acutely infected subjects. Whole unstimulated saliva, collected at 0, 3, 7, 10, and 21 days post recruitment (3ml/participant/time point) underwent SARS-CoV-2 inactivation (1% triton + 0.3% tributyl phosphate, 2 h), followed by screening for salivary cytokine, chemokine and interferon levels measured in duplicate by Luminex using the Human Cytokine 26-plex platform from R&D. We conducted principal component analysis (PCA) to summarize the large dataset. PCA permits us to observe trends, clusters, and outliers that are not readily appreciated using conventional graphics.

Results:
PCA analysis revealed that two out of the seven AV participants, #5 and #8, displayed heightened innate immune responses when compared to the other participants. Particularly interesting was participant #5 who demonstrated extremely high levels at early time points (often a log increase in responses) with diminishing responses over time. Interestingly, #5 had the last dose of vaccination 9 months before the person got infected. Could the waning protection be reflected in the heightened innate responses elicited by #5? PCA analysis revealed that #3, #5 and #7 displayed heightened pro-inflammatory cytokine expression when compared to the others. The HHC participants clustered with the other four AV patients, i.e., showing similar levels of cytokine concentrations over time.

Conclusions:
Heightened pro-inflammatory cytokines, presented in participants who either did not attain full vaccination (at least two shots) prior to infection or became infected six months after the last booster, i.e., when protection waned significantly. Clearly, more participants will be needed to rigorously achieve our goal of correlating oral innate immune response to acute infection with the vaccination status of the participant. Additionally, symptom history over the 21 days, along with viral load information and oral innate responsiveness in non- infected but vaccinated participants will contribute to an improved understanding of the role vaccination plays in innate immunity.

ABSTRACT #66

Phenotype comparison of a human and murine M Opsin mutation

Maya Tang, Hathaway Brown; Sreelakshmi Vasudevan, Department of Ophthalmology; Paul Park, PhD, Department of Ophthalmology

Background:
Cone opsins are G protein-coupled receptors located in the cone outer segments of cone photoreceptor cells in the retina. Mutations in cone opsins have been considered as a cause of defects in color vision. The C203R mutation of M cone opsin (MOP) in humans causes blue cone monochromacy, an X-linked condition that results in impaired vision. The murine ortholog of this point mutation is C198R. The mechanism by which the C203R mutation causes disease is currently unclear.

Goals:
The goal of this study is to compare the cellular localization of human and mouse MOP and their mutants *in vitro*, and to analyze the phenotype of a mouse model of blue cone monochromacy expressing the C198R mutant.

Materials and Methods:
DNA constructs coding for human MOP (wild-type and C203R mutant), and mouse MOP (wild-type and C198R mutant), each tagged with yellow fluorescent protein (YFP), were generated. For confocal microscopy analysis, HEK293T/17 cells were transiently transfected with the MOP vectors on poly-L-lysine treated coverslip glass. Nuclei, endoplasmic reticulum (ER), and plasma membrane (PM) were labeled with DAPI, pDsRed2-ER and wheat germ agglutinin Alexa Fluor 647 conjugate, respectively. Colocalization analysis of microscopy images was conducted using the Coloc-2 plugin in Fiji. The animal experiments were conducted in mice expressing the C198R mutant MOP along with C57Bl/6J control mice. Immunohistochemistry of total cones and MOP was done to evaluate the total cones and M cones in C198R mice.

Results:
Wild-type human and murine MOP behaved differently in cellular localization, but human and murine MOP mutants showed similar cellular localization. C198R mice showed a significant reduction of cones compared to age matched C57Bl/6 control mice.

Conclusions:
The C203R mutation in MOP leads to a condition characterized by early degeneration of cone photoreceptor cells, causing color blindness. *In vitro*, C203R and C198R mutants both exhibited similar cellular localization indicating that the mouse MOP mutant can serve as a model for the human mutant. Developing a murine model to study the pathology, mechanism, and management of C203R induced blindness has significant implications for improving the lives of patients with visual impairments. These findings support the possibility of using murine C198R MOP to study human C203R MOP.

ABSTRACT #67

Repurposable drug discovery following single cell RNA-seq analysis in endometrial cancer

Owen Tolbert, Shaker Heights High School; Jeeda Ismail, Department of Population and Quantitative Sciences; Stefanie Avril, MD, Case Comprehensive Cancer Center; Banu Tamilselvan; Brian Richardson; Cheryl Cameron, PhD, Department of Nutrition; Mark Cameron, PhD, Department of Population and Quantitative Sciences

Background:
Endometrial cancer is one of the most common cancers for women past the age of 55 occurring in the uterus, with more than 200,000 cases in the US annually. African American women have a 12% lower incidence rate of endometrial cancer compared to white women. Still, they have an 86% increased death rate, making it one of the biggest racial disparities in mortality in cancer. African American women are found to be more likely to present with advanced stage of disease and unfavorable tumor molecular subtypes. We hypothesize that characterizing transcriptional (RNA-seq) differences in the endometrial cancer tumor-immune microenvironment will uncover biomarkers and drug targets that may help improve outcomes due to endometrial cancer.

Goal:
Our goal is to identify key transcriptomic biomarkers at the single cell level and apply a bioinformatic method from the Cameron group called drug perturbation Gene Set Enrichment Analysis (dpGSEA). dpGSEA is a computational method for finding repurposable drugs that might be able to target differing gene expression in endometrial cancer patients.

Materials and Methods:
We isolated single cell suspensions (tumor cells and immune cells) from cryopreserved tissue samples obtained from endometrial cancer patients treated at Case CCC institutions. For my project, we started with differentially expressed gene analysis on single cells from 4 patients with endometrial cancer, n=2 with CN-hi molecular subtype (high copy number variation/serous-like) and n=2 CN-lo (low copy number variation/endometroid-like).

Results:
While we have not assayed enough patients yet, African American women have a higher prevalence of the CN-hi molecular tumor subtype (poorest prognosis). Through bulk and single cell RNA-seq we identified differences in the transcriptomic landscape between CN-hi and CN-lo molecular subtype samples. For example, we found MsigDB Halmark pathways changed including Interferon gamma responses, TNFA signaling, Complement, and Inflammatory responses between CN-hi and CN-lo tumor samples. We are now probing these enriched inflammatory biomarkers for candidate repurposable drugs via dpGSEA.

Conclusions:
My project has generated data supporting the use of bulk and single cell RNA-seq and dpGSEA of the tumor-immune microenviroment in discovering candidate drugs that may help improve outcomes of endometrial cancer in the future.

ABSTRACT #68

Microglial Proliferation in Cerebral Organoids Formed with Early Hematopoietic Stem Cells

An Reece Turner, Shaker Heights High School; Jaejin Eum; Anthony Wynshaw-Boris, MD, PhD, Department of Genetics and Genome Sciences

Background:
Microglia are a type of glial cell located in the central nervous system (CNS). Their primary function is managing the extracellular space surrounding the brain and spinal cord, acting both as immune cells and homeostatic regulators. Microglia derive from hematopoietic stem cells. Cerebral organoids are neural organs produced from induced pluripotent stem cells (iPSCs), their development (when produced from human iPSCs) modeling that of the human brain. They provide an *in vitro*, 3D model of the brain, allowing for easier studying of the highly complex, unique human brain. Much like human human brain development, organoid growth is highly variable, and different methods of development are constantly being tested. Cerebral organoids grow differently based on media treatment and initial stem cell composition, and varying any of these factors can provide vastly different patterns of maturation.

Goals:
The goal of this project is to identify the best method for cerebral organoid development based on microglial proliferation for use in future microglia-focused organoid research.

Methods and Materials:
We sectioned organoids produced with early, CD34+ hematopoietic stem cells, as well as ones produced with mature microglia, at 3 weeks, 5 weeks, 7 weeks and ~12 weeks (83 days). We then performed immunohistochemistry on the organoid sections, staining them with 4′,6-diamidino-2-phenylindole (DAPI), a blue fluorescent nuclear marker, as well as ionized calcium binding adaptor molecule 1 (Iba1), a mature microglial surface protein marker, and imaged them under a microscope while illuminated by the corresponding wavelength of light. The images were analyzed computationally, using an Imagej particle analysis macro, and their areas were averaged and compared to provide an accurate assessment of microglial proliferation.

Results:
At the 3 week benchmark, the mature microglia (MG) cerebral organoid line contains a lower microglial density than the CD34+ early hematopoietic stem cell line. At 5 weeks, however, the CD34+ line displays a lower density than its 3 week snapshot, whereas the MG line contains a higher density than before; at this point, both lines contain an approximately equal microglial density. By 7 weeks, both lines have a lower density than their earlier snapshots, but the MG line's average density is higher than that of the CD34+ line. This trend continues into the 12th week, with the MG line containing a higher microglial density than the CD34+ line, but both having a lower density than their previous benchmarks.

Conclusion:
For shorter-form microglial experimentation using cerebral organoids, those created with early hematopoietic stem cells produce better results, but for long-form experiments, organoids made with mature microglia are more useful.

ABSTRACT #69

How the Racial Composition of a City's Police Force Affects Racial Patterns of Arrests and Violence

Mythili Ungarala, Shaker Heights High School; Peter Hovmand, PhD, Center for Community Health Integration; Braveheart Gillani, MSW; Robinson Salazar, PhD, Center for Community Health Integration

Background:
Police brutality has been a long standing issue within the United States. Since 1980, over 30,000 people have died from police violence, and the majority of them being people of color within the United States. Police brutality has historically targeted those of a lower socioeconomic status and the social marginalized. Generally, White officers seem to target African-Americans within numerous communities, sparking the rise of the Black Lives Matter movement, NAACP Chapters, and various other movements and projects. The bigger question that has arised in recent years is whether Black officers generally target Black people as well. Racial bias often exists within a police force's officers. Racial bias is the judgment made based on one's race, and can impact how likely an officer is to arrest a Black person over a White person. Having a lot of racial bias in a police force impacts its city's Black arrest rate and White arrest rate. Creating a more diverse police force has been the goal of many police departments around the country to see if it impacts the racial patterns of arrests and violence within their communities.

Goals:
The goals of this project are to understand the relationship between the racial makeup of a city's police department and racialized arrests. The aim is to identify how severe the relationship is between the two variables and to what extent the rate of violence against African Americans by the police is affected by the race of the officer.

Materials and Methods:
Stella Architect is a modeling software tool used to create simulations and presentations. Stella is going to be used to create the simulations of the data and display the data collected in the form of a simulation model. System dynamics are used to solve complex system problems, or problems that don't change over time. Using quantitative modeling, it creates a representation of a complex system. I used peer reviewed journals from PubMed, Semantic Scholar, and SagePub to gather data about my topic. After collecting data, I created a Causal Loop Diagram (CLD) in Stella. This CLD helped display the connections between the variables. After creating the CLD, I created a Stock and Flow diagram, which displayed the connection between the variables in a different way. After creating the diagrams, I ran the simulations to determine the outcome.

Results:
Experiments in progress, results to be reported.

Conclusions:
Experiments in progress, results to be reported.

ABSTRACT #70

Genetically Modified Mice to Study Cardiac Risk Genes

Mythreyi Ungarala, Shaker Heights High School; Jessica Miley; Can Shi, PhD, Department of Medicine

Background:
Cardiovascular diseases are the leading cause of death in the United States. Heart diseases are a group of conditions that affect your heart and body in different ways. There are many types of heart diseases, including coronary heart disease, strokes, TIAs, aortic disease, and peripheral arterial disease. Key factors for heart diseases are high cholesterol, high blood pressure and smoking. They can also lead to heart attacks, arrhythmia and heart failure.

Goals:
We can't use human test subjects, so we used mice because they are easily attainable and their genes are one of the closest to humans. Our goal is to see if the mice we have injected with these certain heart disease genes will continue to carry the gene. Then we hope we can repair the hurt or lost genes. And our final goal is to repair lost or hurt genes due to cardiovascular diseases in people

Materials and Methods:
We used polymerase chain reaction (PCR) testing to see if the mice carried the gene or not. PCR testing is used to copy small segments of DNA into multitudes of copies for careful molecular and genetic analyses. First we combine a buffer, dNTP mix, primers, ddH_2O, MgCl2 and a Taq polymerase into a core mixture. Then we added in the DNA samples and put them into a PCR machine. The sample is heated so the DNA strand is split into two, then the Taq polymerases and primers build two new strands of DNA. The process is repeated for 35 cycles until we have enough data to analyze. To analyze it, we have to put it in an agarose gel and then use another machine to take pictures and analyze it from there.

Results:
After the PCR testing and analysis, the mice we have definitely carry the gene we injected into them. They match the mice who have the same genes in a lab in New England called the New England BioLabs.

Conclusions:
Knowing now that the genetically modified mice we have carry the same genes as a person with cardiovascular diseases means we can attempt to move forward and try to repair the genes. Since the mice's genes are so similar, this means we're closer to figuring out how to repair the same human genes.

ABSTRACT #71

M.gl Microbiome Prevents the Phenotypic Maturation of Immature Dendritic Cells, Enabling Cancer Malignancy

Sahishnu Vallabhajoysula, Avon High School; Victor Xie, Solon High School; Nathena Murrya BSc; Claire Wolford MS, SOM; Véronique Roche, PhD, SOM; Mei Zhang, PhD, Department of Biomedical Engineering

Background:
Pancreatic cancer ranks only 11th in commonality, but 3rd in mortality. In fact, even with modern therapies, the combined 5-year prognosis of pancreatic cancer patients sits at a meager 11%. Notably, recent studies on pancreatic cancer have reported that patients with microbiome fungal infections caused by *Malassezia globose* (*M.gl*) undergo more rapid disease progression than regular patients. The studies showed that *M.gl* enhances the growth and increases the mortality risk of pancreatic cancer by activating the mannose-binding lectin (MBL) protein and driving the complement cascade which ultimately inhibits a response from tumor-infiltrated immune cells. This study will investigate how the *M.gl* infected cell systems affect a particular antigen-presenting (APC) immune cell in the tumor microenvironment— dendritic cells (DCs). The role of DCs is to phagocytose, process, and present antigens to stimulate cytotoxic t-cell mobilization, becoming quintessential immunotherapeutics. However, in cancer microenvironments this DCs immune function is suppressed, leaving *M.gl* and cancer unregulated. Thus, it becomes paramount to further understand the factors involved in suppressing the dendritic cell immune response in tumor microenvironments, so novel immunotherapeutic targets can be identified.

Goals:
At length, this study will test the hypothesis that *M.gl* infected tumor cell systems affect the maturation & immune response of immature dendritic cells. Specifically, the study will evaluate the effect of M.gl on CD11c, MHC-I, MHC-II, and I-CAM 1 proteins and PU.1, MafB, ERM, ActinF, WASP1, and HS1 genes, which are proteins and genes associated in the DCs maturation process.

Materials and Methods:
Although the lab usually uses murine (KPC) pancreatic cancer models, we studied with the MCF-7 human breast cancer line for the purpose of maintaining the species compatibility of the cells with the human immature dendritic cells used in our study. First, over the course of 7 days, THP-1 monocytes were differentiated into immature dendritic cells using IL-4 and GM-CSF present in cell differentiation media. Then two controls of MCF7 only and *M.gl* only as well as co-cultures of MCF7:*M.gl* at ratios of 2:1, 20:1, and 100:1 were created. The resulting co-culture supernatants were then pulsed with the immature dendritic cells derived from the previous THP-1 culture. Afterwards, we used Fluorescence Activated Cell Sorting (FACS) flow cytometry to calculate the density of cells with CD11c, MHC-I, MHC-II, and I-CAM 1 expression. Furthermore, utilizing Reverse Transcription Polymerase Chain Reaction (RT-PCR) & Quantitative PCR (qPCR) genomic analysis of these novel molecules was studied in conjunction with a proteomic analysis using western blot.

Results:
As of 7/15/2022, only the FACS procedure has been completed; the RT-PCR and WB will be completed within a few weeks. Regardless, the FACS analysis found that in 2:1, 20:1, 100:1, and *M.gl*-only culture conditions the immature dendritic cells showed a lower expression of CD11c, MHC-I, and MHC-II compared to the control. Moreover, the 100:1 condition showed the highest CD11c, MHC-1, and MHC-II expression compared to the other treatment ratios. Conversely, I-CAM expression did not differ significantly between the ratios.

ABSTRACT #71 CONTINUED

Conclusions:

Overall, the FACS analysis found that *M.gl* seems to prevent the phenotypic maturation of immature dendritic cells in our system, but further results (RT-PCR & WB) will give insight into the proteomic and genomic mechanisms behind this relationship. Once the current study has been completed, future steps will be taken to study dendritic cells *in vitro* with patient pancreatic cell lines as well as *in vivo* experiments in mice (KPC) and eventually humans to fully validate these results. Once the relationship has been defined, subsequent novel treatments will be studied and necessary clinical trial steps will be taken. Ultimately, more studies on DCs will facilitate improvements in the immunotherapeutic armamentarium to improve the prognosis of deadly cancers.

ABSTRACT #72

Investigating the Effect of Ionic Strength on GalNAc-Transferase 1 Preferences Towards Charged Substrates and Initial Mucin-Type O-Glycosylation

Mantas Viazmitinas, Westlake High School; Collin Ballard, Department of Biochemistry; Miya Paserba, Department of Biochemistry; Dayna Nguyen, Department of Biochemistry; Kaitlyn Moore, Department of Biochemistry; Thomas Gerken, PhD, Department of Biochemistry

Background:
Mucin-type O-glycosylation is one of the most ubiquitous yet understudied posttranslational modifications of secreted and membrane-bound proteins in metazoans. Structural motifs resulting from O-glycosylation are abundantly found in biological processes such as intracellular signaling and cell-cell interaction. This quasi-regulated process is initiated via a large family of homologous genes encoding the polypeptide N-acetylgalactosamine transferases (GalNAc-Ts), 20 of which have been identified in humans. The GalNAc-Ts are involved in the covalent attachment of the sugar N-acetylgalactosamine (α-GalNAc) to the hydroxyl group of a peptide chain's serine or threonine residues. The GalNAc-Ts play an important role in normal physiology and in many disease states, including cancers, due to mutation, overexpression, and underexpression of specific GalNAc-Ts. Previous studies from the Gerken lab have characterized multiple GalNAc-T specificities that vary with isoform, including preferences for 1) serine or threonine residues, 2) specific peptide sequences, and 3) specific prior remote and/or neighboring glycosylation. Recent studies have also shown that substrate protein charge distributions play a role in this process and have revealed that flanking charges are another factor that can modulate mucin-type O-glycosylation in a GalNAc-T isoform manner. Ultimately, these unique specificities serve to regulate the glycosylation of residues in polypeptide substrates.

Goals:
Recently, the Gerken Lab has begun to investigate the effect of ionic strength on flanking charge preference, specifically with GalNAc-T1, and therefore, the focus of this research was to investigate and understand how elevated ionic strength affects rates of peptide glycosylation.

Materials and Methods:
The analysis was performed using two series of synthetic peptide substrates possessing all possible, different flanking charge combinations, including positively charged arginine (RRR) repeats, negatively charged aspartic acid repeats (DDD), and neutral glycine/alanine repeats (GAG), with one of the series tested under elevated ionic strength. The activity of GalNAc-T1 against these charged peptide substrates was then determined under both conditions.

Results:
GalNAc-T1 demonstrated disruptions in levels of substrate peptide charge distribution preference under elevated ionic strength, with rates of peptide glycosylation increasing for positive flanking charge peptides, decreasing for negative flanking charge peptide substrates, and remaining generally constant for peptides with neutral flanking charge.

Conclusions:

These findings confirm that flanking charges rely on the surface electrostatics of the GalNAc-T1 isoenzyme. They also reveal that ionic strength is another factor that can modulate mucin-type O-glycosylation in a GalNAc-T isoform manner. Thus the initiation of O-glycosylation is modulated by multiple properties of the target peptide and environment. These findings will be useful in predicting sites of glycosylation for the interpretation of O-glycoproteomics data and our understanding of GalNAc-T1 isoform specificity in relation to disease.

ABSTRACT #73

Using a Knowledge Graph-based Computational Framework to Identify Genes and Repositioned Drugs for Alzheimer's Disease

Evan Wang, Beachwood High School; Zhenxiang Gao, Center for Artificial Intelligence in Drug Discovery; Rong Xu, PhD, Center for Artificial Intelligence

Background:
Alzheimer's disease (AD) is a neurodegenerative disorder characterized by memory loss and personality changes leading to dementia. Currently, 50 million people worldwide have AD-related dementia. With the failure of many clinical trials for AD drugs in the pipeline to date, identifying new targets and drug candidates has become imperative to bring about effective AD therapies. With the explosion of large-scale biomedical databases, numerous computational approaches including advanced AI techniques have been developed to systematically analyze biomedical data to identify new targets or new treatments for AD. Our lab has recently developed an advanced knowledge graph-based artificial intelligence system KG-predict for drug repurposing and disease-gene prediction by modeling semantic relationships among tens of thousands of biomedical entities including diseases, genes, chemicals and pathways.

Goals:
In this study, we aimed to predict genes and repurposed drugs for AD by using KG-predict.

Materials and Methods:
We first constructed a knowledge graph by integrating multiple types of entities and relations from various genotypic and phenotypic databases including Gene Set Enrichment Analysis (GSEA), Mouse Genome Informatics (MGI), Gene Ontology Annotation (GOA), Genotype-Tissue Expression (GTEx), Phenomebrowser databases, Human Phenotype Ontology (HPO) database, DrugBank, and TreatKB. The knowledge graph was composed of 1,395,766 interactions between 65,298 entities. We processed these databases using Python and applied the knowledge graph to KG-predict that has established in the lab. We then predicted genes associated with AD, and analyzed gene enrichment pathways of the top-ranked predicted genes. Further, we applied our knowledge graph to KG-predict model to identify repurposing drug candidates for AD.

Results:
Using KG-Predict, we revealed not only known genes, but also new high-scoring predicted genes that are associated with AD. Gene enrichment pathway analysis of the top 100 predicted genes showed that complement and coagulation pathway, ferroptosis and cholesterol metabolism were the top three ranked pathways. In addition, KG-predict also identified the top 20 highest scoring drug candidates for repurposing drug for AD. Of these candidates, memantine has been approved for AD, and nine of the top-ranked drugs have been used in clinical trials for the treatment of AD, validating the effectiveness of KG-predict for drug repurposing.

Conclusions:
The results of our present work identify new genes that may be associated with AD and repurposed drug candidates for AD treatment, complementing the currently available analyses. Our findings may therefore provide valuable insights into the molecular basis of AD and potential therapeutic strategies. Future research includes testing identified candidate genes, pathways and drugs in experimental models of AD, and evaluating top repurposed candidate drugs using patient electronic health records.

ABSTRACT #74

12-year time trend and association of early-onset colorectal cancer with diverticulitis in the United States: 2010-2021

Lindsey Wang, Orange High School; Rong Xu, PhD, Center for Artificial Intelligence; Nathan A. Berger, MD, Center For Science, Health and Society, Case Comprehensive Cancer Center

Background:
The incidence of early-onset colorectal cancer (EOCRC; in patients < 50 years old) has increased at an alarming rate in the past several decades. Multiple factors have been linked to EOCRC including inflammatory bowel diseases, obesity, diet, sedentary lifestyle, alcohol consumption and smoking. Diverticulitis is an inflammation of pouches in the colon wall. EOCRC and diverticulitis share many risk factors including obesity, smoking, lack of exercise, diet (insufficient fibre in diet and red meat and high fat). However, it remains unknown whether diverticulitis itself is associated with increased risk of EOCRC.

Goals:
(1) to examine time trends of incidence rates of new onset EOCRC from 2010-2021 among patients with and without diverticulitis, stratified by gender, race and ethnicity; (2) to examine whether diverticulitis is associated with increased risk of EOCRC by comparing propensity-score matched cohorts with and without diverticulitis.

Materials and Methods:
We used the TriNetX Analytics network platform that contains nation-wide, real-time, de-identified electronic health records (EHRs) of 106 million unique patients from 75 different health care organizations across all 50 states in the US, covering diverse geographic locations, age groups, racial and ethnic groups, income levels and insurance types.
The study population comprised 46,179,351 patients aged 20-49, including 298,117 with diverticulitis. We examined yearly incidence rate of new onset EOCRC (new cases per 100,000 people per year) from 2010 through 2021 among patients with and without diverticulitis. The association between diverticulitis and EOCRC, measured by odds ratio (OR) and 95% confidence interval (CI), was calculated by comparing the risk of EOCRC between propensity-matched cohorts with and without diverticulitis.

Results:
Incidence rates of new onset EOCRC among patients with diverticulitis increased from 100 cases per 100,000 people in 2010 to 402 cases per 100,000 people in 2021 (p<.001), significantly higher than in patients without diverticulitis (24 and 77 cases per 100,000 people in 2010 and 2021, respectively). Higher rates were observed in men and White people. The 5-year risk of EOCRC among patients aged 20-44 with diverticulitis was 1.34%, higher than the 0.84% in propensity-score matched patients without diverticulitis (OR: 1.61, 95% CI:1.31-1.98), especially in left side of colon (OR: 2.56, 95% CI: 1.49-4.42).

Conclusions:
We showed that the incidence of EOCRC continuously increased from 2010 through 2021 in both patients with and without diverticulitis, but with a 4 times higher incidence among patients with diverticulitis. Patients with diverticulitis were at a significantly increased risk for EOCRC compared with matched patients without diverticulitis, suggesting diverticulitis is a risk factor for EOCRC and a driver for the increasing trend of EOCRC from 2010 to 2021.

ABSTRACT #75

Obesity and Cancer Risk in the US from 2010-2021: A revisit in a unified platform

William Wang, Orange High School; Rong Xu, PhD, Center for Artificial Intelligence; Nathan A. Berger, MD, Center For Science, Health and Society, Case Comprehensive Cancer Center

Background:
The prevalence of obesity in the US was 41.9% in 2017-2020, representing a major threat to public health. Cancer is a major public health and economic issue. In 2020 alone, there were an estimated 1.8 million diagnoses and more than 600 000 deaths from cancer in the US. Observational studies have shown that obesity is associated with increased risk for certain types of cancer. However, evidence supporting these associations as well as strength and timing of associations are often inconsistent and sometimes conflicting, which may be due to different data resources, sample sizes, data collection and processing, follow-up time and statistical methods.

Goals:
to examine associations of obesity with 13 types of cancer, including breast, colorectal, endometrial, esophageal, gallbladder, kidney, liver, meningioma, multiple myeloma, ovarian, pancreatic, stomach and thyroid, in a unified data and informatics platform, with longitudinal cohorts and different follow-up times.

Materials and Methods:
We used the TriNetX Analytics network platform that contains nation-wide, real-time, de-identified electronic health records (EHRs) of 106 million unique patients from 75 different health care organizations across all 50 states in the US, covering diverse geographic locations, age groups, racial and ethnic groups, income levels and insurance types. The study population comprised 69,406,337 unique adult patients (≥18), including 6,237,210 with obesity. The obesity population was divided into 7 cohorts based on the year of their diagnosis of obesity: 2010, 2011, 2012, 2013, 2014, 2015, 2016. The associations between obesity and 13 types of cancer in 7 cohorts and 7 follow-up time windows (11-year, 10-year, 9-year, 8-year, 7-year, 6-year, 5-year) were examined by comparing the risk of cancer between propensity-matched cohorts with and without obesity. Odds ratio (OR) and 95% confidence interval (CI) for different time-windows were calculated.

Results:
Obesity is associated with significantly increased risks for 13 types of cancer, except for esophageal cancer. Among patients who had a diagnosis of obesity in 2012 ("2012 cohort"), the associations of obesity with 13 cancers are: breast cancer in women (OR: 1.18, 95% CI: 1.13-1.22), breast cancer in pre-menopausal women (age 18-45) (OR: 1.20, 95% CI: 1.11-1.30), breast cancer in post-menopausal women (≥55) (OR: 1.23, 95% CI: 1.17-1.29), colorectal (OR: o1.53, 95% CI: 1.46-1.60), endometrial (OR: 2.52, 95% CI: 2.30-2.77), esophageal (OR: 0.93, 95% CI: 0.78-1.10), gallbladder (OR: 1.71, 95% CI: 1.20-2.44), kidney (OR: 1.83, 95% CI: 1.68-1.99), liver (OR: 1.63, 95% CI: 1.58-1.69), meningioma (OR: 1.33, 95% CI: 1.20-1.47), multiple myeloma (OR: 1.30, 95% CI: 1.17-1.44), ovarian (OR: 1.42, 95% CI: 1.33-1.53), pancreatic (OR: 1.36, 95% CI: 1.22-1.52), stomach (OR: 1.37, 95% CI: 1.19-1.59), thyroid (OR: 1.37, 95% CI: 1.25-1.50). The strength of association of obesity with cancer varied with timing and follow-up time.

Conclusions:
Leveraging a nation-wide unified platform of electronic health records of over 100 million unique patients and advanced informatics and statistical tools, we showed that obesity is associated with 12 types of cancer, with highest association for endometrial, kidney and liver cancer. The strength of association of obesity with cancer varied with timing and follow-up time.

ABSTRACT #76

Analyzing Potential Gene Biomarkers for Signet Ring Colon Cancer Through Exon Array Analysis in R

Ben Weil, Charles F. Brush High School; Sanford Markowitz, MD, PhD, Departments of Medicine, Genetics; Helen Moinova, PhD, Case Comprehensive Cancer Center

Background:
Signet ring colon cancer (SRCC) is a rare form of colon cancer that is only present in 0.5%-2% of diagnosed cases. It has a poor prognosis because, due to its rarity, it is often not detected until it has already metastasized throughout the body. As a result, it is crucial to investigate potential biomarker genes that could act as a way to detect SRCC before it metastasizes. This study will analyze five genes that are underexpressed in SRCC and will try to determine whether any of them may be able to serve as SRCC biomarkers.

Goals:
There are two main goals of this research. The first is to model the expression of each of the five biomarkers in an SRCC cell line (V451), non-cancer cell lines, regular colon cancer cell lines in each stage of cancer, and colon cancer tumor lines in each stage of cancer. The other is to compare the expression of each biomarker to every other biomarker to establish correlations and better understand the data. Both of these goals will help to refute the claim that SRCC is not different enough from other colon cancers to form the basis of specific treatments.

Materials and Methods:
Lab personnel performed an Affymetrix exon array on 215 cell lines of the types described above. Following the exon array's completion, the data was cleaned up in Excel and graphed in the R package ggplot2. I created three types of graphs to model the above goals. To reflect the first goal, I made a boxplot of the overall trends of the data and a multiple series scatter plot to show each point of the exon array. To reflect the second goal, I created a series of 10 scatterplots to compare the expression of each biomarker in the cell and tumor lines against every other biomarker.

Results:
The graphs are currently still in progress, and results are not available. However, based on the current graph iterations, the genes PTPRO, NKD1, and PPP1R14C might have the best potential as biomarkers for SRCC. These three genes are expressed in V451 far less than in the other cell lines, and they all correlate very similarly. However, as of right now, it is unclear whether this result is statistically valid.

Conclusions:
This study might find biomarker(s) that scientists can investigate in further clinical research. As a result, the performed graphical analysis will provide valuable insight into SRCC and increase the average prognosis for SRCC patients, especially those who did not have their cancer detected before it metastasized.

ABSTRACT #77

Effect of Fungal Microbiome on Maturation of Immature Dendritic Cells

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Background:
When cancer grows and metastasizes, the tumor contains not only tumor cells, but a microenvironment composed of surrounding blood vessels, infiltrated immune cells, fibroblasts, extracellular matrix, and microbiome. Microbiomes typically consist of tumor-infiltrated bacteria and fungi. This study specifically focuses on three components of the cancer microbiome. Cancer cells (MCF-7 cells), fungi (Malassezia globosa or M.gl), and dendritic cells (derived from using THP-1 as a cell model). More specifically, this study asks how fungal-infected tumor cell systems affect the maturation of immature dendritic cells for immunotherapeutic purposes.

Goals:
To examine the effect of fungal infected (M.gl) cancer cells (MCF-7) systems optimized culture conditions on dendritic cells maturation through the determination of cell function and phenotype

Materials and Methods:
MCF-7 cells were cultured at 37°C, 5% CO_2, and 97% humidity. M.gl was then inoculated into the cell culture of MCF-7 in ratios of 2:1, 20:1, and 100:1. The supernatant was harvested after the inoculation and pulsed with immature dendritic cells (THP-1). FACS analysis was used in order to detect markers of maturity on the dendritic cells (CD11c, MHC I, MHC II, ICAM-1). Further analysis will include RTPCR and Western Blot of transcripts/proteins of interest.

Results:
The FACS analysis found that in 2:1, 20:1, 100:1, and M.gl-only culture conditions the immature dendritic cells showed a lower expression of CD11c, MHC-I, and MHC-II compared to the control. Moreover, the 100:1 condition showed the highest CD11c, MHC-1, and MHC-II expression compared to the other treatment ratios. Conversely, I-CAM expression did not differ significantly between the ratios. The study found that M.gl seems to prevent the phenotypic maturation of immature dendritic cells in our system.

Conclusions:
Culturing and inoculation of the MCF-7 and M.gl have been completed along with harvesting of the supernatant. The immature dendritic cells are in the process of being pulsed and FACS analysis will be conducted once pulsing is complete. As opposed to previous research on the tumor microenvironment, our study showed that growing MCF-7 alongside M.gl decreased the maturation of immature dendritic cells when there was a higher abundance of M.gl. This is likely due to the fact that our experiment was performed in vitro in cell culture conditions and M.gl was cultured alongside MCF-7 cells rather than injected into a developed tumor microenvironment. These two factors likely caused the M.gl to compete with MCF-7 rather than increase the proliferation of cancer cells which in turn caused less dendritic cell maturation.

ABSTRACT #78

Determining Whether Postbiotic Supernatants Affect Keratinocyte or Monocyte Cell Response at the Level of Production of Pro- or Anti-Inflammatory Cytokines, as Assessed by PCR

Alexia Zelada, Cleveland School of Science and Medicine; Thomas McCormick, PhD, Department of Dermatology

Background:
Postbiotics are bioactive compounds made when the healthy bacteria in your gut, known as probiotic bacteria, feed on various types of prebiotic food in your colon. Although these bioactive compounds are considered the waste products of probiotic bacteria, they offer various health benefits to your body. However, in the real world, many companies are interested in designing or discovering microbial products that can suppress immune responses thereby using these "natural" products to incorporate into skin creams or other probiotic formulas. If we can discover an organism or a combination of organisms that can mute the immune response, these may be examined further for their potential application in drugs or "nutraceutical" products.

Goals:
The goal of this project is to determine if postbiotic compounds have any direct pro- or anti-inflammatory effect on cells that comprise the skin or immune system. Also, it is to determine if these compounds alone possess the ability to stimulate these human cells and alter their response.

Materials and Methods:
Probiotics were taken to be cultured overnight and the cells were filtered. Subsequently, the probiotics converted into postbiotics after the cells were filtered. These postbiotic supernatants were collected and placed in dilution assays. These cells were harvested after 24-28 hours of being in the dilution assays and were assessed to detect a cytokine response by conducting a Polymerase Chain Reaction (PCR), which is a technique used to amplify segments of DNA.

Results:
Compared to the growth media, the postbiotic did not reduce the expression of any cytokines. However, I believe that the LPS failed to cause a big enough inflammatory response to measure the changes accurately. We will need to redo this experiment, and possibly use a higher concentration of LPS, or another stimulus to trigger a bigger inflammatory response. The big takeaway is that the postbiotic does not appear to cause inflammation on its own, but we cannot yet conclude if it reduces already present inflammation. More troubleshooting and experiments are needed.

Conclusions:
To be determined following the acquisition of results.

ABSTRACT #79

Development of a Prostate Cancer Diagnostic Test for Barbers

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Background:
The Cleveland African American Prostate Cancer Project (CAAPP) is a study that will evaluate the effectiveness of three intervention strategies to increase prostate cancer screening (via PSA test) in the African American or Black community across Cleveland. One approach, a barber-led education, plays an important role in all three interventions. The purpose of partnering with barber shops/salons is to target the population of our study, as barber shops can serve as a community hub for African Americans. Thus, barbers can play a significant role in the health of their clients, especially through training that is designed to help the barbers with communicating sensitive topics, displaying knowledge on prostate health, understanding the PSA testing process, encouraging men to know their risk of prostate cancer, and connecting people with supportive resources.

Goals:
To create a pre/sample test that assesses the base level knowledge that barbers in Cleveland have on prostate cancer and prostate screening.

Materials and Methods:
I have created a literature review in guidance of the creation of a pre-test using PubMed, Google Scholar, and other platforms. With the help of these resources, we were able to design a concise sample test of questions related to basic facts about prostate health. The sample test is a Google Document printed into a physical paper and pencil test. The results will then be analyzed. The tests will take place in local Cleveland barber shops at Urban Kutz Barbershop and Major League Barbershop. Individuals will take the sample test independently.

Results:
Five individuals participated in the sample testing; all participants were male barbers of either Urban Kuts Barber Shop or Major League Barber Shop. For the testing results, the average number of correct answers out of 12 was 6.5. On average, the participants took 5 minutes in completing the test. Most barbers expressed that the test was created well with few limitations that should be worked on.

Conclusions:
Many barbers knew the answers for questions pertaining to the basic information of prostate health. As for questions that were more complex, like symptoms or treatments, they will need to be stated more clearly if it is confusing or eliminated if it is beyond the scope of knowledge that barbers need to learn. Lastly, the questions that were answered completely correct will have less emphasis on the full barber training curriculum. Overall, the test will also need to be revised accordingly based on the results.

ABSTRACT #80

Role of the SARS-CoV-2 receptor ACE2 in regulating thrombosis

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Background:
This research is focused on the receptor activities of angiotensin converting enzyme 2 (ACE2), the main receptor coronavirus disease 2019 (COVID-19) uses to bind to get into a cell. ACE2 regulates systems that may be involved in the thromboembolism in COVID-19: the plasma kallikrein-kinin system (KKS), the renin–angiotensin system (RAS), and the coagulation system. After binding, the virus-ACE2 complex is taken into the cell, where the virus proliferates to lead to greater infection. Therefore, upon COVID-19 infection, the ACE2 receptor decreases in numbers, leaving the lumen of the nasal area or other regions, which may lead to downregulation and imbalance in biological mechanisms locally and, perhaps, systemically.

Goals:
The research is building on previous work on the importance of the renin-angiotensin system in the modulation of thrombosis risk in the intravascular compartment. In the present experiment, we are asking the question if a deficiency of ACE2 makes a mouse constitutively prothrombotic?

Materials and Methods:
Mice of two groups, *ace2*$^{-/-}$ and wild type, were anesthetized using a sodium pentobarbital solution. After exposing the common carotid artery of the mouse and performing a tail vein injection using a rose bengal solution, a laser was targeted on it, as it was flowing through the animal's circulation. At that of the vessel wall, reactive oxygen species are liberated causing injury to the vessel wall. The injury is due to released reactive oxygen species oxidizing the tissues of the artery. We serially check blood flow in the injured artery. The time to vessel occlusion is noted. An online Shapiro-Wilk test was conducted to show whether or not the sample fits a normal distribution (normality vs not normally distributed). Afterwards, an online unpaired parametric t-test, a type of parametric method, was also conducted.

Results:
After conducting the experiments under replicable circumstances and in pairs of mice (one wildtype, one *ace2*$^{-/-}$) for each experiment. The data are presently being analyzed for differences between the two treatment groups.

Conclusions:
The conclusions as to whether the *ace2*$^{-/-}$ mice are prothrombotic will be made once the studies are completed.