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

2023 STUDENT RESEARCH POSTER PRESENTATION

CASE WESTERN RESERVE UNIVERSITY SCHOOL OF MEDICINE

Participating High Schools

Andrews Osborne Academy, Ardsley HS, Avon HS, Beachwood HS, Campus International, Charles F. Brush HS, Cleveland Central Catholic HS, Cleveland Heights HS, Cleveland School of Science and Medicine, Copley HS, Gilmour Academy, Hathaway Brown, 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, Solon HS, Twinsburg HS, University School, Villa Angela-Saint Joseph HS, Westlake HS

Sponsored by

CWRU Center for Science, Health and Society

10900 Euclid Avenue, Cleveland, Ohio 44106-4971

CASE WESTERN RESERVE UNIVERSITY
School of Medicine

July 27, 2023

WELCOME

Welcome to the twentieth 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 81 high school students and six high school teachers participated.

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

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ACKNOWLEDGEMENTS

Program Organizer
Center for Science, Health & Society
Nathan A. Berger, MD, Director
J.T. Render, Program Manager
James Hale, PhD, Case Comprehensive Cancer Center

Advisory and Selection Committee
Nathan A. Berger, MD, Center for Science, Health and Society, CWRU
April Archer-Bailey, Euclid Middle School
Jennifer Cullen, PhD, MPH, Dept. of Population and Quantitative Health Sciences, CWRU
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Mia Flowers, PhD, Cleveland Metro School District
Mike Ford, M.Ed, PhD, Andrews Osborne
Damian Junk, PhD, Case Comprehensive Cancer Center, CWRU
Kristina Knight, PhD, Department of Population and Quantitative Health Sciences, CWRU
Sarah Laux, PhD, University School
Cynthia Owusu, MD, MS, Department of Medicine, CWRU
John Pink, PhD, Case Comprehensive Cancer Center, CWRU
Diana Ramirez, PhD, Warrensville Heights High School
Neena Singh, MD, PhD, Department of Pathology, CWRU
Vivien Yee, PhD, Department of Biochemistry, CWRU

CWRU Faculty Research Mentors
Drew Adams, PhD, Department of Genetics and Genome Sciences
Kristian Baker, PhD, Department of Genetics and Genome Sciences
Nathan Berger, MD, Case Comprehensive Cancer Center
Andrew Blum, MD, PhD, Case Comprehensive Cancer Center
Walter Boron, MD, PhD, Department of Physiology and Biophysics
Susann Brady-Kalnay, PhD, Department of Molecular Biology and Microbiology
Aaron Burberry, PhD, Department of Pathology
Adam Burgener, PhD, Department of Pathology
Mark Cameron, PhD, Department of Population and Quantitative Sciences
Bryan Carroll, MD, PhD, Department of Dermatology
Fabio Cominelli, MD, PhD, Department of Medicine
Jennifer Cullen, PhD, MPH, Department of Population and Quantitative Health Sciences
E. Ricky Chan, PhD, Case Comprehensive Cancer Center
David Danielpour, PhD, Case Comprehensive Cancer Center
Michael Decker, PhD, Department of Physiology and Biophysics
Amar Desai, PhD, Case Comprehensive Cancer Center
Thomas E. (Ted) Dick, PhD, Department of Neurosciences
J. Alan Diehl, PhD, Case Comprehensive Cancer Center
James Driscoll, MD, PhD, Department of Medicine
George Dubyak, PhD, Departments of Physiology, Biophysics and Pathology
Agata Exner, PhD, Department of Radiology
Chris Flask, PhD, Department of Radiology
Mahmoud Ghannoum, PhD, Department of Dermatology
Berkley Gryder, PhD, Department of Genetics and Genome Sciences
Sanjay Gupta, PhD, Department of Urology
Maria Hatzoglou, PhD, Department of Genetics and Genome Sciences
Siran M. Koroukian, PhD, Department of Population and Quantitative Health Sciences

ACKNOWLEDGEMENTS Continued

CWRU Faculty Research Mentors
Thomas LaFramboise, PhD, Department of Genetics and Genome Sciences
John Letterio, MD, Department of Pediatrics
Alan Levine, PhD, Department of Molecular Biology and Microbiology
Yan Li, PhD, Department of Genetics and Genome Sciences
Ganapati Mahabaleshwar, PhD, Department of Pathology
Danny Manor, PhD, Department of Nutrition
Sanford Markowitz, MD, PhD, Departments of Medicine, Genetics
Divita Mathur, PhD, Department of Chemistry
Jason Mears, PhD, Case Comprehensive Cancer Center
Lin Mei, MD, PhD, Department of Neurosciences
Helen Miranda, PhD, Department of Genetics and Genome Sciences
Vincent Monnier, MD, Department of Pathology
Rebecca Obeng, MD, PhD, Department of Pathology
Reshmi Parameswaran, PhD, Department of Pathology
Paul Park, PhD, Department of Ophthalmology
Pola Philippidou, PhD, Department of Neurosciences
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
Sam Senyo, PhD, Department of Biomedical Engineering
Can Shi, PhD, Department of Medicine, Cardiology
Rakesh Shiradkar, PhD, Case Comprehensive Cancer Center
Neena Singh, MD, PhD, Department of Pathology
Andrew Shoffstall, PhD, Department of Biomedical Engineering
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
John (Zhenghe) Wang, PhD, Department of Genetics and Genome Sciences
Wenzhang Wang, PhD, Department of Pathology
Aaron Weinberg, DMD, PhD, Department of Biological Sciences, Dental Medicine
David Wilson, PhD, Department of Biomedical Engineering
Jordan Winter, MD, Department of Surgery
Anthony Wynshaw-Boris, MD, PhD, Department of Genetics and Genome Sciences
Rong Xu, PhD, Center for Artificial Intelligence
Tae Hun Kim, PhD, Department of Biochemistry
Hung-Ying Kao, PhD, Department of Biochemistry
Mei Zhang, PhD, Department of Biomedical Engineering
Yi Zhang, PhD, Case Comprehensive Cancer Center
Xiongwei Zhu, PhD, Department of Pathology

ACKNOWLEDGEMENTS Continued

2023 SEO/YES Lunch & Learn, Career Café, and Science in the News Seminar Speakers

Edward Barksdale, MD, University Hospitals Rainbow Babies and Childrens Hospital
Nathan Berger, MD, Case Comprehensive Cancer Center
Mel Berger, MD, PhD, Pediatrics
Jennifer Cullen, PhD, MPH, Department of Population and Quantitative Health Sciences
Lina Mehta, PhD, Department of Radiology
Samuel Anim, MD, University Hospitals Hematology and Oncology
Cliff Harding, MD, PhD, Department of Pathology
Alex Huang, MD, PhD, Department of Pediatrics
Mark Jackson, PhD, Case Comprehensive Cancer Center
Damian Junk, PhD, Case Comprehensive Cancer Center
Lalitha Nayak, MD, Case Comprehensive Cancer Center
Rebecca Obeng, MD, PhD, Department of Pathology
Cynthia Owusu, MD, MS, Department of Hematology, Oncology
Reshmi Parameswaran, PhD, Department of Pathology
Andrew Pieper, MD, PhD Department of Psychiatry
John Pink, PhD, Case Comprehensive Cancer Center
Kristina Knight, PhD, Department of Population and Quantitative Health Sciences
Fred Schumacher, PhD, Department of Population and Quantitative Health Sciences
Kurt Stange, MD, PhD, Center for Community Health Integration
Erika Trapl, PhD, Department of Population and Quantitative Health Sciences
Jordan Winter, MD, Department of Surgery
George Yendewa, MD, MPH, Department of Medicine

2023 SEO/YES Near Peer Mentors

Oscar Bautista
Sarah McNeer
Gracie Bellino
Ethan Honeycutt
Caitlin Swanberg
Jess LaBella
Danielle Browne
Isioma Akwanamnye
Marnie Williams
Taylor Benske
Raquel Lopez de Boer
Chelsea Chen
Osmary Medina
Heidi Standke
Anelise Hutson
Lane Pierson
Jerrik Rydbom
Alyssia Broncano
Akash Mody
Lauren Proctor
Lawrence Chu
Bailey Klein
Lauren Reilly Jankowiak

2023 Participating High Schools

Andrews Osborne Academy
Ardsley High School
Avon High School
Beachwood High School
Charles F. Brush High School
Cleveland Central Catholic High School
Cleveland Heights High School
Cleveland School of Science and Medicine
Copley High School
Gilmour 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
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 PROGRAM OUTCOMES

2023

30 High School Student Graduates
100% High School Graduation
100% College Matriculation

Colleges Entered by SEO/YES High School Graduates 2023

CWRU 3
Duke 2
University of Notre Dame 1
Notre Dame College 1
University of Pennsylvania 2
University of Cincinnati 1
Dennison 2
Harvard 1
Ohio State 4
George Washington University 1
Cleveland State 3
Kent State 2
University of North Carolina 1
Brown University 1
University of Chicago 1
Colgate 1
Washington University in St. Louis 2
Northeastern University 1

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
David Adegbite	Villa Angela – St. Joseph	
Deborah Adegbite	Villa Angela – St. Joseph	
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	Washington University of St. Louis
Jordan Alexander	John F. Kennedy High School	
Rama Al Ghalayini	Westlake High School	Ohio State
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	
Ahmed Al-Rawi	Westlake High School	
Jessica Amoah	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

Student	High School	College
Zain Anwar	University School	
Marangely Aponte	James F. Rhodes High School	Cuyahoga Community College
Angelica Arana	Cleveland School of Science and Medicine	
Shruthika Araselvan	Hathaway Brown School	University of Rochester
Alexis Armstead	Glenville High School	Cuyahoga Community College Hiram 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
Safa Bahadur	Cleveland School of Science and Medicine	
Nathan Ballman	Shaker Heights High School	
Anusha Bangalore	Westlake High School	Case Western Reserve University
A'Lahna Banks	Campus International	
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	

Student	High School	College
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
Ramon Bhambra	Twinsburg High School	Kent State University
Sahaj Bhambra	Twinsburg High School	Kent State University 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	Brown University
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	Duke University

Student	High School	College
Ava Bribriesco	Shaker Heights High School	
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
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
Anjali Chepyala	Orange High School	
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

Student	High School	College
Ashley Chu	Hathaway Brown	
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
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	Vanderbilt University 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
Jack D'Cruz	University School	
Maxinae DeJesus	James F. Rhodes High School	

Student	High School	College
Jade Del Orbe	Facing History New Tech	Bowling Green
Kayla Del Valle	Cleveland School of Science and Medicine	
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
Solomon Doibo II	Shaker Heights High School	
Mary Draper	John F. Kennedy High School	Indiana Wesleyan University
Amy Duan	Solon High School	Duke University
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
Adrik Dutta	Shaker Heights High School	
Le'Aona DySart	Cleveland School of Science and Medicine	Eastern Michigan
Chloe Echols	Hathaway Brown School	Dennison
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

Student	High School	College
Adam Esa	St. 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
Luke Feran	St. Edward High School	
Brenden Fernandes	Solon High School	
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
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	University of Notre Dame
Anish Ganesh	University School	The Ohio State University
Amie Garcia	James F. Rhodes High School	University of Alaska Cleveland State University

Student	High School	College
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	Notre Dame College
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
Hanna Goje	Hathaway Brown	
Philip Golczak	Mayfield High School	Case Western Reserve University
Wiktor Golczak	Mayfield High School	Case Western Reserve University
Tarini Gowda	Revere High School	The Ohio State University
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
Kalita Griffin	Glenville High School	Cuyahoga Community College Bowling Green State University
Nalin Gupta	Solon High School	Washington University in St. Louis
Nikki Haab	John F. Rhodes High School	Cleveland State University
Jaida Hadley	Cleveland J.F.K.	
Kenneth Hale	Cleveland School of Science and Medicine	Bates College
Bruce D. Hale, Jr.	Cleveland School of Science and Medicine	University of Toledo

Student	High School	College
Quinta Hamilton	Glenville High School	Kent State University
Trevon Hamilton	John F. Kennedy High School	Purdue University
Harper Hammond	Kirtland High School	
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
Hannah Holt	Charles F. Brush High School	Colgate University
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

Student	High School	College
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
Rohit Jain	Westlake High School	
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
Isaac Jang	Orange High School	Case Western Reserve University
Caroline Jang	Orange High School	
Jonathan Jang	University School	The Ohio State University
Che Jarvis	University School	University of San Diego
Asha Jha	Shaker Heights High School	Dennison

Student	High School	College
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
Adam Kabbara	St. Edward High School	
Vishwum Kapadia	University School	
Timofii Karamalak	Facing History New Tech	Cleveland State
Sai Karnati	University School	Brown University
Hari Kasi	North Royalton High School	
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	University of Pennsylvania
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	
Kareem King	Charles F. Brush High School	Harvard University
Veronica Kissoon	North Olmsted High School	Cleveland State

Student	High School	College
Rashon Knight	Benedictine High School	Allegheny College
Wyson Kong	Cleveland School of Science and Medicine	The Ohio State University
Ishita Kopparapu	Hathaway Brown	
Emerson Krauss	University School	
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 Univ. Case Western Reserve Univ. SOM
Adlai Kwofie	Cleveland School of Science and Medicine	The Ohio State University
Graham Lane	University School	University of Chicago
Aditya Lakshmanan	Mayfield High School	
Rayyan Laryea	Cleveland School of Science and Medicine	
Mya Lavender	John F. Kennedy High School	
Bauldwine Lazare	Cleveland Early College	
Lindsey Lemus	Cleveland School of Science and Medicine	
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
Miles Lipman	Shaker Heights High School	
Tamika Littlejohn	Glenville High School	The Ohio State University University of Toledo

Student	High School	College
Karis Liu	Solon High School	Northwestern University
Laura Llapa	James F. Rhodes High School	Miami University
Arik London	Cleveland School of Science and Medicine	
Noah Lockhart	John F. Kennedy High School	
Andrew Loney	Shaker Heights High School	The Ohio State University
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	Cuyahoga Community College Baldwin Wallace University
Henry Massey	University School	Columbia University
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	Cleveland State University
Quinn McDermott	Shaker Heights High School	Muskingum University

Student	High School	College
Shay McDermott	Shaker Heights High School	Case Western Reserve University
Nichola McDowell	Cleveland School of Science and Medicine	Case Western Reserve University
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	University of Chicago
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	The Ohio State University 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	Cuyahoga Community College 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

Student	High School	College
Uwela Mugabo	Cleveland Central Catholic	
Khalil Muhammad	Charles F. Brush High School	
Patrick Murphy, Jr.	John F. Kennedy High School	Cleveland State University
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
Loriane Nouafo	Solon High School	
Micha Nouafo	Solon High School	University of Pennsylvania
Areesha Nouman	Hathaway Brown	
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

Student	High School	College
Richard Ojo	Eleanor Roosevelt High School	University of Maryland
Andrea Okocha	Bedford High School	University of Rochester
Aide Omoijuanfo	Glean Academy	
Ebahi Omoijuanfo	Glean Academy	University of Notre Dame
Ese-Onosen Omoijuanfo	Glean Academy	University of Notre Dame CWRU School of Medicine
Jason Ong	Solon High School	Johns Hopkins University University of Pittsburgh
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
Sharon Orisadipe	Shaker Heights High School	
Kwabena Owusu	Solon High School	Harvard
Nana Owusu	Solon High School	Yale University Columbia University SOM
Sairam Pantham	Solon High School	
John Pape	University School	Colgate
Gabriel Papell	Shaker Heights High School	The Ohio State University
Radha Pareek	Beachwood High School	
Taniya Parker	Glenville High School	University of Akron
Chantae Parsons	John F. Kennedy High School	University of Dayton
Garv Patel	Andrews Osborne Academy	University of Cincinnati
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	

Student	High School	College
Devan Perera	Twinsburg High School	
Angelica Pickett	John F. Kennedy High School	Liberty University Ohio State University
Eric Pieper	Shaker Heights High School	
Justin Pieper	Shaker Heights High School	
Sophia Pinto	Hawken School	
Alaina Pizarro	Hawken School	
Sophia Poindexter	Cleveland School of Science and Medicine	
Chad Porter	Villa Angela/St. Joseph High School	The Ohio State University
Ta'Shiyah Porter	Cleveland School of Science and Medicine	Kent State
Bre-Shay Potts	John F. Kennedy High School	Cleveland State University
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

Student	High School	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	University of North Carolina
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	
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	The Ohio State University
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

Student	High School	College
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 Senthilkumar	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
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	
Tasneema Shaik	Cleveland School of Science and Medicine	
Anshul Sharma	University 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

Student	High School	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
Pranav Sompalle	Mayfield High School	University of Pennsylvania
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	

Student	High School	College
Diya Swain	Shaker Heights High School	Case Western Reserve University
Hans Swain	University School	
Ian Swain	University School	Case Western Reserve University
Eric Swander	James F. Rhodes High School	Cuyahoga Community College Hiram College
Christopher Swetel	Campus International	
Josea Switzer	Glenville High School	Akron University
Maheera Syed	Strongsville High School	John Carroll University The Ohio State University
Rubab Syed	Strongsville High School	University of Toledo 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
Mackensie Thompson	Andrews Osborne Academy	Cleveland State
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	Kent State University
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	Cleveland State

Student	High School	College
Mythreyi Ungarala	Shaker Heights High School	
Sahishnu Vallabhajoysula	Avon High School	Case Western Reserve University
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
Samuel Wales-McGrath	Twinsburg High School	
Kennon Walton	University School	Duke University
Chougyu Wang	St. Ignatius High School	
Evan Wang	Beachwood High School	
Lindsey Wang	Orange High School	Case Western Reserve University
William Wang	Orange High School	
Yinyin Wang	Shaker Heights High School	
Janiece Warfield	Glenville High School	Cleveland State University
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
Mya Williams	Charles F. Brush High School	

Student	High School	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	CWRU University of Cincinnati 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
Adam Yu	Solon High School	Vanderbilt
George Zaky	St. Ignatius High School	
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	George Washington University
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
Julia Zhu	Hathaway Brown	

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
	Harvard – MIT SOM
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
Rachel McKinney	Andrews Osborne Academy
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
Emma Zglinicki	Hathaway Brown

2023 SEO/YES STUDENT RESEARCH POSTERS

1. David Adegbite, Villa Angela-St. Joseph
   Analyzing Social Media User Engagement with Prostate Cancer Education Posts
   Erika Trapl, PhD, Department of Population and Quantitative Health Sciences

2. Debora Adegbite, Villa Angela-St. Joseph
   Abbarnt BORG expression in Breast Cancer Causes Immune Evasion
   William Schiemann, PhD, Case Comprehensive Cancer Center

3. Adesewa Adeweso, Mayfield High School
   Cellular Uptake of Vitamin E: Mechanisms and Pathways
   Danny Manor, PhD, Department of Nutrition

4. Nassim Aidja, Mayfield High School
   Examining the Role of Community Outreach Events in Health Education
   Kristina Knight, PhD, Department of Population and Quantitative Health Sciences

5. Ahmed Al-Rawi, Westlake High School
   Segmentation Aortic Calcifications seen in CT scans in Patients with Severe Stenosis
   David Wilson, PhD, Department of Biomedical Engineering

6. Jessica Amoah, Cleveland School of Science and Medicine
   T and B cells in Tumors and Lungs of Mice
   Rebecca Obeng, MD, PhD, Department of Pathology

7. Zain Anwar, University School
   Interleukin-34 Deficiency Amplifies Severity of Experimental DSS-Induced Colitis
   Fabio Cominellli, MD, PhD, Department of Gastroenterology

8. Anjelica Arana, Cleveland School of Science and Medicine
   Pancreatic Stellate Cells and Type II Diabetes Crosstalk
   Yan Li, PhD, Department of Genetics and Genome Sciences

9. Safa Bahadur, Cleveland School of Science and Medicine
   The Migration of Mature Microglia into NPC Organoid Models
   Toni Wyshaw-Boris, MD, PhD, Department of Genetics and Genome Sciences

10. Nathan Ballman, Shaker Heights High School
    Investigating the Role of TGFbeta Signaling in GI-cancer through an Informatics-driven Analysis
    Andrew Blum, MD, PhD, Department of Gastroenterology

11. A'Lahna Banks, Campus International High School
    Evaluating barber education pre and post-surveys to understand what the training has taught barbers
    Erika Trapl, PhD, Department of Population and Quantitative Health Sciences

12. **Thomas Blossom, University School**
    Evaluating the Role of Dietary Inflammation in Aviator Cognitive and Physical Fatigue over Time
    Michael Decker, PhD, Department of Physiology and Biophysics

13. **Ava Bribiesco, Shaker Heights High School**
    Examining Mutational Profiles of COVID Strains Using Publicly Available Data
    E. Ricky Chan, PhD, Case Comprehensive Cancer Center

14. **Cara Castro, Hathaway Brown**
    Investigating BIRC3 Signaling in Various Cancers
    Reshmi Parameswaran, PhD, Department of Pathology

15. **Anjali Chepyala, Orange High School**
    Elucidating the structure of biomarker LW-1
    Vincent Monnier, MD, Department of Pathology

16. **Ashley Chu, Hathaway Brown**
    Development of Pre-clinical Assays for Quality Control of Cancer Imaging Agents
    Susann Brady-Kalnay, PhD, Department of Molecular Biology and Microbiology

17. **John D'Cruz, University School**
    Live Cell Imaging to Target Drug Resistance in Cancer
    James Driscoll, MD, PhD, Department of Medicine

18. **Kayla Del Valle, Cleveland School of Science and Medicine**
    TBK1 in Alzheimer's Disease (AD) and Frontal Temporal Dementia
    Xiongwei Zhu, MD, Department of Pathology

19. **Manzili Denis, University School**
    Identifying The Target Of Cancer-Targeting Compounds Using a Forward Genetic Screen
    Drew Adams, PhD, Department of Genetics and Genome Sciences

20. **Solomon Doibo, Shaker Heights High School**
    Determining Notch Receptor Regulation of Arterial Reactivity
    Aaron Proweller, MD, PhD, Department of Medicine

21. **Kaitlyn Ernst, Laurel School**
    Characterizing Fascicle Structure of the Laryngeal Nerve at the Single Fiber Level: Advancing Vagus Nerve Stimulation for Enhanced Neuromodulation
    Andrew Shoffstall, PhD, Department of Biomedical Engineering

22. **Adam Esa, St. Edward High School**
    Imatinib Stimulates Release of Interleukin-1β from Neutrophils via Mechanism Dependent on Lysosomal Disruption
    George Dubyak, PhD, Department of Physiology and Biophysics

23. **Adora Ezepue, Ohio State University**
    Chronic differential expression of metabolic genes in the brain after mild traumatic brain injury
    Andrew Pieper, MD, PhD, Department of Psychiatry

24. **Luke Feran, St. Edward High School**
    Raw Cell Stimulation for Immunofluorescent Staining
    Aaron Burberry, PhD, Department of Pathology

25. **Brenden Fernandes, Solon High School**
    Correlating Ferroptosis-Inducing Drug Responses to Osteosarcoma Subtypes
    Berkley Gryder, PhD, Department of Genetics and Genome Sciences

26. **Fahness Freeman, Cleveland Heights High School**
    Effect of receptor protein tyrosine phosphatase γ on phosphorylation of epidermal growth factor receptor 1
    Walter Boron, MD, PhD, Department of Physiology and Biophysics

27. **Isaiah Gilbert, University School**
    Plasmid synthesis from bacteria for DNA nanostructure production
    Divita Mathur, PhD, Department of Chemistry

28. **Hanna Goje, Hathaway Brown**
    Administration of CDDO 2P-Im suppresses the invasion and migration of Diffuse intrinsic pontine glioma (DIPG)
    John Letterio, MD, Case Comprehensive Cancer Center

29. **Philip Golczak, Mayfield High School**
    Improvement of in Vitro Nanobubble Imaging Techniques and Determination of the Stability of Nanobubble-labeled T-cells
    Agata Exner, PhD, Department of Radiology

30. **Tarini Gowda, Revere High School**
    The Impact of Race Concerning Deaths Due to Legal Intervention
    Peter Hovmand, PhD, Center for Community Health Integration

31. **Harper Hammond, Andrews Osborne**
    Modulation of Extracellular matrix proteins by α-Synuclein and the cellular prion protein: Implications for primary open-angle glaucoma
    Neena Singh, MD, PhD, Department of Pathology

32. **Rohit Jain, Westlake High School**
    Winding back the epi-TOC: An Analysis of Epigenetic Age and Cancer Incidence Rates
    Fred Schumacher, PhD, Department of Population and Quantitative Health Sciences

33. Caroline Jang, Orange High School
    Racial, Genetic, and Socioeconomic Disparities in Pediatric Acute Lymphoblastic Leukemia
    Jennifer Cullen, PhD, Department of Population and Quantitative Health Sciences

34. Asha Jha, Shaker Heights High School
    Blocking the Growth of Metastases Colorectal Cancer By Targeting the Liver-Cancer Crosstalk
    Rui Wang, PhD, Department of Genetics and Genome Sciences

35. Adam Kabbara, St. Edward High School
    Comparing Metrics that Measure Variability in the Respiratory Waveform
    Thomas E. “Ted” Dick, PhD, Department of Neurosciences

36. Harikrisnan Kasi, North Royalton High School
    Cloning, Expression and Characterization of Alkaline Phosphatase in Escherichia coli BL21, C+, and Shuffle
    Tae Hun Kim, PhD, Department of Biochemistry

37. Shria Kavaturu, Copley High School
    Monitoring ORAI1 Dynamics In T Cell
    Zhenghe “John” Wang, PhD, Department of Genetics and Genome Sciences

38. Minjun Kim, St. Edward High School
    Glutamine pathways’ assistance of metabolism to resistant IDH1
    Jordan Winter, MD, Department of Surgery

39. Ishita Kopparapu, Hathaway Brown
    Testing a Novel Stem Cell Culturing Medium for Cortical Organoids
    Helen Miranda, PhD, Department of Genetics and Genome Sciences

40. Emerson Kraus, University School
    Inexpensive Protein and DNA Ladders as Molecular Weight Markers
    Yi Zhang, PhD, Case Comprehensive Cancer Center

41. Aditya Lakshmanan, Mayfield High School
    What Role Does MECP2 Play in Cancer?
    Tae Hun Kim, PhD, Department of Biochemistry

42. Lindsey Lemus, Cleveland School of Science and Medicine
    Scientific Breast Cancer Research On Polygenic Risk Scores
    Fred Schumacher, PhD, Department of Population and Quantitative Health Sciences

43. Miles Lipman, Shaker Heights High School
    Sexual Dimorphism in the Hematopoietic Systems of Mice
    Amar Desai, PhD, Department of Biomedical Engineering

44. Eleanor Meges, Padua Franciscan High School
    The Role of Non-Modifiable Factors and Social Determinants of Health in Prostate Cancer Awareness
    Kristina Knight, PhD, Department of Population and Quantitative Health Sciences

45. Ira Mehta, Lake Ridge Academy
    Effect of Opioids on Mucus Production in the Intestinal Epithelium
    Alan Levine, PhD, Department of Molecular Biology and Microbiology

46. Uwela Mugabo, Cleveland Central Catholic High School
    The role of Macrophages-KLF6 in Atherogenesis
    Ganapati Mahabaleshwar, PhD, Department of Pathology

47. Khalil Muhammad, Charles F. Brush High School
    Discovering Health Disparities for African American women and African women in Triple-negative Breast Cancer
    Jennifer Cullen, PhD, MPH, Department of Population and Quantitative Health Sciences

48. Tina Nguyen, Mayfield High School
    Assessing Apoptotic Activity in Pediatric Diffuse Intrinsic Pontine Glioma in Response to Administration of CDDO-2P-Im
    John Letterio, MD, Department of Pediatrics

49. Loriane Nouafo, Solon High School
    Genotyping to Distinguish Wild Type vs miR 211-/- mice
    J. Alan Diehl, PhD, Case Comprehensive Cancer Center

50. Areesha Nouman, Hathaway Brown
    Evaluating Dextran Polymers for Sustained Delivery of Tuberculosis Drugs
    Horst Von Recum, PhD, Department of Biomedical Engineering

51. Niamh O'Donovan, Ardsley High School
    Investigating Chronic Inflammation in Lymphoid Compartments After Acute Traumatic Brain Injury
    Andrew Pieper, PhD, Department of Psychiatry

52. Aide Omoijuanfo, Glean Academy
    Salivary innate immune responses to SARS-CoV-2 in acutely infected participants
    Aaron Weinberg, DMD, PhD, Department of Biological Sciences, Dental Medicine

53. Ebahi Omoijuanfo, Glean Academy
    Examining Stem Cell Properties of Glioblastoma Cells
    Maria Hatzoglou, PhD, Department of Genetics and Genome Sciences

54. Sharon Orisadipe, Shaker Heights High School
    Highlighting community perceptions and feelings around genetic screening
    Erika Trapl, PhD, Department of Population and Quantitative Health Sciences

55. Sairam Pantham, Solon High School
    A New Look at Prognostic Subgroups Within Endometrial Cancer Through the Examination of Immune Cell Gene Expression
    Mark Cameron, PhD, Department of Population and Quantitative Health Sciences

56. Radha Pareek, Beachwood High School
    Investigating Temporal Expression Patterns of KLF Transcription Factors in Phrenic Motor Neurons: Insights into Breathing Abnormalities and Disease
    Pola Philippidou, PhD, Department of Neurosciences

57. Devan Perera, Twinsburg High School
    Genomic and Mitochondrial Characterization of RKO cell line
    Thomas LaFramboise, PhD, Department of Genetics and Genome Sciences

58. Sophia Pinto, Hawken School
    Optimizing an airbrush speckle pattern application for 2D and 3D surfaces to use in DIC imaging
    Bryan Carroll, MD, PhD, Department of Dermatology

59. 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

60. Sofia Poindexter, Cleveland School of Science and Medicine
    The impact of Human Patient Mutations in UPF1 on Nonsense Mediated mRNA decay while using a budding yeast model
    Kristian Baker, PhD, Department of Genetics and Genome Sciences

61. Samara Rivchun, Laurel School
    In vitro Efficacy of an Enfumafungin Derivative Antifungal SCY-247 Against Candida auris
    Mahmoud Ghannoum, PhD, Department of Dermatology

62. Lilly Russo, Gilmour Academy
    Impact of Gut Microbiome on Sex-Based Differences of Immune Profiles
    Theresa Pizarro, PhD, Department of Pathology

63. Hamza Said, Westlake High School
    Multi-Parametric Magnetic Resonance Imaging to Detect and Characterize Chronic Kidney Disease in Children with Youth-Onset Type-2 Diabetes (DetectKID2)
    Chris Flask, PhD, Department of Radiology

64. Anna Saline, Gilmour Academy
    The angiotensin receptor blocker, Losartan, is effective in maintaining reduced fibrosis using a model of DexM-induced remission in Crohn's disease-prone SAMP mice
    Theresa Pizarro, PhD, Department of Pathology

65. Soham Shah, St. Ignatius High School
The Role of Macrophage-KLF6 in Stent-Induced Arterial Injury
Ganapati Mahabaleshwar, PhD, Department of Pathology

66. Tasneema Shaik, Cleveland School of Science and Medicine
The effects of mutations G350D and R710G on dynamin-related protein 1
Jason Mears, PhD, Department of Pharmacology

67. Anshul Sharma, University School
The impact of changes in the social vulnerability index on overall and race-specific one-year survival rates for prostate cancer from 2000-2020
Fred Schumacher, PhD, Department of Population and Quantitative Health Sciences

68. Pranav Sompalle, Mayfield High School
Association of MR image quality measures with diagnostic accuracy and inter-reader agreement of PI-RADS v2.1 for detection of clinically significant prostate cancer
Satish Viswanath, PhD, Department of Biomedical Engineering

69. Diya Swain, Shaker Heights High School
Long-term Androgen depletion in mice is linked with cognitive impairment
Sanjay Gupta, PhD, Department of Urology

70. Christopher Swetel, Campus International
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Siran Koroukian, PhD, Department of Population and Quantitative Health Sciences

71. Maya Tang, Hathaway Brown
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Paul Park, PhD, Department of Ophthalmology and Visual Sciences

72. Mythili Ungarala, Shaker Heights High School
The Effect of the Promyelocytic Leukemia Protein (PML) on Cancer Cell Glycolysis
Hung-Ying Kao, PhD, Department of Biochemistry

73. Mythreyi Ungarala, Shaker Heights High School
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Can Shi, PhD, Department of Medicine

74. Sahishnu Vallabhajoysula, Avon High School
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Mei Zhang, PhD, Case Comprehensive Cancer Center

75. Samuel Wales-McGrath, Twinsburg High School
Optimizing Therapeutic Outcomes in Diffuse Intrinsic Pontine Glioma Through the Assessment of CDDO-2P-Im in Synergistic Radiotherapy
John Letterio, MD, Department of Pediatrics

76. **Evan Wang, Beachwood High School**
    Integrin Beta3-Mediated Cell Senescence and Colonic Abnormalities in Alzheimer's Disease: Insights from Bioinformatics Analysis
    Rong Xu, PhD, Center for Artificial Intelligence

77. **Lindsey Wang, Orange High School**
    GLP-1RA receptors agonists and gynecologic cancer risk in drug-naïve patients with type 2 diabetes: A nationwide retrospective cohort study in the US
    Nathan A. Berger, MD, Center for Science, Health and Society

78. **William Wang, Orange High School**
    Semaglutide and suicidal thoughts: retrospective cohort study
    Nathan A. Berger, MD, Center for Science, Health and Society

79. **Mya Williams, Charles F. Brush High School**
    Genotyping floxed mouse models to create conditional knockouts for cancer studies
    Sanford Markowitz, MD, PhD, Department of Medicine

80. **George Zaky, St. Ignatius High School**
    The Impact of SLX4IP on cell growth of HER2+ Breast Cancer
    William Schiemann, PhD, Case Comprehensive Cancer Center

81. **Amy Zhou, Beachwood High School**
    Investigating the role of C1 esterase inhibitor in regulating thrombosis
    Alvin Schmaier, MD, Departments of Medicine and Pathology

82. **Julia Zhu, Hathaway Brown**
    MFN2 a Potential Therapeutic Target for Alzheimer's disease
    Wenzhang Wang, PhD, Departments of Pathology

ABSTRACT #1

Analyzing Social Media User Engagement with Prostate Cancer Education Posts

David Adegbite, Villa Angela-Saint Joseph High School; Erika Trapl, Kristina Austin, Rebecca Miller, Sydney Evans, Calvin Tornes, Case Comprehensive Cancer Center, Case Western Reserve University

Background:
Prostate Cancer in the US is a big problem, but it affects African American men more. What is Prostate Cancer? Well Prostate Cancer is a type of cancer that develops in the Prostate Gland that affects men from ejaculating or urinating. I'm working with a project called the Cleveland African American Prostate Cancer Project (CAAPP), which reaches out to African American Barber Shops about communicating with their clients about getting tested for Prostate Cancer. I am trying to figure out what type of posts social media users engage with most. To gather more information, a literature review was conducted and the social media sites of the Case Comprehensive Cancer Center were examined. In today's age, a lot of men are on social media, but women are just on social media a teeny bit more. On social media, 51% of Women and 49% of Men are on the app, which is not that big of a difference.

Goal:
To figure out if men are looking at posts about cancer/prostate cancer or informative posts on social media.

Methods and Materials:
To gather literature, I searched using two academic databases: Google Scholar and PubMed. The search terms used included "Age in Social Media" along with "Social Media" "Gender in Social Media" "Social Media in Men" and "Social Media Usage". A total of 5 Articles were used in this review from 2015 - 2023.

Results:
In Process

Conclusions:
Pending

ABSTRACT #2

Aberrant BORG expression in Breast cancer Causes Immune Evasion

Deborah Adegbite, Villa Angela-Saint Joseph High School; Daeho Kim, William P. Scheimann, Department of Biochemistry, Case Western Reserve University

Background:

BMP/OP-Responsive Gene (BORG) was discovered in the late 1980s. BORG is an intergenic lncRNA that was originally thought to be a coding gene. In previous studies, BORG was discovered in triple-negative breast cancer (TNBC) and was later discovered to be an important regulator of TNBC. BORG liberates D2OR cells from their dormant state, which has been shown to cause metastases in the lungs of mice, by conferring a proliferative shift in the cell cycle. D2OR is part of the murine D2HAN series which includes D2OR, D2A1, and D2.1. The different cell lines show cells at different stages of metastasis. D2OR is the dormant stage, D2.1 is moderately metastatic, and D2A1 is highly metastatic. Since D2OR is known to be dormant it can be used to monitor the rate at which BORG affects metastasis.

Methods and Materials:

We cultured cells in serum-free media and then transferred the serum-free media into a proteome profiler panel. To check the BORG expression and IL-6 expression RNA was extracted using a trizol extraction and checked the level of RNA was by using RT-q-PCR. To obtain the conditional media D2OR_Empty/D2OR_BORG were seeded and cultured for 48 hours and the culturing media has been changed to serum-free media for 24 hours. Serum-free media from each cell was transferred to a parent D2OR cell to check the extrinsic transfer of cytokines and chemokines. Parent D2OR cells were cultivated for 12 hours and harvested.

Results:

In the proteome profiler, we found cytokines and chemokines related to M1 Macrophage, which is anti-cancer and inflammatory, have been decreased by contrast M2 Macrophage, which is pro-cancer and immune suppressive, have been increased such as IL-6. In BORG overexpression cells RNA level of IL-6 was elevated. To understand the effect of BORG on other cells we made conditional media and transferred it to parental D2OR and it showed phosphorylation of STAT3 and increased Cyclin D2 which is downstream of STAT3.

Conclusions:

BORG is an important regulating factor in TNBC that encourages dormant cells to metastasize. We have found BORG expression to initiate IL-6 secretion and also the phosphorylation of STAT3 which means the initiation of the STAT3 cascade in tumor cells and other types of cells. In our research, we found the relationship between BORG overexpression in IL-6/STAT 3 cascade elucidated the reason for increased cell survivability and increased rate of metastasis.

ABSTRACT #3

Cellular Uptake of Vitamin E: Mechanisms and Pathways

Adesewa Adeweso, Mayfield High School; Danny Manor, Department of Nutrition, Case Western Reserve University

Background:
Vitamin E is a lipid-soluble antioxidant found in various foods and supplements. α-tocopherol is one of eight forms of vitamin E and is considered the most biologically active form in the body. Although vitamin E's antioxidant abilities are well researched and documented, it has been questioned whether it can have additional activities independent of its antioxidant actions, specifically through the activation of nuclear receptor transcription factors. In order to test this hypothesis our lab performed transcriptional reporter assays with vitamin E and the receptor PPARgamma. To ensure that vitamin E is taken up during these experiments, we utilize a fluorescent analog of α-tocopherol (NBD-tocopherol) in conjunction with fluorescence microscopy.
Vitamin E uptake is a complex process involving absorption, transport, and utilization. Initially, vitamin E is absorbed in the small intestine with dietary fats and then packaged into chylomicrons for transport into the liver. Once in the liver, vitamin E is incorporated into very low-density lipoproteins (VLDLs) for transport to other tissues. Furthermore, vitamin E is taken up by cells through receptor-mediated endocytosis, which is then incorporated into membranes at various locations within cells. This study is significant for several reasons. Fundamentally, vitamin E is an essential nutrient, and sufficient intake is required for optimal health. Insufficient intake can cause vitamin E deficiency, resulting in severe neurological disorders such as ataxia and hyporeflexia. Furthermore, determining the mechanisms by which the vitamin works in our bodies will provide insights into the vital connection between diet and health. By analyzing the fluorescence patterns through the use of NBD-tocopherol, we will gain insights into how cells take up and utilize α-tocopherol. This research could lead to new insights into the importance of a balanced diet.

Goal:
To identify and establish the mechanism by which vitamin E is transported across the cell membrane and taken up by cells.

Methods and Materials:
NBD-tocopherol was diluted with 100% ethanol, and its concentration was determined by a spectrophotometer. Cos-7 cells were seeded in 24-well plates and incubated for 24 hours at 37℃, 5% CO2. After incubation, cells were treated with 50 uM of serum-complexed NBD-tocopherol and incubated at 37℃ for 18 hours. Cells were washed with phenol-red free, serum-free, Dulbecco's Modified Eagle Medium (DMEM) and an image was taken under Leica’s fluorescent microscope to visualize NBD fluorescence.

Results:
NBD-tocopherol effectively enhances vitamin E uptake in Cos-7 cells. The fluorescence microscopy images presented in Figure 1A and Figure 1B serve as valuable visual evidence of the differential cellular response to vitamin E deficiency and NBD-tocopherol treatment.

Conclusions:
Our findings offer novel insights into vitamin E uptake mechanisms, opening avenues for further research into cellular vitamin E metabolism and potential therapeutic applications.

ABSTRACT #4

Examining the Role of Community Outreach Events in Health Education

Nassim Aidja, Mayfield High School; Kristina Austin, Rebecca Miller, Sydney Evans, Calvin Tornes, Erika Trapl, Department of Population and Quantitative Health Sciences, Case Western Reserve University School

Background:
Community outreach events provide opportunities for individuals to connect with professionals when they otherwise would not have access to those services. Events as such can play a critical role in health education and prevention, as early detection and establishing relationships with primary care are essential to reducing the risk of disease. Health education is the process by which one educates others about health, including physical health, mental health, environmental health, etc. By optimizing outreach events to educate the general public regarding important topics, this increased intervention can help save lives. CAAPP, or the Cleveland African American Prostate Cancer Project, is a project which aims to partner with local barbershops to teach barbers about prostate cancer so they can become qualified to teach clients about prostate cancer. If community outreach events can educate individuals more effectively, organizations like CAAPP can offer prostate cancer screenings and educate the public regarding the threat that prostate cancer poses.

Goals:
To determine what people are learning from community outreach events so that they can become more effective in educating individuals regarding prominent health issues.

Methods:
A literature review on community outreach events and their role in health education was conducted based on 7 articles from 2000-2023. A comprehensive search was conducted across academic databases, including PubMed and Google Scholar, using relevant keywords such as *community outreach events*, *health education*, *health promotion*, *community health programs*, and *public health*. At community outreach events, a two-question verbal survey was conducted asking participants the following questions: "What did you learn something from today's event," and "How can we help you learn more from events like this in the future?". A qualitative analysis was conducted afterward to evaluate their answers.

Results:
Feedback was gathered from individuals who attended community outreach events to assess their knowledge about health-related topics and to gather suggestions for improvement. The theme of communication emerged prominently, with participants expressing a desire for better advertising and increased awareness of upcoming events to encourage broader attendance. Additionally, respondents recommended that companies involved in the outreach events collaborate with community leaders to customize materials and advertisements to fit the community's specific needs. They also suggested forming partnerships with churches and schools to reach a wider audience effectively. Moreover, participants proposed providing informational brochures with clear and easy-to-understand infographics to avoid overwhelming attendees. The diverse range of suggestions collected aims to enhance the impact of community outreach events, ensuring they reach more people and potentially save lives.

Conclusions:
Respondents' insights from community outreach events highlight the need for changes to enhance health education. Improved advertising and outreach can reach and educate more individuals. Partnering with community leaders builds trust in organizations at events. The literature review suggests further research on effective types of outreach events to improve health education. CAAPP can utilize these findings to increase screenings and educate more people about their organization's mission.

ABSTRACT #5

Segmentation of Aortic Calcifications seen in CT scans in Patients with Aortic Stenosis

Ahmed Al-Rawi, Westlake High School; Ammar Hoori, David Wilson, Department of Biomedical Engineering, Case Western Reserve University

Background:
Aortic stenosis (AS) is a type of heart valvular disease that narrows the aortic valve due to accumulated calcifications. This heart disease is more commonly found in individuals over the age of 65. Additionally, AS is the second most common valvular disease in the United States. Aortic stenosis is a very serious problem and causes blood flow to decrease in humans. Cardiologists assess the severity of AS based on the valve functionality. AS calcification can be seen and measured through CT scans.

In this project, we are assessing the AS by segmenting the calcifications found in aortic valve using 3D slicer software and analyzing measurements through different patients. This will help researchers to evaluate AS in order to predict future heart failure events and the need for Transcatheter valve replacement replacement (TAVR) procedure.

Our lab helped detect Aortic Stenosis by using segmentation on 3D slicer that will then be used by cardiologists, to get rid of Aortic Stenosis on patients who have this heart valve disease.

Goals:
Segment aortic calcifications for more than 100 patients using 3D slicer, and then analyze some statistical measurements across those patients. This will help the research to proceed with future machine learning projects.

Materials and Methods:
We are using CT scans for 100 patients from the University Hospital (UH). These scans are acquired during routine patient visits. We are using the 3D slicer as a segmentation tool, which is completely free and has comprehensive tools to segment medical images. The first step of the segmentation is to set a threshold range from 130 Houndsfield units (UH) and above to find out the potential place of the calcifications and bone. We then used noise filtering and the eraser tool to clean up any calcifications that are not of our interest. The scissors tool is then used to get rid of the places that would not be possible for the Aortic Stenosis to be found. Finally we figured out the center of the valve which is required for future training to detect the aortic valve location.

Results:
By analyzing patient hearts, we were able to determine if the patients could have Aortic Stenosis and how severe the calcification is from patient to patient. This will help future research to analyze aortic valve calcification and predicting future heart failures.

Conclusion:
We have been able to predict where Aortic Stenosis can occur on multiple patients accurately.

ABSTRACT #6

T and B cells in Tumors and Lungs of Mice

Jessica Amoah, Cleveland School Of Science and Medicine; Dathan Andrews, Rebecca C. Obeng, Department of Pathology, University Hospitals Cleveland, Case Comprehensive Cancer Center, Case Western Reserve University

Background:
Cancer is one of the leading causes of death in humans. Our immune system, specifically T and B cells can control tumor growth. But sometimes, the T and B cells cannot get into the tumors and function well. Therefore, we would like to study ways to increase the number of T cells in tumors. In this project, we study the ability of a molecule called IL-7 to increase the number of T cells in tumors.

Goals:
To get more T and B cells in the tumor
Which treatment works better IL-7 or Sham (control)

Materials and Methods:
We first injected cancer cells in the veins of 6 mice to grow tumors in the lungs. Then we divided the mice into 2 groups. Group 1- three of the mice got a sham treatment (control) and group 2 was treated with IL-7 once a week for 2 weeks. After the treatments, we harvested the lung tissues from the mice and looked at the histology for immune cells. We also performed immunofluorescence, a technique that allows us to visualize the T and B cells in the tumors. We counted the cells with a software called QuPath and then compared the numbers between the control and IL-7 treated groups.

Results:
The results show that there were on average, 65 T cells per mm^2 in the tumors from the mice that got the control treatment and 288 T cells per mm^2 in the tumors from the mice that got the IL-7 treatment. Also, there were 33 B cells per mm^2 in the tumor that got the control treatment and 14 B cells per mm^2 in the tumor that got the IL-7 treatment.

Conclusions:
Based on our results, we conclude that there is no difference in the number of B cells per mm^2 after IL-7 treatment but there is a significant increase in the number of T cells per mm^2 in the tumor samples from mice treated with IL-7. So in all, IL-7 treatment enhances T cell presence within tumors.

ABSTRACT #7

Interleukin-34 Deficiency Amplifies Severity of Experimental DSS-Induced Colitis

Zain F. Anwar, University School; Paola Menghini, Fabio Cominelli, Division of Gastroenterology, Department of Medicine, Case Western Reserve University

Background:

The complex role of Interleukin-34 (IL-34), a ligand for colony-stimulating factor-1 receptor (CSF-1R), in inflammatory bowel disease (IBD) pathophysiology remains enigmatic. While IL-34 and its counterpart, colony-stimulating factor 1 (CSF1), are acknowledged regulators of macrophage proliferation and differentiation, the specific mechanisms through which IL-34 influences gut homeostasis and intestinal injury are largely unexplored. Previous evidence of elevated IL-34 mRNA expression in IBD patients' inflamed mucosa hints at IL-34's involvement in IBD. This study delves into this intriguing aspect, employing dextran sulfate sodium (DSS)-induced colitis in IL-34 knockout (KO) mice as an experimental model.

Goals:

The study aims to elucidate the role of IL-34 within the context of IBD, particularly its involvement in intestinal inflammation, gut homeostasis, and changes in gut microbiota composition.

Materials and Methods:

Both IL-34 KO and C57BL/6 (BL6) mice, 12 weeks of age and sex-matched (n=20/group), were initially subjected to a fecal homogenization protocol to control for gut flora inter-cage variability. Subsequently, experimental mice were treated with 2.5% DSS in drinking water over a week. Numerous parameters, including body weight loss, mortality rate, severity of colitis via endoscopy and histology, and colon samples for MPO and RT-qPCR analyses were observed and recorded. In addition, mesenteric lymph node (MLN) cells were cultured post-anti-CD3/CD28 stimulation to measure cytokine production in the supernatants. Detailed microbiome analysis, utilizing fecal DNA extraction and sequencing techniques, was carried out to identify potential alterations in taxonomic composition.

Results:

As a part of the ongoing research conducted in the Cominelli Lab, my work predominantly focused on the extraction and analysis of fecal DNA. IL-34 KO mice exhibited enhanced susceptibility to DSS treatment, with a higher mortality rate (50% vs. 30%) and significant body weight loss between days 7 and 10 compared to BL6 mice. The inflammation index score in IL-34 KO mice rose significantly to 10.44 ± 1.48, compared to 4.08 ± 0.97 in BL6 mice ($p=0.0028$, $n \geq 10$/group). The endoscopic score was also higher in IL-34 KO mice (6.15 ± 0.47 vs. 4.08 ± 0.54, $p=0.011$, $n \geq 10$/group). Cytokine production analysis via ELISA and RT-qPCR is underway. Notably, the microbiome analysis revealed considerable taxonomic variation between the two cohorts, with BL6 mice hosting more gut-friendly bacterial species.

Conclusion:

Our findings suggest that IL-34 deficiency predisposes mice to exacerbated DSS-induced colitis, indicating IL-34's potential protective role during acute intestinal inflammation. These insights contribute novel perspectives on the role of IL-34 within IBD contexts, suggesting IL-34 as a critical element in disease progression and gut microbiota regulation. However, these findings stand in contrast to previous studies proposing that IL-34 blockade might confer protection from induced colitis. Consequently, further studies are warranted to thoroughly elucidate the role of IL-34 in intestinal inflammation and its resolution.

ABSTRACT #8

Pancreatic Stellate Cells and Type II Diabetes Crosstalk

Angelica Arana, Cleveland School of Science and Medicine; Hanxiao Liu, Yan Li, Department of Genetics and Genome Sciences, Case Western Reserve University

Background:
Insulin is made when glucose is absorbed from our guts into the bloodstream, when the blood glucose level rises then it signals the β cells in the pancreas to produce insulin. When a person can't produce insulin (Type I diabetes) or poorly responds to insulin (type II diabetes (T2D)). Diabetes mellitus can lead to additional health issues and around 37.3 million Americans have T2D. T2D can affect the islet of the pancreas, can cause the loss of the β cells from apoptosis, or cause poor function of the β cells. Also in the pancreas and islet, there are pancreatic stellate cells (PSCs), PSC is known as a neogenesis for β cells as well as being around seven percent of parenchyma cells in the pancreas. PSCs were first identified in the mouse duck in 1982. There are different types of PSCs one is quiescent PSC and the second is activated PSCs. Quiescent PSC gives interstitial support. While the activated PSC can release inflammation that could damage the β cells. PSCs have supportive effects such as supplying blood flow and providing scaffolding for epithelial integrity.

Goals:
To see if we can use PSCs to improve the function of β cells.

Materials and Methods:
We can use a Mercodia Ultrasensitive C-peptide ELISA and an Apoptosis test. With the Mercodia Ultrasensitive C-peptide ELISA. We can see if the PSCs can improve the β cells by how much β cells will secrete insulin. With this, you can have different control groups with different percentages of PSCs with the β cells. For the Apoptosis test, we have the β cells together with the PSCs cells and have control groups with the same different percentages we use in the Elisa to measure the cell deaths of the β cells with the different amounts of PSCs. To see if the amount of Psc can help cause less death to the β cells.

Results:
Further data is to be collected, based on what we know and the information we do have. We do expect the higher percentage of PSCs with the β cells should improve the β cell's secretion of insulin as well as lessen the death of the cells.

Conclusion:
Eliza's kits shows with beta cells that have 10 percent of PSC produces more insulin contact than 1% 5% and beta cells by themselves. We infer higher percentage PSC help beta cells insulin contact more than lower PSC.

ABSTRACT #9

The Migration of Mature Microglia into NPC Organoid Models

Safa Bahadur, Cleveland School of Science and Medicine; Ya Chen, Anthony Wynshaw-Boris, Department of Genetics and Genome Sciences, Case Western Reserve University

Background:
Microglia (MG), a type of glial cell is the main form of immune defense for the central nervous system, making them an essential component of the brain as they aid in the preservation of neurons and protect the brain from infections. Neuron progenitor cell (NPC) organoids, miniature versions of the brain that mimic its key functions and structure, are helpful in precisely modeling neurological diseases. In vivo during embryonic development, microglia migrate into the developing brain after originating from myeloid progenitor cells in the yolk sac. While prior research had cultured progenitor microglia and NPC simultaneously to develop an advanced organoid model, our study intends to provide an alternative approach that cultures them separately in a natural environment. Due to the preliminary nature of our data, further research is recommended.

Goals:
Our objective is to create brain models that imitate the human organ more precisely. To achieve this, we aim to monitor the migration of mature microglia into the brain organoid, replicating the natural embryonic process. Mature microglia were introduced to NPC organoids to test the natural assimilation of glia into the brain, enabling future comprehensive neurological research.

Methods and Materials:
Several NPC organoids were cultured over 47 days using the Gibco Protocol. On day 48, 2 organoids were designated as control and the 5 experimental organoids were given equal distribution of mature microglia cells. Red Fluorescent Protein (RFP) and Green Fluorescent Protein (GFP), two biological markers were present in the glial cells to help track the location of microglia in the organoids as they were systematically observed at different time points from day 5 to day 17. The 5th experimental organoid was sectioned to confirm thorough microglia migration. When the NPC organoids reached day 65, each organoid received additional media and was kept in the incubator. Epifluorescent microscopy and quantitative analyses were used.

Results:
We expect the results to support that at early time points microglia will gather on the surface of the organoid, and the presence of microglia will be higher inside the organoids later on. Additionally, we anticipate the 5th organoid's sectioning to confirm that the microglia have thoroughly and successfully migrated inside organoids.

Conclusions:
Microglia's integration helps us better understand neurological conditions and diseases. Further research with specific neuronal cells is needed to prove the natural assimilation of microglia into the brain. If additional research is successful, these enhanced brain organoid models will advance studies on major neurological conditions, such as Parkinson's, Alzheimer's, and Autism.

ABSTRACT #10

Investigating the Role of TGFbeta Signaling in GI-cancer through an Informatics-driven Analysis

Nathan Ballman, Shaker Heights High School; Andrew Blum, Division Gastroenterology, Department of Medicine, Case Western Reserve University

Background:
Gastroesophageal cancers, in particular Gastroesophageal adenocarcinomas (GEA) are among the most common and deadly forms of cancer around the world. The Transforming Growth Factor Beta (TGFbeta) signaling pathway is implicated in many cancers as both a tumor suppressor in pre-cancerous cells and as a maintainer of tumor carcinogenesis, allowing for many of the traditional hallmarks of cancer including promotion of growth, evasion of the immune system, and maintenance of cancer stem cells. Our group has shown that TGFbeta is activated in GEA, even at the pre-malignant dysplastic stage of the disease, and so these cancers may be uniquely susceptible to anti-TGFbeta based therapeutics. Since TGFbeta signaling is complex and context specific, affecting each tissue type differently, defining a GEA specific TGFbeta gene signature may ultimately have utility as a biomarker to predict tumor biology or response to therapy.

Goals:
The first aim is to demonstrate that a TGFbeta gene-signature can adequately predict and delineate cancers into groups dependent on TGFb for proliferation or otherwise specific to GEA Secondary aims include defining clinical and molecular trends in GEA as well as prognostic impact based on such classification as described in the first aim.

Methods:
A TGFbeta gene signature was obtained by performing RNAseq using a panel of GEA cell lines selecting genes with increased expression following TGFB1 ligand treatment. The resulting 26 gene signature was then applied to perform hierarchical clustering on mRNA expression profiles from 498 cancer samples collected by the TCGA including both Esophageal adenocarcinoma (EAC) and Stomach Adenocarcinoma samples (STAD) to separate the samples into a TGFbeta-gene-signature-low group and a TGFbeta-gene-signature-high group. After which characterization of both groups was performed. Among the analyzed data was survival time, prevalence of co-occurring mutation, histologic grade, as well as Gene Set Enrichment Analysis (GSEA) and Gene Ontology (GO) profiling.

Results:
The gene list derived from cell lines shows differences in prognosis (the TGFbeta gene-signature high groups had an increased rate of mortality), and GSEA profiling. The gene signature also predicted mutations in the TGFbeta pathway with high accuracy.

Conclusions:
This approach has been validated in GEA as similarly effective to prior approaches in detecting classical results. As such targets on this list may be candidates for future therapeutic agents.

ABSTRACT #11

Evaluating barber education pre and post-surveys to understand what training has taught barbers

Alahna Banks, Campus International High School; Kristina Austin, Rebecca Miller, Sydney Evans, Calvin Tornes, Erika Trapl, Department of Population and Quantitative Health Sciences, Case Western Reserve University

Background:
Prostate cancer is the leading cancer diagnosis among African American/Black men in the US and the second leading cause of cancer-related death (ACS Medical Content and News Staff, 2022). It is one of the most common cancers among the male population and occurs more frequently in AA men compared to White and Asian men. The goal of The Cleveland African American Prostate Cancer Project (CAAPP) is to understand more about the barber education sessions, as its purpose is to develop and implement an education program for barbers to support conversations with their clients and educate them about the importance of prostate cancer screening. The training is also being used to increase barber knowledge about the prostate, prostate cancer screening, and prostate cancer disparities. In addition, CAAPP captured the type of information barbers retained from the training and how they inform their clients about the importance of prostate cancer screening. However barber training is only one part of CAAPP, as CAAPP also organizes outreach events to inform males about prostate cancer along with getting them screened.

Goals:
To understand what barbers have learned from CAAPP's barber education training compared to what they already knew using Pre & Post surveys.

Methods:
The pre and post surveys scores were compared to see what the barbers learned about prostate cancer compared to what they already knew. A literature review was conducted with articles from Pubmed, google scholar, the National Library of Medicine, and science direct to understand how barber shops have made so many previous studies successful. Furthermore, the role play that the barbers do in the training provides an overview of how barbers will talk to their clients about prostate cancer. On July 10, 2023, an in person observation of the barber education training was conducted to see how the barbers would react to the education session and observe the full 4 hour session, along with the activities given throughout. After that, I will look at the boosters that happen 2-3 weeks after the training to see what information the barbers retained. The adult learning theory will be researched through Phoenix.edu to see the difference in how adults learn versus how children learn and to compare the methods CAAPP has used to teach their barbers versus other methods they could have used. By doing this, a comparison can be made between the most effective approaches.

Results:
The Pre & Post surveys taken by CAAPP barbers show that while many men got most answers correct there were still a few who got them wrong during the pre survey. During the post-survey, they received after the training some people's answers changed which led to them getting it correct but, some people who got it correct in the pre-survey got it wrong on the post-survey. This shows that though the training was effective, but some barbers may have forgotten material or simply made an error while filling out the post-survey. The reason many researchers have chosen to use barbers in their studies is because of the relationships that the barbers have with their clients and the community. The education session involves a role play, which is used in the training to help prepare the barbers on how they will talk about prostate cancer with their clients. The training on July 10th showed that barbers have learned an abundance of information from the training, as they had a lot of questions that were answered to the best of our navigators' abilities.

ABSTRACT #11 CONTINUED

Conclusions:

There isn't a lot of public information on the effectiveness of training like CAAPP's. Nonetheless, the current research suggests that barbershops and salons are places that have helped in disseminating health-related information. Other studies, including CAAPP, have been successful in the usage of barbershops and salons. CAAPP usage of barbers to get men screened, has been a great resource to the community and provides additional opportunities for outreach. When people go to barbers they trust their barber so, when they bring up a serious topic they are more likely to listen and take it seriously. The training isn't only to tell others about Prostate cancer, it also informs the barbers right along with the client, as many barbers walk out of the training knowing 10x more than what they knew walking into the training.

ABSTRACT #12

Evaluating the Role of Dietary Inflammation in Aviator Cognitive and Physical Fatigue over Time

Tommy Blossom, University School; Elizabeth Damato, Michael Decker, Department of Physiology and Biophysics, Case Western Reserve University

Background:
Aviators who are exposed to multiple long duration, high altitude military flights ("sorties") have been found to experience cognitive fatigue post-sortie. This cognitive fatigue poses a threat to aviator safety and performance. Increased levels of proinflammatory cytokines have shown a correlation to greater cognitive fatigue levels. Various outside factors such as sleep or diet could also have an effect on this cognitive fatigue or these proinflammatory cytokines. 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 and various factors that could affect this response.

Goals:
The goal of this analysis is to examine factors that contribute to increased levels of daily dietary fluctuations and their relation to cognitive fatigue.

Methods: Aviators (n = 28) were assessed 12 times over a two week period (Starting Sunday, excluding Saturday) in which they had regularly scheduled sorties. The assessment included a 24-hour diet recall and a self-administered five-category multidimensional fatigue index (MFI) test. Aspects of the fatigue levels test were examined to look for relationships with dietary inflammation scores (DIS). These scores were obtained using each dietary component's calculated weight based on their strength of association with proinflammatory biomarkers. Scores are summed using each component's weight and can be negative (anti-inflammatory) or positive (pro-inflammatory).

Results:
Aviators were analyzed separately based on week (1 and 2). No significant differences in inflammatory diet scores were found when comparing to perceived general fatigue scores for either week. Also, there were no significant differences between perceived physical fatigue scores and dietary inflammation scores for either week.

Conclusion:
The analysis found no significant relationship between perceived general fatigue or physical fatigue and diet inflammation scores over week 1 and week 2. However, physical fatigue averages trended upward over the two week period. Also, on various data points, lower DIS scores showed lower levels of physical fatigue (Day 10), and higher DIS scores showed higher levels of physical fatigue (Day 4). This suggests that further interrogation of the study could reveal significant relationships between this dietary inflammation and fatigue.

ABSTRACT #13

Examining Mutational Profiles of COVID Strains Using Publicly Available Data

Ava Bribriesco, Shaker Heights High School; E. Ricky Chan, Department of Population and Quantitative Health Sciences, Case Western Reserve University

Background:
In 2019, the first infection of COVID-19 was reported in Wuhan, China. Throughout the next few years, a worldwide pandemic affected billions of people. During this time, COVID infections were reported to public repositories such as NCBI, NextStrain, and GISAID by generating a consensus sequence which represented the major strain of the virus, and often disregarded the possibility of minor strains or sequence variability in the infection. This legacy method of reporting originated due to limited technology, but with the advent of next-generation sequencing, strain profiles can be examined in much more depth than ever before. Deep sequencing of samples from COVID infected individuals have revealed extensive variability in allele frequencies across multiple positions along the viral genome which supports the idea that infections are complex in composition. In order to compare, contrast, and properly describe the complex nature of patient samples to known major strain lineages reported in the database, a comprehensive analysis of the available data is crucial to establish the profile of these major strain lineages across geography and time.

Goals:
To examine the genomic sequences of the COVID virus using publicly available data to generate mutational profiles for each of the major COVID lineages across geography and time.

Materials and Methods:
The full global data set for COVID was downloaded from NextStrain, a publicly available repository for COVID sequences and sample metadata. This site provides regularly updated data on COVID lineages with respect to location distribution, chronological surveillance, and mutations within the genome of COVID. Over 7.7 million viruses have been deposited at the time of download early June 2023. To process the data, a combination of Unix command line functions and custom python scripts were written using VSCode IDE. The frequency of each mutation along the genome was calculated for every lineage reported. The NextStrain data uses the Wuhan reference genome and all positions and reported mutations are in the context of the Wuhan genome. The data was further examined and broken down by geographical location as well as date of sample collection. Positions where the mutation frequency was greater than 5% were implemented for the final analysis. Parsed data were visualized using ClustVis and RAWGraphs.

Results:
A total of 7,778,511 viruses were examined from NextStrain. We identified 28,735 different mutations across 20,572 unique positions (certain positions had different mutations). With the COVID genome length of 29.9kb this suggests that mutations have been observed in nearly ⅔ of the genome. For the scope of this study we focused on only positions in which the mutation frequency exceeded 5% in any given strain as we wanted to focus on the major signature for each lineage. This is not to suggest that positions that are currently less than 5% are not important or that they may not at some point reach a higher frequency. We also observe shifts in the mutation frequency over time for each lineage suggesting that lineage profiles change during the course of the pandemic. Our results also show the distribution of mutations across geography and time.

Conclusions:
COVID is a complex virus, and the description of profiles for strains are more complicated than traditionally reported. With data collected from publicly available sites, we have generated a comprehensive picture of the major lineages that have been described. This profile will be used to help accurately describe the complex nature of infections that we currently observe in patient samples and potentially help us anticipate future variants of concern as well as provide insight as to how mutations arise and propagate through the course of a pandemic.

ABSTRACT #14

Investigating BIRC3 Signaling in Various Cancers

Cara Castro, Hathaway Brown; Claire Fritz, Akshaya Radhakrishna, Dan Feinberg, Reshmi Parameswaran, Department of Pathology, Case Western Reserve University School of Medicine

Background:
The BIRC3 protein is a part of the inhibitors of apoptosis (IAP) family, which help with regulation in various signaling pathways and controlling cell survival. These IAPs play a role in anti-apoptotic mechanisms that can lead to uncontrolled proliferation, the growth of cancer, and resistance toward therapies. Demonstrated through the limited resources on BIRC3 in cancer, it has been proven that BIRC3 affects different cancers in different ways. In glioblastoma multiforme (GBM), if there are high levels of BIRC3 then the cancer is more radio and chemo resistant, however, this is not always the case. In chronic lymphocytic lymphoma (CLL), low BIRC3 mRNA expression has shown to increase CLL disease progression. BIRC3 is a part of the non-canonical NFκB pathway, which helps the cell to grow and develop.

Goals:
The goal of the project is to determine how different cancers utilize BIRC3 signaling, so that therapeutics related to the BIRC3 pathway can be developed in the future to curb cancer growth.

Materials and Methods:
The cell lines Jeko (mantle cell lymphoma), Raji (Burkitts lymphoma), Mino (mantle cell lymphoma), PGA (CLL), Mec (CLL), and RS411 (Acute lymphoblastic leukemia) were used. These cells were cultured in media containing RPMI with 10% FBS and 1% P/S. The cells were kept at 500,000 cells/mL and kept in an incubator at 37ºC. The cells were plated on a 6 well plate with the conditions of no treatment and BAFF. The treatment stayed in the cells for 14-16 hrs and were used to make lysates, along with RIPA and protease inhibitors. A BCA was done to determine the concentration of the lysate samples. The samples were placed in a 10% acrylamide gel to go through electrophoresis. The proteins in the gel were transferred to a PVDF membrane. The membrane was put in the primaries of BIRC3, GAPDH, and p100/p52, and their corresponding HRP- conjugated secondary antibodies (anti-rabbit or anti-mouse). The different conditions were developed using the ECL reagent and imaged on the Chemidoc.

Results:
In the Raji cells, both the untreated and BAFF treated samples displayed similar expression in BIRC3. In the Jeko cells, the untreated samples showed no expression of BIRC3, while the BAFF treated samples had some expression.

Conclusion:
Determining the ways in which BIRC3 signals differ in various cancers will help in the process of developing new therapies in future studies.

ABSTRACT #15

Elucidating the structure of biomarker LW-1

Anjali Chepyala, Orange High School; Deepitha Nelson, Vincent Monnier, Department of Pathology, Department of Biochemistry, Case Western Reserve University

Background:
AGEs, or advanced glycation end products, are formed by non-enzymatic reactions between reducing sugars and amino acids or proteins. Able to accumulate in tissues and organs, AGEs have been correlated with various diseases, such as polycystic ovary syndrome, cardiovascular disease, schizophrenia, cancer, and more. LW-1, a type of AGE, is a collagen-linked fluorophore whose levels increase with age, diabetes, and end-stage renal disease. LW-1 correlates with the long term progression of microvascular disease and subclinical cardiovascular disease, such as the thickening of the carotid in type 1 diabetes. Despite this, very little is known about the molecular structure of LW-1. Therefore, it is of extreme importance to continue research into elucidating the chemical structure of the compound.

Goals:
To extract and highly purify LW-1 from collagen samples and to elucidate the chemical structure of LW-1.

Materials and Methods:
This experiment was conducted using 150 grams of collagen samples from 14 diabetic and cardiovascular diseased patients. Multiple enzymes were used to break down the collagen at specific temperatures, and the digest was then filtered using 0.45 um filters. The digest was then acidified and passed through a glass column packed with TC18 resin. Fractions were eluted and desalted, then passed through an HPLC (high performance liquid chromatography). The fractions were then tested for fluorescence and absorbance at a certain wavelength. Fractions that tested positively (peaking at the specific wavelength) were separated, then passed through the HPLC again to purify it further. Most reactive fractions were once again separated, and then freeze dried.

Results:
Currently, LW-1 has been extracted and purified through the methods mentioned above. However, due to the ongoing nature of the experiment, the chemical structure of LW-1 has yet to be encountered.

Conclusions:
Based on prior data, we can conclude that LW-1, like other AGEs, has a lysine residue in an aromatic ring coupled to a sugar molecule. Additionally, LW-1 has been established as a glucuronide, which is a substance produced when glucuronic acid is linked to another substance with a glycosidic bond. We also expect LW-1 to have a molecular weight of 623.3 DA, as established in former experiments. Further studies are needed to elucidate the molecular origin of the compound.

ABSTRACT #16

Development of Pre-clinical Assays for Quality Control of Cancer Imaging Agents

Ashley Chu, Hathaway Brown; Kathleen Molyneaux, Susann Brady-Kalnay, Department of Molecular Biology and Microbiology, Case Western Reserve University School of Medicine

Background:
Glioblastoma is the most common primary brain tumor, with an average survival rate of 14.6 months after treatment. Prior research has shown that a protein, PTPμ, is cleaved in tumor tissue, and the fragments are very abundant, allowing them to serve as a tumor biomarker. PTPμ, a receptor protein tyrosine phosphatase, acts as a homophilic cell adhesion molecule (CAM) and an enzyme. This cleavage causes the glioblastoma to rapidly migrate and proliferate, making it difficult for surgeons to fully resect the tumor. Peptides derived from a short portion of PTPμ's amino acid sequence are thought to bind to the fragments. By conjugating these peptides into fluorophores, surgeons can better easily find what they need to resect.

Goal:
The goal of this study is to identify a way to detect peptide interactions with PTPμ in hopes to improve imaging agents for glioblastoma resection.

Materials and Methods:
An in vitro bead aggregation assay was used to evaluate the effect of certain buffers and peptides on PTPμ aggregation. Each buffer was diluted to a final concentration of 0.01% Tween, a detergent used to prevent non-specific sticking of the beads to each other or the plastic. Protein G MonoMag beads were coated with the extracellular domain of PTPμ (PTPμ_fc), diluted in the appropriate buffer, and added to a 48 well plate with the peptides being tested. The fc domain of the PTPμ is able to bind to the Protein G, allowing for the beads to aggregate when rotated on the orbital shaker for 30 minutes at 150 rpm. 20x images of each well were taken both after the bead preparation and aggregation (T0 and T30). By putting these images into ImageJ, we were able to quantitate the number and average size of the aggregates. Due to the lack of peptide effects on aggregation, we have moved onto a fluorescent bead binding assay to determine peptides' ability to bind to PTPμ_fc coated beads.

Results:
Of the four buffers being tested (Grace's Media, DMEM, HBS, and PBS), Grace's Media produced the fewest but largest aggregates. This indicates that the beads in that buffer are further along in the aggregation process compared to those in buffers such as HBS with a greater number of small aggregates. We are yet to see a significant effect of the peptides in the bead aggregation assay, but there is a potential trend where meglumine increases the number of aggregates, maintaining a similar size. Results from the fluorescent bead binding assay show that SBK4 has a strong affinity to PTPμ_fc coated beads.

Conclusion:
The results of this assay suggest that there is a possible effect of meglumine on the increase in number of aggregates. Further experimentation is needed to be able to confidently conclude its effects on aggregation. Grace's Media induces the best aggregation whereas HBS induces poor aggregation. Using the fluorescent bead binding assay, SBK4 has been shown to have a strong binding signal to PTPμ_fc coated beads. The results of this assay may contribute to determining which peptides will be best to improve clinical imaging agents.

ABSTRACT #17

Live Cell Imaging to Target Drug Resistance in Cancer

Jack D'Cruz, Solon High School; James Ignatz-Hoover, Priyanka Rana, James Driscoll, Department of Medicine, Case Comprehensive Cancer Center, Case Western Reserve University

Background:
Multiple myeloma (MM) is an incurable cancer of malignant plasma cells. These plasma cells secrete huge amounts of monoclonal antibodies, making them highly sensitive to changes in protein homeostasis. The 26S proteasome is a massive holoenzyme consisting of over ninety subunits responsible for the vast majority of protein degradation. Since MM cells secrete vast amounts of immunoglobulins, MM depends heavily on proteasomes for survival. Proteasome inhibitors (PIs), such as FDA-approved bortezomib, inhibit catalytic activity of the proteasome leading to the accumulation of misfolded proteins which promotes stress in the endoplasmic reticulum (ER), triggers the unfolded protein response, and eventually culminates in apoptosis. Most MM patients will receive a PI as part of their chemotherapy. Unfortunately, many patients ultimately develop resistance to PIs and relapse which reduces patient outcomes. Thus, identifying novel actionable therapeutic targets that can prevent or overcome drug resistance is essential for the advancement of MM treatment. Prior studies in the Driscoll lab using clinical datasets suggested PSMC2, a regulatory ATPase correlated with poorer MM patient survival when overexpressed. We hypothesized that increased PSMC2 levels may make MM cells more resistant to PI treatment.

Goals:
Here, we conduct *in vitro* experiments utilizing live-cell imaging to model the effects of PSMC2 on MM response to PI treatment, ER stress induction and cell viability.

Methods and Materials:
Proteasome gene expressions were compared to overall survival data in MM patients from APEX and CoMMpass studies. We then modeled expression of our lead subunit, PSMC2, *in vitro* by overexpression using a third-generation, FLAG-tagged lentivirus, and an empty vector control in ARH-77 and U266 cells. Cells were treated with bortezomib or the ER stress inducer tunicamycin and incubated in the Incucyte live cell imager. Cell viability was assessed over 48h by propidium iodide staining. To determine the effect of PSMC2 overexpression on ER stress, cells were transfected with a baculovirus ER stress reporter and challenged with either bortezomib or tunicamycin and were assessed via flow cytometry.

Results:
Data collected on proteasome genes compared to overall survival in APEX and CoMMpass trials revealed that increased PSMC2, correlated with poorer overall survival in MM patients. Using our *in vitro* model, we show PSMC2 overexpression in MM cell lines increased drug resistance against bortezomib and tunicamycin in cell viability and ER stress assays.

Conclusions:
Our data supports PSMC2 as a negative prognostic biomarker in MM and that it promotes drug resistance. This was supported by large patient data sets and *in vitro* models measuring cell viability and ER stress. With this information, we are led to believe PSMC2 plays a role in MM becoming drug resistant, and that PSMC2 should be a target of future research and drug development.

ABSTRACT #18

TBK1 in Alzheimer's Disease (AD) and Frontal Temporal Dementia (FTD)

Kayla Del Valle, Cleveland School of Science and Medicine; Fengqin Wu, Yubing Lu, Xiongwei Zhu, Department of Pathology, Case Western Reserve University

Background:
Alzheimer's disease is the most common type of dementia and it causes a decrease in a person's memory, thinking, behavior, and social skills over time. This type of dementia can gradually change how a person functions and their ability to live normally. The most common symptom of Alzheimer's disease is memory loss, which is why people with AD tend to be less capable of doing daily activities over time because they forget how to do them. This can be noticed early on if the person has trouble remembering something that has just happened or has been said. AD typically occurs at an older age (65 and up) unlike other types of dementia affecting a person's personality, behavior, and language. FTD can sometimes be misdiagnosed as Alzheimer's disease, which is one thing that makes them comparable. It often begins early in life between the ages of 40 and 65 but can also occur later on like AD. One thing you should know about FTD is that 40% of people with FTD, also have a family history of the condition. This is called familial FTD, also known as fFTD. Both of these conditions are related in themselves and to my project because we are looking at the different types of dementia, the causes, and how we can help people with dementia.

Goals:
From this experiment, we would like to use different methods to help better understand AD as a condition. We will do this by looking at functions of certain genes-specifically TBK1 and its role in AD- and using many more methods.

Materials and Methods:
One method used was IHC staining (Immunohistochemistry). This method requires us to take our samples of tissue sections and process them properly. Each slide of tissue sections has different samples on it that use different antibodies. First we must rehydrate them, then use antigen retrieval if necessary, use primary antibodies, secondary antibodies, PAP Complex, Development, and finally dehydration. I will go more into depth about these steps as I get further into my research. This process takes 2 days, allowing for your slides/tissue to be viewed for years to come. IHC staining allows us to see protein markers, as well as detect antigens. Another method used was Western Blot. This method uses many different buffers and sample preparation which gives us the ability to identify proteins but also knockout cells. Knocking out cells is extremely important as it lets us figure out a genes specific function.

Results:
There is a robust TBK1 expression as detected by TBK1 antibody but low level of TBK1 activation as measured by phospho-TBK1 in the brain. We are still comparing TBK1 and p-TBK1 between AD and control.

Conclusions:
My experiments went extremely well and while I can't say there is anything specific to be taken away from them, I do know how valuable the research is.

ABSTRACT #19

Identifying the Target of Cancer-Targeting Compounds Using a Forward Genetic Screen

Manzili Denis, University School; Matthew Pleshinger, Department of Pharmacology; Ralston Goldfarb, Drew Adams, Department of Genetics and Genome Sciences, Case Western Reserve University

ABSTRACT:

New cancer-killing molecules are constantly being discovered. Some have unique cytotoxic effects yet, these compounds can only be used in a clinical setting if the target is found and its mechanism of action is understood. The purpose of this project is to find compounds with unique toxicity as well as identify their targets. Many compounds can eliminate cancer, yet many do so by attacking common pathways. We can filter out common toxicity mechanisms that can lead to death by adding solutions such as nicotinic acid or using nucleobase rescue which will prevent cell death by certain compounds However, if the addition of a compound still leads to cell death, the compound targeting a potentially unique pathway. By using the Forward Genetic Screen the new pathway can be identified. The Forward Genetic Screen is an unbiased approach in which a compound is added to a hypermutated cell line where surviving cells have a mutation that would cause them to be resistant to the compound. Isolated cell colonies will share mutations in a common target. Through this process of elimination and using the Forward Genetic Screen approach, we can identify unique compounds with interesting mechanisms of action.

ABSTRACT #20

Determining Notch Receptor Regulation of Arterial Reactivity

Solomon Doibo, Shaker Heights High School; Susmita Chakrabarti, Aaron Proweller, Department of Medicine, Case Western Reserve University

Background:
Understanding arterial reactivity, including processes of constriction and dilation, is crucial for comprehending physiological and pathological phenomena related to blood flow, blood pressure, and vascular system function. High blood pressure (or hypertension) is a global health concern associated with severe conditions such as heart disease and stroke, and a heightened state of arterial vasoconstriction characterizes it. While hypertension medications exist, many individuals are unable to achieve blood pressure-lowering goals and further research is necessary to address this issue effectively. The Notch signaling pathway has been implicated in modulating arterial function. The pathway includes membrane-bound ligands interacting with receptors (Notch 1-4) on neighboring cells. Within the arterial wall, the Jagged1 ligand instructs Notch receptors on smooth muscle cells (SMCs) to contract, leading to vessel constriction. However, the specific Notch receptor(s) engaged by Jagged1 is not known.

Goals:
Our study aims to investigate the Notch pathway's molecular mechanisms and its potential role in regulating vasoreactivity and blood pressure. By elucidating the specific molecules and sequential steps involved in this pathway, our overall goal is to lay the foundation for future drug development targeting individuals with high blood pressure. Based on preliminary data from our laboratory, we hypothesize that the Jagged1 ligand specifically stimulates the Notch1 receptor on smooth muscle cells to promote contraction.

Materials and Methods:
To test our hypothesis, we performed *in vitro* Notch ligand induction assays. Briefly, tissue culture plates were seeded with Jagged1 ligand (Fc-J1) or control-only (Fc). Next, aortic SMCs (rat A10 or mouse primary) were layered onto the plates and incubated for 48 hr at 37 C, 5% CO2 followed by SMC harvest and protein isolation. Protein lysates were subjected to Western blotting to measure phosphorylated myosin light chain (P-MLC), the molecular indicator of contracted muscle. To test the requirement of Notch1 for mediating P-MLC production induced by Jagged1, a subset of A10 cells were subjected to siRNA treatment targeting Notch1. Densitometric quantification of relative P-MLC/ Total (T) -MLC levels were performed using Image J software.

Results:
Compared to control Fc, Fc-J1 stimulated A10 SMCs displayed a near 50% increase in P-MLC (n=1). Similarly, Fc-J1 induction of mouse primary aortic SMCs resulted in an approximate 70% enrichment of P-MLC (n=3; p=0.024). Lastly, targeted reduction in Notch1 levels by siRNA (15 nM) treatment achieved nearly 80% loss of Notch1. Experiments to determine P-MLC levels in Notch1-deficient SMCs are in progress using the ligand induction assay.

Conclusions:
The Jagged1 ligand is implicated in promoting the constrictor phenotype in SMCs. Through continued use of the Notch ligand induction assay, we will be able to determine whether Jagged1 requires the Notch1 receptor for its function. Through these efforts, we will continue to gain insight into the molecular mechanisms underlying arterial constriction. We anticipate our findings will contribute to future drug development efforts targeting Jagged1-Notch1 for the treatment of hypertension.

ABSTRACT #21

Characterizing Fascicle Structure of the Laryngeal Nerve at the Single Fiber Level: Advancing Vagus Nerve Stimulation for Enhanced Neuromodulation

Kaitlyn Ernst, Laurel School; Eleana Cintron, Jennifer Coleman, Andrew Shoffstall, Department of Biomedical Engineering, Case Western Reserve University

Background:
Vagus nerve stimulation (VNS) has emerged as a promising neuromodulation therapy for various conditions, including epilepsy, depression, chronic pain, and inflammatory disorders. VNS modulates neural activity by delivering electrical stimuli to the vagus nerve; however, existing VNS techniques do not consider the underlying spatial arrangement of fascicles and fibers during stimulation. The configuration of fibers in relation to organs innervated is unknown, resulting in limited therapeutic efficacy of VNS devices and significant side effects from non-targeted organs. Specifically, unintended stimulation frequently affects adjacent structures in the larynx and induces severe side effects concerning voice production, swallowing, and breathing. By characterizing the neural composition of the laryngeal nerve, with a specific focus on differentiating the superior and recurrent laryngeal nerve, we aim to optimize neuromodulation strategies and minimize complications associated with VNS.

Goals:
The objectives of this project are two-fold: 1) investigate the differences in fascicle composition and architecture between the superior and recurrent laryngeal nerve, and 2) quantify the frequency, diameter, and type of nerve fibers within each fascicle, differentiating between myelinated efferent, myelinated afferent, unmyelinated efferent, and unmyelinated afferent fibers.

Materials and Methods:
Gross samples of laryngeal nerves were obtained from cadavers and then embedded and sectioned for histological analysis. Staining with hematoxylin and eosin (H&E) and myelin basic protein (MBP)/neurofilament (NF) was conducted to visualize the cellular components and myelin sheaths, respectively. A semi-automated, machine-learning-based image analysis program, including fascicle segmentation and axon detection, using QuPath and ImageJ was developed to efficiently analyze gathered slides. Statistical analysis was then performed to determine the significance of the results.

Results:
Experiments in progress, results to be reported.

Conclusion:
Characterizing the neural makeup of the laryngeal nerve and elucidating the differences between the superior and recurrent laryngeal nerve will have significant implications for neuromodulation research. The findings will contribute to the development of refined techniques that selectively target desired neural pathways, reducing the risk of unintended stimulation and improving therapeutic outcomes. Furthermore, the knowledge gained from this research may apply to other branches of the vagus nerve, expanding the scope of future neuromodulation studies.

ABSTRACT #22

The Chemotherapeutic Drug Imatinib Stimulates Release of Interleukin-1β from Neutrophils via a Mechanism Independent of Inflammasomes but Dependent on Lysosomal Disruption

Adam Esa, Saint Edward High School; Brandon A. Miller, Katherine Horan, George Dubyak, Department of Physiology and Biophysics, Case Western Reserve University

Background:
Neutrophils are granulocytic myeloid leukocytes that are important in the body's first line of defense against invasive pathogens: the innate immune system. Inflammation is the result of the immune system to try to combat infections. Myeloid cells within the innate immune system can respond to stimuli through the assembly of oligomeric cytosolic sensor proteins known as inflammasomes. One type of inflammasome within myeloid cells is the nucleotide-binding domain, leucine-rich–containing family, pyrin domain–containing-3 (NLRP3) inflammasome. The NLRP3 inflammasome can be activated in response to a number of stimuli, however, a common theme of activation is a perturbation in cellular homeostasis. These disruptions include, most commonly, potassium efflux, but also other ionic fluxes, mitochondrial dysfunction, and lysosomal damage. Canonically in monocytic myeloid cells, activation of the NLRP3 inflammasome will result in the release of Interleukin-1β (IL-1β) and lytic cell death known as pyroptosis, but neutrophils have been observed to release IL-1β without notable cell lysis in response to NLRP3 activating stimuli. Additionally, the response of neutrophils to lysosome disrupting stimuli has not been fully investigated. Recently, Imatinib, a commonly prescribed chemotherapeutic for myeloid leukemias, has been reported to activate the NLRP3 inflammasome in dendritic cells via lysosomal disruption. As Imatinib is a treatment for myeloid leukemias, we find it prudent to understand how this drug interacts with neutrophils.

Goals:
To characterize the neutrophil response to Imatinib and to determine the role of the NLRP3 inflammasome in IL-1β release.

Materials and Methods:
We used neutrophils isolated from either wildtype mice or mice with genetic knockouts of inflammasome signaling components. Mice were euthanized by CO_2 asphyxiation and processed for removal of their femurs and tibia. Then we extracted neutrophils from the bone marrow using a negative selection kit. After that, we cultured the neutrophils in media and primed the cells with lipopolysaccharide (LPS). We then added any inhibitors if needed and stimulated the cells with ATP as a positive control for NLRP3 inflammasome activation, Leu-Leu-o-Me (LLME) which is known to rapidly disrupt lysosome integrity, or Imatinib. After stimulation, we collected the supernatant to be used for Sandwich IL-1β ELISA, LDH release, and Western blot of inflammasome components.

Results:
Based on our results, Imatinib and LLME are able to stimulate IL-1β secretion and cell lysis, even with the inhibition of the NLRP3 inflammasome and caspase-1. This demonstrates an alternate mechanism of IL-1β secretion in neutrophils that opposes the canonical NLRP3 inflammasome activation by ATP. This data suggests that lysosomal disruption may also lead to granule disruption allowing the neutrophils to release serine proteases into the cytosol to override the need for the NLRP3 inflammasome.

Conclusions:
This research demonstrates how lysosomal disruption in Neutrophils does not activate the NLRP3 inflammasome as previously thought. Fully understanding how drugs such as Imatinib affect inflammation in different myeloid leukocytes will allow for better chemotherapy treatment for diseases such as myeloid leukemia.

ABSTRACT #23

Chronic differential expression of metabolic genes in the brain after mild traumatic brain injury

Adora Ezepue, The Ohio State University; Kate Lindley, Harrisburg Academy; Samyuktha Lyer, Edwin Vázquez-Rosa, Kalyani Chaubey, Sarah Barker, Coral Cintrón-Pérez, Youngmin Yu, Jiwon Hyung, Louis Stokes Cleveland VA Medical Center, Harrington Discovery Institute, University Hospitals Cleveland, Institute for Transformative Molecular Medicine, School of Medicine; Daniel Gordon, Joseph Ives, Minseo Yang, Kevin J. O'Donovan, Reed Dolph, Department of Chemistry and Life Science, United States Military Academy; Jennifer Garbarino, Noori Sotudeh, AtlasXomics; Andrew A. Pieper, Department of Psychiatry, Case Western Reserve University

Abstract:

Approximately 2 million patients are diagnosed with traumatic brain injury (TBI) every year in the United States. Most of these cases are mild TBI and characterized by relatively rapid recovery of acute symptoms. However, damage after mild TBI frequently continues to evolve into a chronic neurodegenerative condition that can last the lifetime of the patient. This places patients are at significant risk of developing later complications, including increased risk of developing neurodegenerative diseases of aging (i.e. Alzheimer's disease and Parkinson's disease). However, the underlying basis for this conversion of acute injury to chronic neurodegeneration is not known. In our laboratory, we are investigating the chronic consequences of mild multimodal TBI (mmTBI) using an overpressure chamber that generates a precisely calibrated and readily reproducible mixture of global concussion, acceleration / deceleration, and early blast wave exposure. Mice exposed to this injury develop progressive and chronic cognitive impairment associated with axonal degeneration, DNA damage, oxidative stress, and microglial lipid droplet accumulation, as well as peripheral metabolic changes similar to human TBI. Here, we report the results of high spatial resolution analysis of chronic changes in chromatin accessibility after mmTBI. Applying deterministic barcoding in tissue with spatial omics sequencing (DBiT-seq) to brain tissue from mice 12 months after mmTBI reveals altered expression of genes associated with metabolic impairment. This provides new insight into the underlying basis for chronic impairment after mild TBI.

ABSTRACT #24

Raw Cell Stimulation for Immunofluorescent Staining

Luke Feran, Saint Edward High School, Blake McCourt, Aaron Burberry, Department of Pathology, Case Western Reserve University

Background:

Amyotrophic Lateral Sclerosis (ALS) is a neurodegenerative disease that hinders movements and leads to paralysis and death. ALS primarily affects motor neurons in the brain and the spinal cord. Although patients diagnosed with ALS sometimes have no family history of the disease, in about ten percent of cases the people have a mutation in *Chromosome 9 Open Reading Frame 72* (*C9ORF72*). The *C9ORF72* mutation may cause motor neuron loss because of toxic proteins made from the mutation or reduction of the C9ORF72 protein itself. The C9ORF72 protein works in macrophages to control movement of CD80, another protein that activates T cells which can lead to autoimmune diseases that also occur in some ALS patients. Here I study macrophages with loss of *C9ORF72* to see where CD80 exists in the cells using markers of lysosomes, endosomes, and plasma membrane.

The purpose of this experiment is to elicit an immune response in the cells and observe the cells under such conditions. We use the toll like receptor 2 (Tlr2) activator Pam3csk4 (synthetic triacylated lipopeptide) at 1000 ng/mL which is a saturating concentration for overnight stimulation.

Goals:

The goal of this experiment is to move various antigens including CD80 into Raw 264.7 cells that had *C9ORF72* mutations induced by CRISPR/Cas9 surfaces by eliciting a Tlr2 immune response. The antibodies to be used are purified anti-mouse CD80, purified anti-mouse CD107a (LAMP-1; lysosome), biotin anti-mouse CD-14 (plasma membrane), and purified anti-mouse CD68(endosome). Prior to stimulation with Pam3csk4 acting as a pro-inflammatory transcription factor activator, the Raw 264.7 cells will be cultured in DMEM media for approximately two weeks.

Methods:

Raw Cells were plated and incubated overnight in DMEM. Cells were harvested, then replated with select antibodies, then analyzed by immunofluorescence for CD-14 and CD-68 location.

Results and Conclusions:

I was able to see CD-14 and CD-68 staining of stimulated Raw 264.7 cells. The location of this marker was consistent with where lysosomes are expected to be within cells. In the future, I could change the amount of time the cells are cultured for to try and improve the staining. I could also test different antigens such as CD-80 to assess receptor-building biology relevant to ALS.

ABSTRACT #25

Correlating Ferroptosis-Inducing Drug Responses to Osteosarcoma Subtypes

Brenden Fernandes, Solon High School; Yaw Asante, Berkley Gryder, Department of Genetics and Genome Sciences, Case Western Reserve University

Background:
Ferroptosis is a type of regulated cell death characterized by the buildup of reactive oxygen species and their pernicious interactions with polyunsaturated fatty acids. Although a newly uncovered mechanism, ferroptosis has gained attention for its potential as a promising pathway towards treating cancers such as Osteosarcoma (OS). OS is the most widespread bone cancer that primarily affects children, teenagers, and young adults. Therapeutically serving patients has been challenging, so a viable option is needed to treat those with a poor prognosis.

Goals:
The objective of this study is to identify the correlation between the expression of key genes, notably RUNX2 and FOSL1, in OS and the cell line's susceptibility to ferroptosis-inducing drugs (FIDs) including Erastin, Methotrexate, and Salinomycin. By doing so, we aim to determine how to effectively exploit ferroptotic vulnerabilities when treating subtypes of this cancer.

Materials and Methods:
We used public data from Broad Institute's DepMap to examine the trend between gene expression levels in OS tumors and cell lines and their sensitivity to different FIDs.

Results:
Our findings revealed an inverse relationship between expression levels of RUNX2 and OS cancer cells' sensitivity to Salinomycin and Erastin. On the contrary, Methotrexate exhibited the opposite pattern. Consequently, we compared the properties of these drugs to propose potential reasons for these trends.

Conclusions:
The data suggest that OS cancer cell lines can be subcategorized based on gene expression as well as by their differing responses to ferroptosis inducers. RUNX2 appears to be the more aggressive subtype and generally corresponds to a worse patient prognosis. Furthermore, we concluded that a decrease in RUNX2 expression level leads to weaker cellular responses to DNA damage and may result in a reduced chance of metastasis. Additional work is necessary to figure out if certain transcriptomic profiles are associated with an increased response to FIDs, which would suggest new approaches for chemotherapeutic regimens against this disease.

ABSTRACT #26

Effect of receptor protein tyrosine phosphatase γ on phosphorylation of epidermal growth factor receptor 1

Fahness L. Freeman, Cleveland Heights High School; Fraser J. Moss, Eva Gilker, Walter F. Boron, Department of Physiology and Biophysics, Case Western Reserve University School of Medicine

Background:
Phosphorylation is a post-translational modification (PTM) in which a kinase adds a phosphate group to a protein. Dephosphorylation is the removal of the phosphate group and is done by phosphatases. These two processes allow cells to transmit and amplify signals, triggering various responses including gene expression and cell growth. Acid-base homeostasis is the regulation of the body's pH. The CO_2/HCO_3^- system is the major contributor to acid-base balance, in which the lungs are responsible for CO_2 concentration in the blood and the kidneys are responsible for HCO_3^- concentration in the blood. Previous evidence suggests that receptor tyrosine phosphatase gamma (RPTPγ) functions as a sensor of CO_2 and HCO_3^-, and is capable of initiating signaling pathways involved in acid-base homeostasis through its role of dephosphorylating tyrosine residues on other protein targets. One potential target of RPTPγ is epidermal growth factor receptor 1 (ErbB1), which is a receptor tyrosine kinase.

Goals:
The goal of this study is to determine how to presence of RPTPγ affects the phosphorylation status of ErbB1. We hypothesize that RPTPγ will interact with and dephosphorylate ErbB1 at Tyr1172.
Methods: To accomplish this, we transiently transfected Human Embryonic Kidney (HEK) cells with the DNA of ErbB1 conjugated to a Citrine fluorophore (ErbB1Cit), or ErbB1Cit plus RPTPγ conjugated to an Aquamarine fluorophore (RPTPγAqua). We then treated the cells with media that contained (1) epidermal growth factor (EGF), which is an agonist of ErbB1 (2) PD168393, which is an inhibitor of ErbB1, or (3) no additives for 20 minutes. After fixing the cells, they were stained with an antibody against pTyr1172-ErbB1.

Results:
Results showed that treatment with PD168393 decreased the amount of phosphorylated ErbB1, while ErbB1Cit dishes treated with EGF or regular media showed no difference in phosphorylated Try1172. In the dish that contained ErbB1Cit and RPTPγAqua, treated with regular media, we observed that increased amounts of RPTPγ expression led to decreased amounts of phosphorylated ErbB1.

Conclusions:
This work demonstrates that RPTPγ is either directly or indirectly dephosphorylating ErbB1 at Try1172, and it will be interesting to see how the phosphorylation of ErbB1 is altered during different acid-base conditions.

ABSTRACT #27

Plasmid synthesis from bacteria for DNA nanostructure production

Isaiah Gilbert, University School; Divita Mathur, Department of Chemistry, Case Western Reserve University

DNA origami is a nanotechnology that utilizes the principles of base pairing in DNA molecules to create intricate and precise nanostructures. DNA origami allows for the incorporation of various functional elements, such as proteins, nanoparticles, or chemical groups, to give the finished structures specific properties and/or functionalities. The overall aim for this project is to create DNA origami. The way that this would be done is to first create purified plasmids from bacteria samples, and then utilize these purified plasmids in order to make our DNA origami. The bacteria will initially be taken from a smaller sample and placed into growth media and incubated overnight to grow the sample. Plasmid purification will then be conducted by using a miniprep kit. Then, these plasmids will be used in the process of making DNA origami. The procedure was successful in the creation of DNA origami for later research. In conclusion, our procedure was successful as we did make DNA origami. This research's community impact is large as it impacts the field of cancer research, potentially giving us access to a safe drug delivery system and to reducing the side effects of chemotherapy, thus making cancer treatment a safer and smoother process all around. This means that not only would DNA origami be impacting the field of cancer research, but also the field of medicine as a whole due to its capability to be a new drug delivery system.

ABSTRACT #28

Administration of CDDO 2P-Im suppresses the invasion and migration of Diffuse intrinsic pontine glioma (DIPG)

Hanna Goje, Hathaway Brown; John Letterio, Department of Pediatrics, University Hospitals Cleveland, Case Western Reserve University

Background:

Diffuse intrinsic pontine glioma (DIPG) is a high-grade pediatric glioma; DIPG cells have a limited response to radiation therapy and are inoperable due to their location in the brain stem. When DIPG is exposed to radiation it activates chemokine or CCL2 which has a key role in radiation induced inflammation; the inflammation and recruitment of microglia and macrophages helps its growth and its resistance to radiation. CDDO-2p-Im. This synthetic oleanane triterpenoid (SOT) is known as CDDO-2P-Im or '2P-Im'. 2P-Im is an orally administered drug that has the potential to enhance the radiation response of DIPG and to suppress the activation of macrophages and microglia, through suppression of CCL2 production.

Goals:

The goal of these experiments is to test the potential dose dependent effect of CDDO-2P-Im on DIPG cell migration. With the drug's ability to cross the blood brain barrier (BBB) 2P-Im would be a new treatment alongside the standard care for DIPG. In order to investigate the anticancer properties and the dose dependency of this drug, we conducted a scratch assay with multiple doses to observe the drug's effect on migration. We tested with doses 12.5nM, 25nM, 50nM, 100nM, 150nM, and a control. The 150nM dose lowered the wound closure percentage by 16.4%.

Materials and Methods:

Cells were incubated in 12-well plates with media then incubated for 24 hours until confluent. Once confluency was reached the cell layer was scratched with a pipette tip in four straight perpendicular lines. Then the media was removed and the plates were next gently washed with phosphate-buffered saline (PBS) to get rid of any floating cells and debris, then the cells got more media. Cells were imaged using *Keyence BZ-X810, a fluorescent microscope* and incubated for 24 hours. A photo was taken of the cells and then they were incubated. Photos were taken every 24 hours and incubated in between to see migration.

Results:

The administration of 2P-Im greatly reduced the migration of DIPG in the wells, at its highest the wound closure percentage dropped from 27.60% to 11.20%.The next step for this drug would be for it to be tested in clinical trials.

Conclusions:

The data support the hypothesis that the administration of 2P-Im inhibits invasion and migration of Diffuse Intrinsic Pontine Glioma also known as DIPG.

ABSTRACT #29

Improvement of in Vitro Nanobubble Imaging Techniques and Determination of the Stability of Nanobubble-labeled T-cells

Philip Golczak, Mayfield High School; Dorian Durig, Agata Exner, Department of Radiology, Case Western Reserve University

Background:

Immunotherapies such as CAR-T cell and TCR-T Cell therapy are widely used to treat blood cancers (e.g. Acute B lymphocytic leukemia). However, there are limitations to this treatment such as reduced efficacy in solid tumors due to the acidic tumor microenvironment causing T-cell exhaustion. Additionally, neurotoxicity and on-target-off-tumor toxicity, are conditions caused by the improper targeting of tissues by CAR-T cells and their movement throughout the body which can pose a major risk to patient health. Thus, it is vital to monitor the traffic of CAR-T cells within the body, enabling a better understanding of their behavior in proximity to solid tumors as well as CAR-T Cell congregation in the body due to improper targeting. Labeling the cells with ultrasound contrast agents such as nanobubbles (NBs) may be an effective method to locate and track the CAR-T cells. NBs consist of an inert gas core encapsulated by lipids, polymers, or proteins. Notably, due to the ultrasound wave the NB experiences areas of low and high pressure causing the gas core to expand and contract stretching the flexible shell and producing nonlinear resonance echos due to the NB's oscillation allowing them to appear brightly on ultrasound imaging. Additionally, due to their small size (~290nm), they are uptaken by CAR-T cells, thus labeling them and making them visible on ultrasound(1). However, the stability of NBs in labeled T-cells in vivo remains unknown and could affect the viability of NB-labeling as a method of tracing T-cells throughout the body. Furthermore, many in vitro imaging techniques are unreliable and provide unclear images, making it more challenging for physicians and researchers to determine whether the T-cells are labeled.In our study, we aim to observe the contrast of NB- labeled T- cells using ultrasound imaging at various incubation periods, in order to replicate in vivo temperature conditions. Additionally, these T-cells will be imaged in vitro using an agarose solution poured into a custom mold designed to minimize noise and provide for clear and consistent imaging.

Goals:

Determine the stability of NBs in labeled T-cells after various incubation periods, which simulate body temperature conditions. Additionally, we aim to evaluate a custom mold that is easily manipulated and provides clear images. This will enable improved visualization and enhance the ability of researchers and physicians to accurately determine the presence of labeled T-cells.

Materials and Methods:

T-cells were thawed and added to complete media consisting of RPMI media, 10% FBS, and 1% Pen strep. Then they were centrifuged and once the supernatant was removed, incomplete RPMI media was added and the cells were counted. The cells were then resuspended in incomplete RPMI media for a concentration of 5 million cells per mL and a total of 20 million cells. Next, the 4mL of cell solution was added to a falcon tube, and 444 uL of NBs were added for a concentration of 10000 NBs per cell. The T-cells were labeled with NBs consisting of a C_3F_8 gas core and lipid shells consisting of DPPA, DPPE, DBPC, and DSPE-mPEG2K. The NBs were activated through mechanical agitation using a Vialmix shaker and separated from microbubbles (MBs) through centrifugation. Then 2 mL of the sample were added to 2 wells and were incubated at 37 degrees 5% CO2 for 1 hour being manually shaken every 15 minutes. Immediately after incubation the entirety of the sample was removed from the wells and added back into one tube. Then each well was rinsed with 1ml of incomplete RPMI media which was then added to the same tube as the sample. The sample was then centrifuged and the supernatant was removed and placed into a separate tube. Next, 1mL of complete media along with cytokines was added to the sample to dilute it to 20 million cells per mL. The cells in the sample and supernatant were then counted to verify the count. This was repeated for additional samples which were taken after an extra 30-minute, 1-hour, 2-hour, 4-hour, and 6-hour incubation. For imaging of the T-cell samples, an

ABSTRACT #29 CONTINUED

agarose tissue-mimicking phantom was made from a solution containing 3g of agarose dissolved in 200mL of deionized water which was heated and poured into the custom mold. The samples were imaged on the VisualSonics Vevo-2100 Ultrasound. The 3 wells of the phantom were rinsed with incomplete RPMI media to ensure that no deionized water from storage remained in the wells. The phantom was arranged to the side of the MS250 transducer and the sample was resuspended before addition to each well. The acquisition lasted 300 seconds with the first and last frames of the acquisition being imaged as well. The settings used to image the samples were Contrast mode, Frequency: 18MHz, Power: 4%, Gate: 4, Beam width: wide, Frame Rate: 1, Contrast Gain: 35dB, 2D gain: 18dB, Depth and width: the size of ROI, sensitivity = 1, and Line density = high.

Results:

The agarose gel phantom produces clear images with little noise blocking the view of the labeled T-cells on the Vevo-2100. Further results are pending as a consequence of the ongoing nature of experimentation.

Conclusions:

Conclusions are yet to be made as all testing is still to be finished.

ABSTRACT #30

Microbiome Composition and Fecal Bacteria Contamination of Common Surfaces in the Workplace

Tarini Gowda, Revere High School; Tobi Taylor, Adam Burgener, Department of Pathology, Case Western Reserve University School of Medicine

Background:
The environment is composed of numerous bacteria from various sources; this could include bacteria from human skin, for example, *Staphylococcus* and *Corynebacterium*; Food, for example, *Salmonella*; From water, for example, *Shigella* and *E.coli*; and From soil, for example, *Azotobacter* and *Azospirillum*. As known, our environment contains all kinds of bacteria differing from air to fecal matter. The fecal microbiome is known to be composed of *Clostridium* coccoides, *Bacteroides* fragilis, *Bifidobacterium*, *Prevotella*, *Bacteroides* vulgatus, *Bacteroides* uniformis, *Faecalibacterium* prausnitzii, *Bacteroidetes, Firmicutes*, *Actinobacteria*, *Proteobacteria*, *Fusobacteria*, *Atopobium*, *Eubacterium*, *Ruminococcus*, *Peptococcus*, and *Peptostreptococcus.* The goal of this project is to study the similarities of the fecal microbiome with the microbial composition of the environment and to answer the following questions: Are the bacteria we find present in the feces what we find in our environment? What areas of the environment most correspond with the fecal microbiome and why?

Goals:
To determine which surfaces have the highest bacterial load as measured by raw bacterial 16S rRNA reads. Sub-hypothesis: I expect to find the most fecal bacteria on our chairs, because our bottoms are always in contact with the chair.

Materials & Methods:
Direct analysis using 16S vs. Culturing bacteria
Standard procedure for collecting samples (Look at papers to start)

1. **Wet-dry sample collection procedure:**
    a. **Dry Surface: One swab would be dipped in 1x PBS and streaked across the area for 10 seconds and put into a cryovial; One swab for 16S.**
    b. **Wet Surface: A dry swab would be swabbed across the wet surface for 10 seconds and placed into the cryovial. One swab for 16S.**
    c. **Expected: 1 swab for 16S for each sample.**
2. **Use 16S swab for analysis.**

Results:
The top 10 bacteria found in our samples were Staphylococcus, Corynebacterium, Halomonas, Enhydrobacter aerosaccus, Lawsonella, Streptococcus, Alishewanella, Agathobacter, Escherichia/Shigella, and Lactobacillus. Most of these bacteria are found on human skin and digestive tracts. The rectal swabs are similar to the Lab Coat Person 008, Positive Control Toilet Bowl, Environmental Control 16SBH, IH and Chair Person 002. The rectal swabs are most similar to the 16S Bench and Proteomic Bench.

Conclusion:
After day 5, all the plates had bacteria growing except for the control plates. In conclusion, our phones tend to have a significant presence of bacterial colonies associated with them. This observation raises awareness about the potential for cross-contamination between the fecal microbiome and frequently touched surfaces like phones.

ABSTRACT #31

Modulation of Extracellular matrix proteins by α-Synuclein and the cellular prion protein: Implications for primary open-angle glaucoma

Harper Hammond, Andrews Osborne Academy; Priya Katiyar, Neena Singh, Department of Pathology, Case Western Reserve University

Alpha-synuclein (α-Syn) is implicated in Parkinson's Disease (PD), a neuromotor disorder associated with intracellular aggregation of α-Syn and death of dopaminergic neurons. PD is also associated with visual symptoms, but most remain unexplained. In the brain, dysfunction of α-Syn due to aggregation impairs neuritogenesis by altering the composition of extracellular matrix (ECM) proteins. A similar process in the eye, especially in the trabecular meshwork (TM), could compromise the contractile function of TM cells and impair the outflow pathway of aqueous humor (AH), resulting in increased intraocular pressure (IOP) and primary open-angle glaucoma (POAG). We hypothesize that dysfunction of α-Syn activates the Ras homolog gene family member A (RhoA)-associated coiled-coil containing kinase (ROCK) signaling pathway directly or indirectly, altering the characteristics of ECM proteins in the TM. In previous studies, we reported that the prion protein (PrP^c) regulates the RhoA/ROCK pathway to prevent excess phosphorylation of cofilin as deposition of phospho-cofilin (p-cofilin) impairs the ability of actin filaments to undergo depolymerization. I confirmed this phenomenon further by checking the ratio of p-cofilin and cofilin in the brain tissue of wild-type and PrP^c-knock-out (PrP^c-KO) mice by Western blotting (WB).

To evaluate the role of α-Syn in altering this pathway, we transfected neuroblastoma cells to overexpress either PrP^c or α-Syn, and used the WB technique to detect levels of cofilin, and p-cofilin. The results showed that increased expression of α-Syn increased p-cofilin dramatically. PrP^c-overexpressing cells, on the other hand, showed an increase in cofilin relative to p-cofilin. These results show a novel function of α-Syn in the modulation of ECM proteins. An unexpected finding was that levels of α-Syn were upregulated in PrP^c-KO brain tissue relative to wild-type controls. We are in the process of confirming this result, and whether levels of cofilin and p-cofilin are altered as well. Our research is essential as it could help us develop a preventative medication for POAG with new knowledge of the functions of α-Syn, and it could also possibly be applied to PD treatment. The next steps would be to repeat the experiment in the more delicate TM cells and possibly in living mice and to experiment further to find the exact mechanism by which α-Syn interacts with cofilin and p-cofilin.

ABSTRACT #32

Winding back the epi-TOC: An Analysis of Epigenetic Age and Cancer Incidence Rates

Rohit Jain, Westlake High School; Fredrick Schumacher, Department of Population and Quantitative Health Sciences, Case Western Reserve University

Background:
Cancer incidence varies across organs, thus indicating differences in etiology and exposure impact among different tissues and cell types; for example the lifetime risk of being diagnosed with cancer is 0.6% in the pelvic bone, 1.08% for thyroid, and 6.9% for lung. A major factor underlying cancer incidence is the complex process of aging. Recently, whole-genome methylation has been utilized to develop biological clocks to determine inter-individual aging processes. The second-generation of these biological clocks have focused on better modeling the tissue specific cumulative number of stem cell divisions. As hypothesized, an increase in the stem-cell mitotic replication rate increases the risk for cancer as an indicator of aging, which is supported by work which investigated how the more a cell divides, the higher the likelihood that cell would develop cancer-like abnormalities. However, these biological aging clocks have not been correlated with tissue specific stem-cell mitotic replications rates. The epiTOC (Epigenetic Timer of Cancer) methylation clock can directly estimate the cumulative number of stem cell divisions in a tissue.

Objective:
We aim to examine estimates of tissue specific aging with site-specific cancer incidence rates and evaluate the association between finding the relationship between the calculated epiTOC for a patient's tissue and their cancer incidence.

Methods:
The Cancer Genome Atlas (TCGA) database, containing 10,957 sets of patient data, was sorted into different types of cancer and the stage of cancer at time of diagnosis. Following this part of the research, I assisted in using the R coding language to calculate the epiTOC values for all of the patients, finding the mean to be 43% under the "normal" value when adjusting for age and demographics.

Results:
From the database of 10,000 patients, we were able to find a positive correlation with the epiTOC calculations and the incidence rates, with a linear correlation of around 0.71 [0.54-0.83]. As a result of this process, we found that the largest subgroup of patients were those affected with breast cancer, at 4.8%, and the most prevalent stage of cancer was stage 2 at 35.7%.

Conclusions:
There is a deeper connection between the number of stochastic events in tissues and the incidence of cancer. Models such as epiTOC offer invaluable benefits for furthering research into how we can create new testing to catch cancers quicker in the future and hopefully implement a system where these values can offer physicians a much stronger and effective approach in preventing and dealing with cancers of all types and stages. Furthermore, this research builds on the groundbreaking paper published by Cristian Tomasetti and Bert Vogelstein, "Variation in cancer risk among tissues can be explained by the number of stem cell divisions," which showed a positive correlation in the amount of stem cell divisions and the lifetime risk of cancer by proving the same relationship is true with tangible measurements that can be taken with less invasive methods.

ABSTRACT #33

Racial, Genetic, and Socioeconomic Disparities in Pediatric Acute Lymphoblastic Leukemia (ALL)

Caroline Jang, Orange High School; Jennifer Cullen, Department of Population & Quantitative Health Services, Case Western Reserve University

Background:
Acute lymphoblastic leukemia (ALL), characterized by the overproduction of lymphocytes, is the most common cancer among children and adolescents. While survival rates have improved, disparities persist among different population groups.

Goals:
Our goal was to conduct a systematic review to view how factors such as race/ethnicity, genetics, and socioeconomic status (SES) impact mortality/survival measured in Overall Survival (OS) and event-free survival [EFS] and incidence rates in pediatric ALL.

Materials & Methods:
The database PubMed was utilized to search candidates for relevant studies, with the key phrase, "childhood acute lymphoblastic leukemia and disparities." From these initial candidates, predetermined inclusion and exclusion criteria were applied. Only studies with a pediatric population of ALL that were published within the last twenty years were included (with an exception). The resulting studies focused on potential factors were selected.

Results:
Of the initial 175 candidate articles, 17 were chosen for the review based on the inclusion and exclusion criteria. Many (11 out of 17) studied more than one disparity. Regarding race/ethnicity, non-Hispanic Black (NHB) and Hispanic patients were consistently reported to have inferior OS and EFS rates and higher proportions of relapse in comparison to non-Hispanic Whites (NHW). Hispanic patients additionally suffered higher incidence rates, which has been partly associated with single-nucleotide polymorphisms (SNPs) in their genes. Native Americans were also found to have lower 5-year OS, although data on EFS and incidence rates are lacking. Non-Hispanic Asians (NHA) have been a disputed group, with some sources split between citing similar survival rates or lower survival rates, both compared to NHW patients (although not to the same extent as Hispanic and NHB patients). Patients of a low SES/high-poverty area were reported to have a lower 5-year OS compared to those of a high SES/low-poverty area, as well as a higher proportion of relapses.

Conclusions:
In our study, racial/ethnic diversity was identified as a factor for different ALL outcomes; non-White children generally suffer lower survival rates, higher incidence rates, and higher relapse rates, with varying accounts for NHA. Patients from a lower socioeconomic background and/or high-poverty area also suffered inferior survival rates. Studies focused on Native Americans with pediatric ALL as well as other miscellaneous factors (e.g gender) are needed. This study similarly highlights the need for disease-specialized treatment and the importance of providing access to clinical trials and treatment.

ABSTRACT #34

Blocking the Growth of Metastatic Colorectal Cancer by Targeting the Liver-Cancer Crosstalk

Asha Jha, Shaker Heights High School; Samantha Smith, Izzy Smith, Josh Cabacungan, Rui Wang, Department of Surgery, Case Western Reserve University

Background:
Colorectal Cancer (CRC) is the second leading cause of cancer-related deaths in the U.S. One major factor that makes CRC so deadly is how quickly it spreads from the primary site to other parts of the body, known as metastatic CRC (mCRC) and as such, possess different genetics and phenotype to adapt to the microenvironment. The liver is the most common site of mCRC and has a unique endothelium-rich microenvironment. Recent studies determined that endothelial cells (ECs) in the liver secrete a soluble protein called Leucine Rich Repeats And Immunoglobulin Like Domains 1 (LRG1), which in turn promotes tumor growth by binding and activating with the CRC-associated receptors human epidermal growth factor receptor 3 (HER3). LRG1- and HER3-specific antibodies reduced but did not completely eradicate the growth of CRC tumors. Subsequent analysis revealed that CRC tumors subjected to LRG1-HER3 inhibitions had elevated mitochondrial oxidative phosphorylation (OXPHOS) activities, which is a pro-survival metabolism pathway observed in other types of cancer in the liver.

Goals:
It's hypothesize that elevated OXPHOS activity mediates CRC cell survival even in the presence of HER3 inhibition, thus, combining HER3 and OXPHOS inhibitions may lead to significant anti-tumor effects in CRC liver metastases.The main objective is to see if blocking the metabolic pathway will restrict the growth of CRC tumors completely.

Materials and Methods:
The HCT116 cell line, a human colorectal cancer cell from an adult male, is grown in a 25 cm^2 flask. The cells are split into a T-25, a 10 cm dish, and seeded into a 96-well plate in a 3 x 5, 15 wells, with each column intended for a different treatment: (1) CRC control media, (2) EC control media, (3) EC control media and MM-121, a HER3-specific antibody that has significant on-target effects in human trials, (4) EC control media and Metformin, and (5) EC Control media, MM-121, and Metformin. Then, after incubating it for a day with fresh Dulbecco's Modified Eagle Medium (DMEM) with 5% Fetal bovine serum (FBS), the media in the 96-well is replaced with 1% FBS DMEM, then incubated the cells overnight. Meanwhile, the 10 cm dish's media is also replaced with 1% FBS DMEM and incubated overnight, that way the media can be used as control for the experiment. After that, the 1% media from the 10 cm dish is pipetted into a vial and spun in the centrifuge to separate the liquid from the debris, to which then it's pipetted into the 96-well plate. After incubating the wells for another day, the media is aspirated and each inhibitor is pipetted into their respective columns, and then incubated over the weekend, for 72 hours. Once done, a PicoGreen Assay was done to quantitate how many cells are in each well and compare how each drug did on the cancer cells.

Results:
According to the assay, the treatments with MM121 and Metformin have reduced the cell growth by 80% compared to the control cells growing in plain EC condition media. However, with the treatment that combines both the drugs, there is an even greater reduction, with the graph showing the trend, proving that combining all three agents greatly reduces cancer cell growth.

Conclusion:
Overall, the data showed that the treatment of combining both HER3-specific antibodies and metformin had significant anti-cancer effects, potentially synergistic compared to monotherapies. As both the HER3 antibodies and metformin have been used in human trials for other types of disease, findings suggest the combination of these two drugs as a potential therapy for treating patients with mCRC.

ABSTRACT #35

Comparing Metrics that Measure Variability in the Respiratory Waveform

Adam Kabbara, Saint Edward High School; Caitlin Clifford, Cara Companaro, Rishi R. Dhingra, Frank J. Jacono, Thomas E. Dick, Department of Neurosciences, Case Western Reserve University

Background:
Biological variability is a physiologically relevant signal that has multiple definitions. There are two types of biological variability: Linear and Nonlinear. Linear is identified as being stochastic or random and unpredictable. On the other hand, nonlinear can be time-dependent or chaotic. Thus, biologic variability is not a homogeneous property but complex mix, whose elements are hard to separate. We have developed an analytical tool that measures the nonlinear complexity in variability of the respiratory pattern. We refer to the output of this tool as the nonlinear complexity index (NLCI).

Goals:
I hypothesize Total Variance Index (TVI) tracks the increase in NLCI, e.g., the predictability of the ventilatory waveform. The goal was to analyze the difference in breathing patterns at different hour marks with different doses of Ecoli. Specifically, we used linear cycle-triggered averages to determine the predictability of the breathing waveform.

Methods:
The data were available from the laboratory were recordings of the ventilator wavform obtained using plethysmography. I analyzed these waveforms using commercially available software (Spike 2 & Excel). The brearthing waveforms were obtained from naïve rats, as well as rats with 0, low-, and high-doses of *Escherichia coli* (*E. coli*). Ideally a section of data to analyze should be stationary. Using Spike 2, I marked inspiratory to expiratory phase transitions, and generated cycle-triggered averages of the waveform for 50 breaths. The difference between the standard deviation and the average was normalized and used as an index of total (linear and nonlinear) variance, which I refer to as the total variance index (TVI). The nonlinear complexity index (NLCI) is a statistic that measures the predictability of the ventilator wave form and was provided to me.

Results:
I generated figures showing the relationship of TVI, NLCI and fR to doses of *E. coli* and increasing the duration of infection. In rats with sterile implants (*Ec*0), TVI, NLCI and fR were consistent across time and indistinguishable from naïve rats (Fig 1). In rats given a low dose inoculation (*Ec*25 cfu), TVI remained low, NLCI increased at 6 hrs, and fR was highest at 12 hrs (Fig 2). In rats given a high dose inoculation (*Ec*100 cfu), TVI, NLCI, and fR were highest at 12 hrs (Fig 3). Finally, TVI correlated negatively to NLCI (Fig. 4)

Conclusion:
The goals were fulfilled by analyzing the data of rats at different hours with different doses of *E coli*. The analysis showed no direct correlation of time to NLCI, neither did it show correlation of NLCI to TVI. TVI decreased as NLCI increased, thus we conclude that NLCI and TVI are correlated negatively but the dynamic range of TVI is narrow and the slope is shallow. Furthermore, TVI did not have a strong relationship with time as the data points varied between the similar values across time.

ABSTRACT #36

Cloning, Expression and Characterization of Alkaline Phosphatase in *Escherichia coli* BL21, C+, and Shuffle

Hari Kasi, North Royalton High School; Tae Hun Kim, Department of Biochemistry, Case Western Reserve University

Background:
Alkaline phosphatase, a critical enzyme, is primarily known for its dephosphorylation abilities. By catalyzing the removal of phosphate groups, it plays a central role in numerous essential cellular processes. In the realm of molecular biology, alkaline phosphatase is a powerful tool for dephosphorylation of DNA during cloning, ensuring precise fragment insertion. Within cells, it regulates phosphate levels, influencing metabolism and maintaining homeostasis. Furthermore, it contributes to intercellular communication by dephosphorylating extracellular signaling molecules. Alkaline phosphatase's diagnostic significance extends to its association with liver and bone disorders.
Goals:
This study aims to investigate the expression of alkaline phosphatase (AP) in three different cell lines and evaluate its activity. Previous attempts to express AP in our laboratory were unsuccessful, showing a lack of functional enzyme activity. Therefore, the primary objective of this experiment is to optimize the expression conditions and achieve successful production of active AP in these specific cell lines. By doing so, we seek to gain insights into the factors influencing AP functionality and enhance our understanding of its role in cellular processes.

Methods:
In this study, our objective was to express alkaline phosphatase (AP) and evaluate its activity in three different cell lines: C+, shuffle, BL21 competent E. coli, and a proprietary cell line. To optimize the expression process, in contrast to previous expression attempts, we employed an osmotic shock method for cell lysis instead of sonication. Following cell lysis, the lysate was thawed on ice for 5 minutes to maintain enzymatic integrity and maturity of AP. Subsequently, AP was purified using nickel column affinity chromatography, followed by gel filtration chromatography to further enhance purity. The activity of the purified AP protein was assessed using a pNPP (p-nitrophenyl phosphate) assay, which measures the enzyme's capacity to dephosphorylate pNPP. Additionally, we conducted a DNA phosphorylation experiment to validate AP's enzymatic functionality.

Results:
The expression and activity of alkaline phosphatase (AP) were successfully achieved in this study. Different concentrations of AP, ranging from 0.1 to 4 µM, were tested to evaluate their efficiency. Results indicated that AP exhibited functional enzymatic activity within the concentration range of 1 to 4 µM, with 4 µM showing the highest efficiency. At concentrations below 1 µM, notably at 0.5 µM, AP demonstrated a significant reduction in enzymatic function, indicating a dose-dependent relationship.

Conclusions: In this study, we successfully expressed and assessed the activity of alkaline phosphatase (AP) in three different cell lines: C+, shuffle, and BL21 competent E. coli. Previous attempts to express AP in our laboratory had yielded non-functional enzyme activity, highlighting the need for optimization. By employing an osmotic shock method for cell lysis and carefully thawing the lysate on ice, we achieved improved AP functionality. Our results indicated that AP exhibited the highest enzymatic efficiency at concentrations between 1 and 4 µM. At concentrations below 1 µM, notably 0.5 and 0.1µM, AP demonstrated a significant reduction in function. These findings emphasize the importance of maintaining an optimal AP concentration to ensure maximal enzymatic activity. Moreover, we confirmed AP's enzymatic function through pNPP assays and DNA phosphorylation experiments.

ABSTRACT #37

Monitoring ORAI1 Dynamics in T Cell

Shria Kavaturu, Copley High School; Yicheng Chen, Zhenghe John Wang, Department of Genetics and Genome Sciences, Case Western Reserve University

Background:
Causing the deaths of over 600,000 people, cancer was the second leading cause of death in the United States in 2022. Throughout the 21st century chemotherapy and radiotherapy, using chemicals and radiation, respectively, to attack cancer cells, have been the forerunners in cancer treatment. But more recently new treatments such as immunotherapy to fight cancer. Cancer immunotherapy requires the activation and expansion of cancer-specific T cells, which kills cancer cells by recognizing antigen targets expressed on cancer cells. Critical to T cell activation, Ca^{2+} rapidly activates and integrates numerous signaling pathways to generate widespread changes in T cell gene expression and function. The mechanism of ORAI1, an important calcium ion channel, in the process of T cell activation, requires further exploration.

Goals:
This study aims to investigate the localization and movement of ORAI1 during T cell activation by expressing ORAI1 fused with fluorescent protein tags in T cells. Real-time live-cell imaging techniques will be employed to monitor the dynamics of ORAI1 during the process of T cell activation.

Materials and Methods:
Retrovirus is an important tool for introducing genes of interest into T cells. We constructed the ORAI1-mscarlet fusion gene by PCR and inserted it into the retroviral expression vector MSCV using the method of restriction enzyme digestion and ligation. We transfected the vector into the virus packaging cell line PT67. After antibiotic (Zeocin) selection, we obtained cell clones capable of stable virus production. After collecting the culture supernatant of PT67, we performed virus enrichment and purification from the cell supernatant using Retro X-100. The purified virus will be used for infecting Jurkat T cells. The expression levels can be evaluated through western blot analysis and fluorescence microscopy.

Results:
Our research is still ongoing at this point in time so concrete results are not available. At this point in time we have successfully identified the vectors with the highest viral presence and will be infecting the jurkat cells to see how long the infected T cells can survive.

Conclusion:
If successful, this treatment offers a less aggressive form of treatment for those diagnosed with blood cancers and can potentially prevent relapses of cancer as the cells will persist in the body long term.

ABSTRACT #38

Glutamine pathways' assistance of metabolism to resistant IDH1

Minjun Kim, St. Edward High School; Semmer Ali, Omid Hajihassani, Jonathan J. Hue, Hallie Graor, Alexander W Loftus, Mehrdad Zarei, Luke D. Rothermel, Jordan Winter, Department of Surgery, Division of Surgical Oncology, University Hospitals Cleveland, Case Comprehensive Cancer Center, Case Western Reserve University

Background:
Pancreatic ductal adenocarcinoma (PDAC) is one of the most aggressive types of cancer with a five-year overall survival rate of less than 5%. Isocitric Dehydrogenase 1 (IDH1) is an important cytosolic enzyme that protects 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. Our work has previously shown that AG-120 (ivosidenib), an FDA-approved mutant IDH1 inhibitor, is actually a potent wild-type IDH1 inhibitor, under low magnesium and nutrient levels that are present in tumor microenvironment. The targeted therapy of AG-120 inhibits the IDH1 pathway to reduce ATP production and eventually causes cell apoptosis. However, even with the great decrease in tumor size, cells became adaptable to the stress and inhibition that were caused by AG-120. Therefore, a hypothesis was built to show that other pathways, which we assume are ASCT-2 transporter and GSL-1 glutamine pathways, are activated to support energy to the alpha-ketoglutarate.

Goals:
This study aims to see if the Glutamine pathway GSL-1 and transporter ASCT-2 assist the metabolism of the resistant IDH1 cell. The primary purpose of this research is to find a different pathway that cancer cells gain energy when the clinical trial patients develop resistance or are resistant to the AG-120 drug.

Materials and Methods:
To ascertain the cell dependence on the glutamine pathway GSL-1 and ASCT-2, The MIA PaCa-2 and Panc-1 cancer cells were used as the primary cell line separated into two groups labeled as parental and IDH1 resistant cells. The IDH1-resistant cells were given by our lab, which was modified by gradually increasing the dosage of AG-120 from 0μM to 80μM, and the resistance of cells to AG-120 was proven by the long and short-term cell viability. The cells were also planted into 6-well plates and it was treated with different Glutamine concentrations to determine if a decrease in glutamine concentration causes cell apoptosis, or in general if the resistant cells have any relation with glutamine level. Western blot analysis of ASCT-2 and GLS-1 was performed to show that it is the right pathway to target.

Results:
The short-term cell viability data proved that IDH1-resistant cells are resistant to the AG-120 drug since around 20% of the parental cells treated with AG-120 and around 75% of the resistant cells treated with AG-120 survived. The data suggest that parental cells are not resistant to the AG-120 and IDH1-resistant cells, when compared to parental, are resistant to AG-120. The long-term cell viability data demonstrate that a decrease in glutamine concentration causes cell apoptosis in the resistant cells that were treated with AG-120 compared to when parental cells are treated with glutamine-modified media since it didn't show any signs of decrease. The western blot expression was still in progress when this abstract was submitted. However, I assume that it will show that when cells become resistant to AG-120, the expression of GLS-1 and ASCT-2 are increased as compared to the parental cells.

ABSTRACT #38 CONTINUED

Conclusions:

When the pancreatic cancer cells, MIA PaCa-2 and Panc-1, become resistant to AG-120, the reason behind the resistance is partly due to the activation of glutamine pathways of ASCT-2 and GLS-1. For the future research direction, I would like to use CB-839 (Telaglenastat), GLS 1 inhibitor to see if GLS-1, my primary focused enzyme is the right enzyme to target. Suppose GLS-1 is the right enzyme to target, I will treat the resistant cell with a combination therapy of AG-120 and CB-839 and see if it has a synergistic effect in decreasing cell survival in vitro. I will use patient-derived xenograft (PDX) athymic nude mice to see if the combination therapy is effective compared to monotherapy agents, through in vivo studies.

ABSTRACT #39

Testing a Novel Stem Cell Culturing Medium for Cortical Organoids

Ishita Kopparapu, Hathaway Brown; Helen Miranda, Department of Genetics and Genome Sciences, Case Western Reserve University

Organoids are a 3D stem cell model which recapitulate the physiology of human organs. Animal models such as mice have limitations due to the inaccurate representation of the human brain. 2D models such as iPSC-derived cell types only capture one or two cell types whereas organoids present a unique model as they are closer to that of a human organ's physiology in composition and cell-to-cell interactions. Thus, organoids allow human diseases to be tested in the most human-like model. The purpose of this project was to optimize a cortical organoid differentiation protocol to be implemented in neurodevelopment and further disease progression studies. This project builds off a protocol for cortical organoids that has cost effective advantages by using a novel stem cell media supplement provided to our lab that is considerably cheaper than the ones in the market now. In this project, embryonic stem cells were cultured until completely confluent and later differentiated into cortical organoids to study neurodevelopment. Two culturing media, an established commercial media and a novel commercial media, were tested and when observing the organoids, growth and cell type antibodies were studied to identify neurodevelopment and progression of differentiation. Preliminary results showed that at day 30, the progenitor cells within the organoid began to migrate for both types of media. During the differentiation process, the novel commercial media showed more neural rosettes compared to the established commercial media. Neural rosettes indicate neural development as they are known to be representative of the neural tube. Future directions include looking at day 75 and comparing iPSC to ESC differentiation.

ABSTRACT #40

Evaluating Homemade Protein and DNA Ladders as Molecular Weight Markers for Size Exclusion-Chromatography

Emerson Krauss, University School; Udaya Balamurugan, Yi Zhang, Department of Biochemistry, Case Western Reserve University

Background:
Commercial protein ladders are expensive. The result of creating this protein ladder would efficiently cut down lab prices while still managing to create accurate measurements of different proteins. Past homemade protein ladders did not attempt to use the ladder for chromatography. Commercial DNA ladders are equally expensive. Past homemade DNA ladders have omitted steps of expressing the cell culture to get the plasmids used in the DNA ladder.

Goals:
Having a protein ladder is vital for identifying the size of proteins on SDS-PAGE gels. By observing the size of the proteins, we can then be able to separate that protein from others. Observing the size of the protein is also essential to better understanding the structure of this protein. DNA ladders in Agarose Electrophoresis Gels are equally important in confirming if the correct DNA molecule is in a sample. So, we will create inexpensive protein and DNA ladders.

Methods:
The methods for the creation of the protein weight markers are divided into two main steps: Expression and Purification. In expression, we grow cell cultures to produce the proteins we need as molecular weight markers. Purification involves separating these proteins we need as weight markers from impurities. Concentration on the purified proteins to improve the visibility of these weight markers on an SDS-PAGE gel. The methods for creating the DNA weight markers similarly have the step of expression, but contrast by the cutting of the plasmids. Expression is the same by growing the cell culture we need. Then purification takes place to separate out the RNA and other impurities from the sample. We then cut the plasmids using restriction enzymes resulting in the molecular weight markers to be used in the final DNA ladder. We also ran a protein ladder through HPLC having the machine separate it out.

Results:
We found that the proteins migrated down the SDS- PAGE gel properly when compared to the commercial protein ladder. These proteins did not fragment at all and were shown as distinctive markings that did not fragment. The weight markers showed up successfully. Specific protein markers showed up as lighter than preferred so we would then concentrate those proteins more so that they would appear properly. After testing again, they were extremely visible. We found that for the DNA ladder that the plasmids migrated properly and were visible. HPLC did not workout possibly due to incompatibility of the proteins to the HPLC machine.

Conclusions:
The data indicates the protein ladder was partially successful. The protein weight markers were visible and migrating on par with the commercial protein ladder suggesting to be a viable alternative. The DNA ladder migrated properly although the plasmids were a little faint.

ABSTRACT #41

What Role Does MECP2 Play in Cancer?

Aditya Lakshmanan, Mayfield High School; Helen Park, Alexandra Belardo, Chathuni Jayathilaka, Tae Hun Kim, Department of Biochemistry, Case Western Reserve University

Background:

Mecp2 is a methyl binding protein that suppresses genes by binding to methylated sites. Genes can be suppressed through DNA methylation, where a methyl group is added to cytosine residues in a CPG sequence. Mecp2 is one of the proteins involved in this process. DNA methylation is relevant to cancer as it disrupts normal methylation patterns. DNA methyltransferases (DNMT) are enzymes responsible for DNA methylation, including DNMT1, DNMT3A, and DNMT3B. Methylation typically occurs in gene promoter regions, controlling transcription. Hypo- or hypermethylation of genes can lead to cancer, affecting oncogenes and tumor suppressor genes. Mutations in DNMTs or Mecp2 can disrupt methylation. In our lab, we study Mecp2 protein and its impact on the body, exploring how mutations may contribute to cancer.

Goals:

Our short-term goals were to purify Mecp2, and then store that protein for any later use, or any experiments we need to run. For Mecp2, there are many experiments that could be run, but all of them fall under the context of how Mecp2 relates to cancer by affecting nucleosomes and how it impacts the nucleosomal structure.

Materials and Methods:

There were many materials that were used in order to purify Mecp2. Some of them include, Centrifuge, Sonicator, Spectrophotometer, Columns, Lysis/Wash Buffer, Autoclave IPTG, as well as a MicroPipet. Mini Prep is a technique used to isolate small plasmid DNA from bacteria, minimizing protein and genomic DNA contamination. Heat Shock Transformation enables molecular cells to uptake circular plasmid DNA from the surrounding environment, allowing genes of interest to be introduced into bacteria for expression and replication. The cells are made competent using Calcium Chloride Treatment (CA2+) to bring the plasmid into close proximity with the outer membrane. After plating onto LB agar, colonies are picked, and multiple colonies are selected to account for potential mutations. The process is scaled up by transferring cells to larger flasks, inducing protein production with IPTG (lac operon). Centrifugation concentrates the cells, and sonication breaks open the cell membrane, releasing the protein. The supernatant is then subjected to size exclusion chromatography using a Gel Filtration Buffer.

Results:

Mecp2 was successfully extracted and copied and as a result, there is an ample amount of Mecp2 to do research on. Because of this purification, we now know that MECP2 Replication works best with the cell line of Codon plus, E.COLI.

Conclusions:

During the purification we induced the plasmid DNA into 2 different cell lines of E.Coli, to see which would replicate faster, so that in the future, if there is an emergency in need of Mecp2, we would know which E.Coli cell line would prove to be more useful. The two cell lines we used were codon plus, as well as BL 21, and Codon Plus proved to be much faster.

ABSTRACT #42

Scientific Breast Cancer Research on Polygenic Risk Scores

Lindsey Lemus, Cleveland School of Science and Medicine; Fred Schumacher, Department of Population and Quantitative Health Sciences, Case Western Reserve University

Background:
As stated by the National Cancer institute; Cancer is a disease caused when cells divide uncontrollably, spreading to surrounding tissue. Breast Cancer is a severe disease among many women, starting at age 49; and also in men, 1 in 100 males can be impacted. In 2020, there were 2,261,419 new cases, affecting a multitude of demographics and glaring racial health disparities. An ongoing obstacle in healthcare is the idea that racial minorities in America are more likely to be overlooked than white patients. This is due to their inability to access or afford healthcare. Healthcare is not accessible to many patients around the world. The average cost of a mammogram in the United States is $150 dollars with insurance, and without insurance, $499 dollars.

Goals:
Our goal is to help develop a medical plan accessible to all patients to further their understanding of Breast Cancer and the apprehension of when to seek help. Identifying a possible system of approach for Breast Cancer using affected individuals, while providing guidance to patients on accessibility will help to discourage the use of racial discrimination in healthcare.

Methods:
Provide the most economical yet effective plan to attack Breast Cancer, without adding more expenses and physical health affiliations. A Polygenic score (PGS) or Polygenic risk score (PRS) is a varied estimate of an individual's genetic liability to a genetic trait or disease which is calculated by accessing their genotype and crossing it with any other known genotype cancer trait. In addition, a Polygenic Risk Score can not only be helpful with Breast Cancer but Prostate Cancer, Coronary Artery Disease, Obesity, Type 1 and 2 Diabetes, and Alzheimer's Disease. This may be an approach to help lower the cost of mammograms done monthly or even yearly. This allows independent individuals to get a PRS evaluation to determine the number of times they need to receive a mammogram. Individual A is shown to have a higher trait and more ancestral aggressive breast cancer leading them to be checked more often, whereas individual B has a lower trait and some known ancestral breast cancer, being checked every two years. Computing the number of alleles at risk for the cancerous phenotype, and weighting the estimated size of the cancer would be an effective and inexpensive way to identify and help patients. Overall, the emphasis would be to ensure access to healthcare for all and eliminate socioeconomic inequalities. With this approach, cancer patients and communities benefit from the lower cost and are ensured they receive equal and effective treatment.

Results:
Studies show that Polygenic Risk Scores are 95% effective this would demonstrate that there have been just results that helped and guided patients. For the remaining 5% of patients on which it did not accurately work on would indicate the high polygenic score they have but security of not receiving the cancerous phenotype trait. As there are disadvantages to all tests there are also advantages, Polygenic risk Score Test would allow the patients to measure the risk of any cancerous genes, which would potentially save their lives. This would also allow for a wider polygenic diversity by introducing our world to genotype variations amongst a population. Furthermore, 10 studies were done amongst three types of cancer: Prostate, Colorectal and Breast. The Results showed that out of the 10 studies done, receiving a PRS was "Likely to be the most cost-effective than alternatives."

Conclusions:
The information listed above shows the breakdown of how we can help advocate for our community by not only making it more accessible but finding ways for others to get involved. In conclusion this could help lower breast cancer demographics and bring awareness to the effectiveness of Polygenic testing. Saving millions of lives yearly with more cost-effective methods of approach.

ABSTRACT #43

Sexual Dimorphism in the Hematopoietic Systems of Mice

Miles Lipman, Shaker Heights High School; Brittany Cordova, Bailey Klein, Amar Desai, Case Comprehensive Cancer Center, Case Western Reserve University

Background:
The hematopoietic system is the physiological system responsible for the production of blood cells, including red blood cells and the components of the immune system. The system relies on the production of these blood cells from hematopoietic stem and progenitor cells (HSPCs), a type of cell belonging to the lineage$^-$ c-Kit$^+$ Sca-1$^+$ (LSK) classification. This group of stem cells can be split into two categories, long-term hematopoietic stem cells (LT-HSCs), which are capable of self-renewal, and short-term hematopoietic stem cells, which are not. These cells and the cells they produce are essential for proper functioning of the body and for recovery after injury, making treatment of hematological disorders and acceleration of hematological recovery after injury or transplantation essential. However, prior studies have determined that sex differences in the hematological system can lead to different results in males and females. This investigation focuses on sex differences in gene expression and concentrations and types of HSPCs and immune cells in the bone marrow (BM), peripheral blood (PB), and spleen. Analysis of these targets can assist in understanding the most effective treatments for patients by determining sex-related differences in their capacity for hematopoietic regeneration and immune function.

Goals:
The goal of this investigation was to determine the differences in the function of the various hematopoietic components between male and female mice. This was accomplished by categorizing the differences in cell types and gene expression in different parts of the hematopoietic system between healthy male and female mice.

Methods and Materials:
Spleens, bone marrow (BM), and peripheral blood (PB) were harvested from two male and two female mice. In order to determine differences in hematopoietic cell generation and immune function, flow cytometry was performed on samples from these tissues stained for LSK, LT-HSC, ML, and B and T cell content. Real-time PCR analysis was performed on cDNA samples from the spleen and BM in order to determine the relative expression of various genes involved in immune regulation, hematopoiesis, and angiogenesis.

Results:
qPCR results indicate a trend toward increased expression of angiogenic, hematopoietic, and immune genes in male spleens and BM, as well as increased expression of the inhibitory gene Pf4. In the female BM, though, there is a trend toward increased expression of Ptn, an angiogenic gene. The results of flow cytometry demonstrate a trend toward similar frequencies of LSKs and LT-HSCs in the spleen and the PB, but markedly higher concentrations of both LSKs and LT-HSCs in male BM. Flow cytometry results also indicate a trend toward higher frequencies of immune cells in the female PB.

Conclusions:
The differences in gene expression, especially in the expression of the Il6, Kitl and Angpt1 genes, indicate that males trend toward higher expression of genes involved in hematopoietic activity, angiogenesis and immune cell maturation in the spleen and BM. Some of these genotypic differences can be observed in the much higher frequencies of LSKs and LT-HSCs in the male BM. However, males also trend toward increased expression of the negatively regulatory gene Pf4, which inhibits angiogenesis, hematopoiesis, and T cell maturation. The higher frequencies of stem cells are likely tied to this increased expression of Pf4, which would cause stem cells that would have otherwise differentiated during hematopoiesis to remain undifferentiated. Meanwhile, females trend toward

ABSTRACT #43 CONTINUED

increased expression of Ptn in the BM, which promotes angiogenesis, indicating that female and male angiogenesis may be promoted by different genes in the BM. Females also trend toward higher frequencies of immune cells in the PB, indicating a more active immune system. Further study is necessary to determine the full extent of the phenotypic differences in male and female hematopoiesis and their effects on medical treatment, especially transplant results.

ABSTRACT #44

The Role of Non-modifiable Factors and Social Determinants of Health in Prostate Cancer Awareness

Eleanor Meges, Padua Franciscan High School; Rebecca Miller, Kristina Austin, Sydney Evans, Rachel Gardenhire, Calvin Tornes, Erika Trapl, Kristina Knight, Department of Population and Quantitative Health Sciences, Case Western Reserve University

Background:
Prostate cancer is cancer that begins in the prostate gland within the male reproductive system. It is a significant public health concern worldwide, affecting a substantial number of individuals assigned male at birth each year. While knowledge about prostate cancer— including risk factors, symptoms, screening, and treatment options— is crucial for early detection and optimal management, awareness levels vary across different demographic groups. Prostate Specific Antigen Tests (PSAs) are blood tests used to detect antigens specific to prostate cancer. African American men, who face a higher risk of developing prostate cancer and are more likely to be diagnosed at advanced stages, often exhibit lower levels of knowledge of prostate cancer compared to their White counterparts. The Cleveland African American Prostate Cancer Project (CAAPP) aims to alleviate this disparity by training barbers to promote PSAs as well as genetic screening to their primarily black clientele and to connect them to healthcare resources.

Goals:
This research paper aims to determine the role of non-modifiable factors and social determinants of health in influencing knowledge of prostate cancer and prostate cancer screening. This research focuses on non-modifiable factors such as age and race, as well as social determinants of health such as socioeconomic status and education.

Methods:
CAAPP quantitatively assessed study participants' baseline knowledge and awareness of prostate cancer through a pre-screening enrollment survey. By studying how people's background relates to what they already know about prostate cancer, we can identify differences in knowledge and awareness within the Cleveland community. Additionally, a literature review was conducted using academic research articles from Google Scholar and PubMed to determine how social determinants of health and non-modifiable factors influence knowledge of prostate cancer. Finally, analysis of the 2020 Ohio Behavioral Risk Factor Surveillance System (BRFSS) was completed. The BRFSS is the world's largest random-digit dial telephone survey. They surveyed male participants over 40 about whether they had a PSA screening within the last 2 years and this study determined how answers to this question were impacted by differences in race, age, educational attainment, and income. Significance was determined at $p<0.05$ based on non-overlapping confidence intervals. Data analysis will be completed with Excel and SPSS.

Results:
The BRFSS data reveals that, in Ohio, black men over 40 are significantly less likely to have gotten a PSA screening within the last two years than their white counterparts. Men younger than 60 were significantly less likely to receive a PSA screening than men 60+. Individuals with lower income levels and educational attainment, were significantly less likely to have had a PSA screening. Groups that were less likely to have gotten a PSA screening are likely less aware of prostate cancer and PSA screenings. The literature review supported these findings and showed that they support national trends in prostate cancer awareness. CAAPP's data is still undergoing analysis.

Conclusions:
Learning which groups lack certain types of knowledge can help CAAPP and similar programs more strongly target educational interventions. In the future, more localized assessments can be completed on a larger scale to assess knowledge within the Cleveland community.

ABSTRACT #45

Effect of Opioids on Mucus Production in the Intestinal Epithelium

Ira Mehta, Lake Ridge Academy; Alan D. Levine, Department of Molecular Biology and Microbiology, Case Western Reserve University

Background:
Ulcerative Colitis (UC) is a chronic inflammatory bowel disease that is characterized by inflammation and ulcers on the inner lining of the large intestine. An estimated 1 million people in the United States are diagnosed with UC. In active UC, mucus protein production is reduced in inflamed and non-inflamed segments, the numbers of sentinel goblet cells are deceased, and the goblet cell secretory response to microbial challenge is attenuated. Mucus provides lubrication and protects the epithelium from digestive enzymes, acids, microorganisms, and infiltrating bacteria. Mucus production depends on *muc2* expression, which is the gene that codes for the protein mucin2. Mucin2 polymerizes with other proteins to create mucus. Opioids are known to induce mucus secretion, but how mucin production is regulated is poorly understood. There are three opioid receptors: MOR, KOR, DOR. Each receptor has a different function, and it is unclear as to which opioid receptors are responsible for triggering mucus production.

Goals:
To address the inflammatory distress in patients with UC, the goal of this project is to investigate the mucus-inducing effects of opioids on the epithelial cells that line the gastrointestinal tract.

Methods:
Human colorectal carcinoma T-84 cells were used as a model of the human intestinal epithelial barrier. The cells were maintained in DMEM/F-12 (Dulbecco's Modified Eagle Medium/Nutrient Mixture F-12) supplemented with 5% fetal bovine serum (FBS.) Intestinal epithelial cells were grown in 6-well plates and treated with a dose curve of 0, 10, and 100 uM morphine. After 4 and 24 hours, RNA was isolated and cDNA synthesized. RT-qPCR was used to quantify *muc2* gene expression.

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

Conclusions:
Pending results

ABSTRACT #46

Role of macrophage-KLF6 in atherogenesis

**Uwela Mugabo, Cleveland Central Catholic High School; Kartik Bhat, Solon High School;
Hang Pong Ng, Ganapati Mahabaleshwar, Department of Pathology, Case Western Reserve University**

Background:
Atherosclerosis is an arterial disease that occurs due to the buildup of lipid-filled plaques. The process of building up plaque is known as atherogenesis. Plaque development for most people starts in childhood and becomes worse as they age. In the United States, about 610,000 people die from atherosclerosis each year. Atherosclerosis affects all major arteries that supply blood to vital organs such as the heart and brain. Atherosclerosis can mostly be found in the arteries because blood flows with high pressure and more turbulently, which are favorable conditions for plaque development. Further, elevated levels of fatty substances in blood could also increase blood viscosity as well as deposit fatty materials on the arterial walls. The deposition of these fatty substances attracts macrophages as a part of the fat clearance mechanism. However, the accumulation of these macrophages initiates chronic inflammation that contributes to plaque development. Initially, macrophages attempt to break down fat in the arteries, which prompts them to bloat and become foam cells. These foam cells can also prompt an inflammatory response. Here, we are examining the importance of macrophage Kruppel-like factor 6 (KLF6) in the regulation of inflammatory gene expression and high-fat diet-induced atherogenesis.

Goals:
Examine the role of macrophages-KLF6 in atherogenesis.

Methods and Materials:
The Lyz2Cre and Klf6FlFl: Lyz2cre mice on Apoe-null background were fed on a high-fat high-cholesterol diet. The en-face preparation of the aorta from these mice were stained with Sudan IV and lesion areas were quantified and charted using Image software. The aortic sinuses were cryosectioned and stained with Oil Red O lipid accumulation, and anti-F4/80 antibody for macrophage accumulation. Image software was used to quantify aortic sinus plaque and macrophage area. The macrophage inflammatory gene expression was quantified by RT-gPCR analysis.

Results:
Macrophage-KLF6 deficient mice are protected from high-fat diet-induced atherosclerotic plaque formation. Macrophage-KLF6 deficient mice also exhibited significantly diminished aortic root macrophage accumulation as well as lipid-rich plaque formation. Moreover, KLF6 deficiency significantly attenuated inducible pro-inflammatory gene expression in macrophages.

Conclusions:
Our study provides initial evidence that macrophage-KLF6 promotes atherogenesis.

ABSTRACT #47

Discovering what causes health disparities for African American women and African women in Triple-negative Breast Cancer

Khalil Muhammad, Charles F. Brush High School; Jennifer Cullen, Department of Population and Quantitative Health Sciences, Case Western Reserve University

Background:
Breast cancer is one of the leading causes of death among women, and it is also most commonly diagnosed amongst women. Triple-negative breast cancer (TNBC) is one of the most aggressive and least treatable subtypes of breast cancer. TNBC is also least commonly diagnosed amongst African American women and African women, but they are more likely to die from TNBC as compared to white women. The reasoning behind this disparity is many like race, socioeconomic status, genetics, environmental factors, and biological factors.

Goals:
The goal of this study was to find the most prominent reason found across most studies that link African American women and African women to having higher mortality rates and less incidence rates with TNBC. Hopefully in finding out the overarching reason as to why African American women and African women have higher mortality rates and lower incidence rates with TNBC, will help better decrease and eventually eliminate this disparity.

Materials and Methods:
Using the PubMed (PubMed (nih.gov)) search database. PubMed is a free biomedical search engine used to inform users using published scientific articles. Many searches were conducted under the search terms: (i) African American women and (ii) triple-negative breast cancer, and (iii) disparities. 117 published papers were found. These papers were then grouped in relevant sections. These sections were biology, socioeconomic status, and genetics. The papers also had to have been published within the last 6 years. The years of the published studies ranged from 2017-2023. After finding the most commonly linked factor to TNBC, it will be examined to see what effects factor on rates being higher in black women for TNBC, and TNBC mortality.

Results:
Out of 117 papers only 70 (60%) were examined. Out of 36 articles of 117 (30%) said biological factors are linked to TNBC incidence rates being lower for African American women and African women, but having a higher mortality rate. 33 articles out of 117 (28%) said genetic factors are linked TNBC incidence rates being lower for African American women and African women but having a higher mortality rate. Out of 117 articles 17 (14%) said socioeconomic status is linked to TNBC incidence rates being lower for African American women and African women but having a higher mortality rate. Out of the three factors examined, biological factors, socioeconomic status, and genetic factors were most commonly linked to TNBC incidence rates being lower for African American women and African women but having a higher mortality rate.

Conclusions:
Overall the most commonly linked factor to TNBC incidence rates being lower for African American women and African women, but having a higher mortality rate is biological factors. Truthfully the overarching link to TNBC incidence rates being lower for African American women and African women, but having a higher mortality rate is unknown due to racial disparities being a gap in knowledge. With more research hopefully the gap in knowledge around racial disparities will close and the full truth on why African American women and African women TNBC incidence rates are lower, but have higher mortality rates.

ABSTRACT #48

Assessing Apoptotic Activity in Pediatric Diffuse Intrinsic Pontine Glioma in Response to Administration of CDDO-2P-Im

Tina Nguyen, Mayfield High School; Bhavya Sharma, Stevie Rieger, John Letterio, Department of Pediatrics, Case Western Reserve University School of Medicine

Background:
Pediatric diffuse intrinsic pontine glioma (DIPG) is a form of childhood brain cancer that begins its formation in a patient's brain stem, a structure responsible for regulating bodily automatic functions like breathing and heart rhythm. Annually, only approximately 200 to 300 cases of DIPG arise within the United States, with the majority of these DIPG patients surviving for less than one year. Symptoms of DIPG are induced by the dysfunction of pontine structures, which can contribute to facial paralysis and hyperreflexia. These symptoms will largely be presented among patients less than four weeks after their initial diagnosis. A treatment of interest with regard to addressing DIPG is CDDO-2P-Im, a synthetic oleanane triterpenoid. Previous research has demonstrated that CDDO-2P-Im induces apoptosis in human leukemia cells by disrupting intracellular redox balance through the activation of an extrinsic caspase-8 pathway. In this study, the apoptotic properties of 2P-Im were analyzed with DIPG utilizing the immunofluorescence of Cleaved Caspase 3 (CC3), an enzyme required for the hallmarks of apoptosis.

Goals:
We propose that the use of CDDO-2P-Im in an *in vitro* model will support the notion of increased antineoplastic efficacy and, if administered with other therapies like radiation therapy (RT), will improve treatment response for patients who have DIPG.

Materials and Methods:
1x10^6 DIPG cells were plated per well on a six-well plate. The control well was treated with dimethyl sulfoxide (DMSO). The remaining wells were treated with ten microliters of 2P-Im at 12.5 nM, 25 nM, 50 nM, 100 nM, and 150 nM concentrations of the drug. Cells were subsequently incubated over an 18-hour period and lysed using RIPA+protease inhibitor. Protein lysate was stored in an Eppendorf tube at -80 degrees Celsius. Lysates were denatured by boiling in SDS loading buffer at 95 degrees Celsius for five minutes. Samples were run in an electrophoresis gel at 80 mA for two hours. Proteins were transferred onto membrane at 30V overnight in the cold room. The membrane was incubated with primary antibody, washed, and then incubated with secondary antibody. Chemiluminescent signals were captured with film in a dark room.

Results:
At increasing nanomolar concentrations of 2P-Im, higher levels of cleaved PARP were expressed, with decreasing levels of PARP enzyme. Greater cleaved PARP is indicative of higher apoptotic activity *in vitro*, lending to optimal treatment response and greater antitumor efficacy.

Conclusions:
Future work with DIPG treatment using 2P-Im may further investigate the dose-dependent cytotoxicity of the drug in animal models, like mice. Doing so can ascertain the optimal dosage with the greatest efficacy of treatment, as well as possible side effects that could not be observed in an *in vitro* model. As DIPG currently exhibits low levels of response to treatments like RT, the use of such therapies in combination with CDDO-2P-Im can help to increase radiosensitivity, ultimately improving overall patient prognosis and quality of life.

ABSTRACT #49

Genotyping to Distinguish Wild Type vs miR $211^{-/-}$ mice

Loriane Nouafo, Solon High School; Neekkan Dey, J. Alan Deihl, Department of Biochemistry, Case Western Reserve University

Background:

Genotyping is a process done to identify differences in DNA sequences between different individuals or populations. This method can be used to identify variations or mutations that have been made into an organism's genetic material.

Goals:

To identify Wild Type (WT) or miR $211^{-/-}$ genotype mice among four unknown mice pups.

Materials and Methods:

DNA was isolated from tail fragments of four different mice pups (19 days old) using appropriate miR-211 specific primers to amplify the desired region of the miR-211 gene. The sequence of the primers used for the amplification are miR-211- Fw: *5'CTTGTGCCAGATCTACCCCC3'* and miR-211- Rv: *5'CACTGGGCTAAGCCATGAAT3'*. PCR was performed using the T100 Thermal Cycler and the conditions were 98^0C for 2 minutes, denaturation at 98^0C for 12 sec, annealing at 63^0C for 15 sec (35 cycles), extension at 72^0C for 60 sec and 4^0C for storage.. After PCR, the amplicons from each reaction sample were run on 1.5% agarose gel for 30 min at 100 V, followed by imaging them under ChemiDoc MP Imaging System.

Results:

Figure 1. shows Well 1, the 100 bp DNA Ladder (New England Biolabs); Well 2, Unknown Sample 1, Well 3, Unknown Sample 2, Well 4, the water control that has no template, Well 5, Unknown Sample 3, Well 6, Unknown Sample 4, and Well 7, 100 bp DNA Ladder. In the first and seventh wells, the two darkest markers are known to be the 500 bp (basepair) and 1 kb (kilobase). In the fourth well there were no bands because there was no DNA template. In the second and third wells, the bands were observed to be at about 940 bp. However, in the fifth and sixth wells, the observed bands were at about 757 bp.

Conclusions:

Out of the four tail samples of unknown genotype, we conclude that two belong to Wild Type mice (Samples 1 and 2) and the other two belong to miR-211 $^{-/-}$ mice (Samples 3 and 4). As the miR-211 gene fragments had been knocked out from the DNA of certain mice, we know that the mice with the miR-$211^{-/-}$ will have shorter fragments (amplicons) than the Wild Type mice.

ABSTRACT #50

Evaluating Dextran Polymers for Sustained Delivery of Tuberculosis Drugs

Areesha Nouman, Hathaway Brown School; Emmanuel Opolot, Horst von Recum, Department of Biomedical Engineering, Case Western Reserve University

Background:
Infectious diseases pose a major threat worldwide because of their health risks and the lack of accessibility to resources among many populations. One of these diseases is tuberculosis (TB), a global epidemic. Current treatment strategies for TB, mainly oral route administration, are often inefficient because of medications' side effects, high dosages, and patient non-compliance with treatment duration. These weaknesses in treatment prompt exploration of areas of improvement and the need for more efficient drug delivery systems. Dextran, a glucose polymer, is being studied as a viable option for a long-term polymer drug delivery system.

Goals:
This project aims to determine if dextran improves the outcomes of TB treatment through controlled release, consisting of drug loading, drug release, and bactericidal assays.
The goal of this research project was to, in vitro, analyze dextran's performance as a polymer drug delivery system, including its drug release kinetics and bactericidal efficiency.

Materials and Methods:
The methods included polymer synthesis, drug loading, drug release, and bactericidal assays. First, the dextran discs were formed by crosslinking dextran and punching out the gel into discs. The discs were then loaded with the TB drugs pyrazinamide, isoniazid, ethambutol, cefotaxime, and cefixime by submerging the discs into the drug and its solvent. The loading efficiency was determined. The discs were then placed into phosphate buffer saline (PBS), replaced daily. The drug concentration of each PBS sample was measured using a plate reader machine. Simultaneously, *E. coli* and *Staph aureus* bacteria were plated with drug-loaded discs placed on top. Following overnight incubation, the zones of inhibition were measured. The process was repeated daily, with the same discs placed on new plates. Using the data, daily averages and standard deviations were graphed for each drug to analyze the rate of release.

Results:
The results, both visual and statistical, indicated dextran's successful ability as a polymer drug delivery system for TB medications. After drug loading, the discs' weights increased significantly. Plate reader data analysis showed a steady rate of drug concentration, with the highest amount of drug released within the first few days. The drug release from the discs also demonstrated bactericidal activity, with cefotaxime having the highest zones of inhibition for both *E. coli* (zone of inhibition > 13 mm) and *Staph aureus* (zone of inhibition > 10 mm).

Conclusions:
In conclusion, dextran showed promising results of extended TB medication release. Not only did the polymer effectively load drugs, but it was also able to perform controlled release and kill bacteria. This research and experimental study suggest possibilities for improved treatment strategies, especially for infectious diseases such as tuberculosis, that have the potential to revolutionize drug delivery systems in the medical field.

ABSTRACT #51

Investigating Chronic Inflammation in Lymphoid Compartments After Acute Traumatic Brain Injury

Niamh O'Donovan, Ardsley High School; Kailey Takaoka, Tufts University; Sofia Corella, Edwin Vazquez-Rosa, Andrew Pieper, Department of Pathology, Case Western Reserve University

Background:
Traumatic brain injury (TBI) is a leading worldwide cause of death and TBI-related issues have an annual cost of $80 billion in the United States alone. Annually, 3.5 million people in the United States sustain a TBI and 5.3 million people are currently living with TBI-induced disabilities. Injuries associated with TBI range from acute to chronic, with acute referring to damage directly after insult and chronic referring to damage that progresses for years or even a lifetime after injury. The mechanisms behind the transition from acute to chronic TBI are unclear. However, chronic neuroinflammation, which can cause prolonged damage to the brain, is a conceivable cause. Immune cells in our bodies are responsible for mounting an inflammatory response during infection or tissue damage and are derived from the hematopoietic system. This crucial and complex system comprises lymphoid organs (e.g. bone marrow) and hematopoietic stem cells from which blood cells, including immune cells, are derived. Our preliminary data suggests that TBI impairs the hematopoietic system in a manner that contributes to peripheral immune dysfunction, which could potentially cause chronic neuroinflammation. Specifically, we show that 3 weeks after TBI, mice exhibit increased neutrophils and neutrophil chemokines in peripheral blood, indicating chronic systemic inflammation. There is also an increase in T cells in the bone marrow, suggesting local inflammation in this primary lymphoid compartment.

Goals:
We hypothesize that TBI induces inflammation in the bone marrow compartment, which then propagates chronic systemic inflammation. After confirming our preliminary data, we will test our hypothesis by examining inflammatory factors in the bone marrow of mice subjected to TBI or sham-injury, 3 weeks after injury.

Methods:
Bone marrow was isolated from wild type 8-week-old mice 3 weeks after being subjected to multimodal TBI model (mmTBI), or sham-injury (5 mice per group). This model of TBI incorporates aspects of acceleration/deceleration, blast wave exposure, and concussive impact to inflict a complex brain injury that is reminiscent of TBI experienced by people and also has been established to drive transition of acute TBI into chronic neurodegeneration over the lifespan of mice. In order to assess gene expression of inflammatory factors, RT-qPCR was performed. RNA was isolated from the tissues and reversed transcribed into cDNA using reverse transcriptase. PCR-amplified cDNA was then mixed with probes that identified a specific DNA sequence of selected inflammatory factors. The pro-inflammatory factors analyzed were IL-1β, IL-6, TNF-α, CXCL1, and IFN-γ.

Results:
Bone marrow analysis of sham-injury and mmTBI mice 3 weeks post-injury indicate no statistically significant changes in inflammatory factors. However, tumor necrosis factor (Tnf) trends towards being increased in the bone marrow 3 weeks post-injury.

Conclusion:
Although no statistical significance for pro-inflammation in the bone marrow was detected, TNF-α trends towards significance, suggesting that this inflammatory factor could potentially be increased in the bone marrow 3 weeks after TBI. Therefore, we should reassess Tnf, and probe for other pro-inflammatory factors. At this time, we cannot confidently conclude that there is no inflammation in the bone marrow 3 weeks post TBI, thus, future studies are warranted. Additionally, we probed for interferon-gamma (Ifng), however this target gene was not identified in the bone marrow as indicated in our raw qPCR data.

ABSTRACT #52

Examining Stem Cell Properties of Glioblastoma Cells

Ebahi Omoijuanfo, Glean Academy; Maria Hatzoglou, Department of Genetics and Genome Sciences, Case Western Reserve University

Background:
Glioblastoma (GBM) is the most common form of brain tumor in adults. GBM is a difficult cancer to treat. Two main problems with GBM treatments arise. 1. The doctor cannot cut a large perimeter around the brain tumor. 2. Radiation and drug therapy are virtually useless against GBM. The recurrence rate is very high and the recurring brain tumor is much worse and often drug resistant. The recurrence rate is due not only to the difficulty of removing the whole tumor and surrounding area but also to Cancer stem cells (CSCs). Stem cells are cells with the ability to develop into several different types of cells. CSCs multiply indefinitely and have similar properties to cancer cells and stem cells. These cells are believed to contribute to the majority of GBMs. Sox2 is a transcription factor in multipotential neural stem cells.

Goals:
The goal of this study is to determine whether Sox 2 can be detected in patient derived GBM cells and therefore confirm that GBM cells do indeed possess Stem cell like abilities.

Materials and Methods:
A Western Blot will be run with patient derived GBM cell samples and the amount of Sox 2 will be compared to tuba, a housekeeping protein, alpha-tubulin, which will be our loading quantity control.

Results:
We expect to see Sox 2 expression.

Conclusions:
Based on our results we can conclude that GBM cells primarily come from stem cell like cells and this is potentially responsible for the high rate of recurrence.

ABSTRACT #53

Salivary innate immune responses to SARS-CoV-2 in acutely infected participants

Aide Omoijuanfo, Glean Academy, David Fletcher, Tracey Bonfield, Jeffrey Jacobsen, Christopher L. King, Jonathan Karn, School of Medicine, Santosh K. Ghosh, Aaron Weinberg, School of Dental Medicine, Case Western Reserve University

Background:
The oral mucosa was recently shown to be a primary site of SARS-CoV-2 (CoV-2) infection. Studies have revealed that toll-like receptors 7 and 8 and RIG1-like receptors (RLRs) are critical for CoV-2 recognition and activation of pro-inflammatory cytokines and IFN-type 1 and -III production. Additionally, it appears that CoV-2 can evade and suppress innate immunity through expression of specific antagonists of interferons. These findings have all been related to nasal and upper airway epithelium, with little to no information as to the virus' impact on innate responses of the oral cavity. We hypothesize that the cytokine/interferon and antimicrobial peptide (AMP) responses of the oral cavity during an acute CoV-2 infection will shed light on early processes to fight infection and protect the patient from severe illness.

Goals:
This study's main goal is to determine breakthrough (vaccinated and infected) participants' responsiveness to CoV-2 infection based on their salivary innate immune responses, clinical outcomes and viral load determinations.

Methods and Materials:
Following IRB protocol approval, we collected saliva samples from 11 acutely infected COVID-19 participants within 7 days of testing positive, at zero-time, day 7 and days 14 or 21. Salivary cytokines/chemokines, interferon and AMP levels were measured (in duplicate) by the Luminex® platform using Human Cytokine 34-and 14 Plex (R&D) [total of 48 analytes] according to the manufacturer's instructions. Innate immune marker profiles were also measured in saliva samples of 32 pre-covid era participants as controls. Data were analyzed using Graph Pad Prism software.

Results:
Levels of most of the salivary analytes of acutely infected participants were distinctly different than respective analyte levels in the pre-covid saliva samples (control). There was interpersonal variability in the trajectories of analytes from the "breakthrough" participants; some responded vigorously while others were weak, and in many cases fell within the control levels.

Conclusions:
Salivary Innate immune markers can be instructive in determining the host's responsiveness during the early stages of a CoV-2 infection; i.e., a persistently high level of pro-inflammatory salivary analytes may predict a worse prognosis in patients with COVID-19, as demonstrated by persistently high salivary viral loads. While preliminary findings are intriguing, we intend to recruit a larger cohort of Cov-2 acutely infected participants to establish the statistical robustness of these findings and their association with vaccination status, viral loads, viral variants, symptoms, and strength and durability of adaptive immune responses.

ABSTRACT #54

Highlighting community perceptions and feelings around genetic screening

Sharon Orisadipe, Shaker Heights High School; Rebecca Miller, Kristina Austin, Sydney Evans, Calvin Tornes, Erika Trapl, Department of Population and Quantitative Health Sciences, Case Comprehensive Cancer Center, Case Western Reserve University

Background:
Genetic screening can use a saliva test to tell you about genes that could be associated with heritable cancers. This can be used for early detection and prevention. Many people correlate historical mistreatment in research with their understanding of genetic screening. In addition, misconceptions and perceptions of genetic screening greatly impact an individual's willingness to undergo screening. As a result, they are limiting themselves from the use of genetic screening for the purposes of better understanding their cancer risk. Previous studies have reported fear of eugenics and human mortality and not wanting to know their future (1). The Cleveland African American Prostate Cancer Project (CAAPP) wants to give community members more information with the goal of making them more comfortable participating in genetic screening.

Goals:
From a sample of community members, we sought to better understand what concerns they held about genetic screening, related to prostate cancer. In response to their concerns, CAAPP hopes to give them more resources, to give them more confidence in getting screened.

Methods:
To find helpful information, a Literature review was done using google scholar and using PubMed. There were multiple different search terms such as “genetic screening”, “African Americans and genetic screenings”, “what is genetic screening”, “communication and genetic screening” and “education and genetic screening”. Papers ranging from 2000 to 2023 were included in the search criteria. A total of seven primary sources were selected for inclusion in the literature review process. The CAAPP team conducted a listening tour to gain knowledge on how the community feels about genetic screening. Using a de-identified transcript from Listening tour recordings and the articles found, the information was analyzed using standard qualitative analysis techniques in order to understand how communities, especially the black community, perceive genetic screening.

Results:
CAAPP found out that based on the listening tours, in which 79 community members attended, their perceptions of genetic screening were based on previous historical mistreatments and fears around future mistreatment of their community. The best way to get more people to come and get screened is through better communication. Explaining to the community what genetic screening is and how it can help people understand the importance of early prevention.

Conclusions:
Based on CAAPP’s sample of community members, there was a large range of emotions. There was concern about what would be done with their information. We are working to better inform the community, especially the African American community, that their information will not be used against them or their family.

ABSTRACT #55

A New Look at Prognostic Subgroups Within Endometrial Cancer Through the Examination of Immune Cell Gene Expression

Sairam Pantham, Solon High School; Michael Rubsamen, Mark Cameron, Department of Population and Quantitative Health Sciences, Case Western Reserve University

Background:
A rising problem in the fight against cancer is that of endometrial adenocarcinoma, an increasingly common cancer within the female genital tract and the only gynecologic cancer with rising incidence. Considering that, by 2030, the number of cases of endometrial cancer within the United States is predicted to rise to 122,000 cases, it's become increasingly imperative for the formation of effective prognostic criteria. To this end, the Cancer Genome Atlas has identified 4 molecular subtypes within endometrial cancer: POLE, MSI, CN low, and CN high. However, information is still lacking on differences in immune system responses to endometrial cancer, information that is potentially critical to the formation of prognostic subgroups.

Goals:
This study aims to identify differences between endometrial cancer patients in regards to gene-expression signatures relevant to anti-tumor immune responses. This involves the isolation of endometrial tumor samples from various patients and the analysis of single immune cell RNAseq data through experimental software designed by Partek, whose performance was also evaluated.

Materials and Methods:
RNAseq libraries were prepared using Chromium Next GEM Single Cell 3' Reagent Kits, designed by 10x Genomics, from tumor samples isolated from patients at Case Comprehensive Cancer Center membership institutions. Subsequent gene counts from each individual sample were then analyzed with Partek's software using hierarchical clustering and gene specific analysis (GSA).

Results:
Gene specific analysis performed between different samples and different cell types within samples revealed important differences between endometrial cancer patients regarding the expression of metabolic factors such as EIFB21, MDH1B, and RPP24 and factors directly influencing the anti-tumor immune response, such as CXXC4, SLC22A16, TMIGD2 and IL7R.

Conclusions:
Results suggest that the expression of the aforementioned factors is critical for understanding immune responses to endometrial cancer and forming prognostic subgroups within endometrial cancer, potentially allowing clinicians to provide crucial information to their patients in the future.

ABSTRACT #56

Investigating Temporal Expression Patterns of KLF Transcription Factors in Phrenic Motor Neurons: Insights into Breathing Abnormalities and Disease

Radha Pareek, Beachwood High School; Raquel Lopez De Boer, Polyxeni Philippidou, Department of Neurosciences, Case Western Reserve University School of Medicine

Background:
Breathing abnormalities are observed in various neurological disorders, including sleep apnea, muscular dystrophy, and amyotrophic lateral sclerosis (ALS), characterized by muscle weakening and respiratory failure. Understanding the specific motor neurons involved in breathing control, particularly phrenic motor neurons (PMNs) responsible for diaphragm innervation, is crucial for targeted therapeutic interventions. However, limited research exists on the genes and transcription factors maintaining PMN identity throughout an individual's lifespan. Previous studies from Dr. Philippidou's lab highlighted the importance of Hox5 transcription factors in establishing PMN organization and their connection with inhibitory premotor neurons. Interestingly, transcriptomic analysis of Hoxa5 mutants revealed a modified gene signature, including the Krüppel-like factor (KLF) family of transcription factors. Although KLFs have been implicated in cell differentiation, proliferation, and survival, the identification of KLF gene expression in PMNs during development is a new discovery and has the potential to shed light on the molecular mechanisms underlying breathing control and associated disorders.

Goals:
This study aims to explore the temporal expression patterns of KLF family transcription factors in PMNs and ascertain their putative role in maintaining the identity of these neurons. By elucidating the regulatory mechanisms underlying PMN identity maintenance, we aim to contribute to a better understanding of breathing regulation and pathogenesis.

Methods:
The Digoxigenin (DIG) In Situ Hybridization (ISH) technique was employed to examine cervical segment samples of the spinal cord from wild-type mice. Specific DIG-labeled mRNA probes, including KLF5, KLF6, and KLF16, were used to detect probe-target binding. The localization of PMNs was confirmed using the Vesicular acetylcholine transporter (VAChT) probe as a marker.

Results:
Qualitative analysis of frozen spinal cord sections revealed positive signals for KLF5, KLF6, and KLF16 throughout neuronal development from embryonic day 15.5 to post-natal age of one month. Expression of KLF family transcriptome was more concentrated in grey matter neurons. The microscopic analysis identified regions within the PMN circuit displaying probe-target binding, suggesting the potential involvement of these transcription factors in regulating PMN identity.

Conclusions:
Ongoing studies aim to characterize statistical significance further and establish the functional relevance of KLF expression in PMNs. However, unraveling the temporal expression patterns and putative roles of KLF family transcription factors in PMNs expands our understanding of breathing regulation. Further investigations into the functional significance of KLF transcription factors and their interactions with other crucial players in PMN identity maintenance are essential for advancing knowledge and translating findings into effective clinical interventions.

ABSTRACT #57

Genomic and mitochondrial characterization of RKO cell line

Devan Perera, Twinsburg High School; Maryssa Shanteau-Jackson, Vedant Thorat, Thomas LaFramboise, Department of Genetics and Genome Sciences, Case Western Reserve University

Background:
Colorectal cancer is expected to cause nearly 52,550 deaths in just 2023. Colorectal cancer can be very deadly, but different cancer cell lines have different mutations causing them to behave differently. Some of these mutations occur in the Mitochondrial genome of a cell and are often looked over; however, without inspecting the mtDNA, knowledge about the cell line may remain limited. Therefore, it is important to look into the mitochondrial DNA to find discrepancies between cell lines. RKO is a cell line of colorectal adenocarcinoma. The cell line was derived from a 63-year-old man with poorly differentiated cancer cells in the epithelial tissue of the colon. RKOs have a doubling time of about 36 hours. The cells also have MSI (Microsatellite Instability), which is when the number of repeated DNA bases in a small sequence of DNA is different from when the Microsatellite was inherited. This can be caused by mistakes that are left uncorrected in DNA Replication. This Cell Line is typically cultured in a supplemented medium.

Goals:
This project aims to culture the RKO cell line and sustain them in order to later screen the cell line for mitochondrial and nuclear DNA mutations such as the p53, KRAS, and TRβ genes. Doing so will allow for comparison with a similar colorectal cancer cell line SW480s.

Materials and Methods:
Cell culture was conducted to sustain both the RKO and SW480 cell lines. In silico analysis was carried out to determine genomic differences between cell lines. Thereupon, PCR and Sanger sequencing were used to confirm mutations found in the genomes. Finally, a mitochondrial stress test was performed to determine which cell line was more metabolic and to compare oxygen consumption rates in the mitochondria.

Results:
The data displayed that the SW480s were the more energetic cell line as they had a higher basal metabolic rate, higher OCR (Oxygen Consumption Rate), and a higher spare respiratory rate. Overall, due to a MT-TP mutation in the mitochondrial genome of the RKOs that affected the tRNA, RKOs were significantly less energetic.

Conclusions:
Overall, the results of the experiments illustrated that RKOs were much less metabolic due to mutations in the mtDNA that caused the cell line to have limited OXPHOS in the mitochondria. Because OXPHOS was limited, the cells struggled to keep up with the SW480s' production of ATP, so the RKOs lagged behind as the weaker metabolic line.

ABSTRACT #58

Optimizing an airbrush speckle pattern application for 2D and 3D Surfaces to use in DIC imaging

Sophia Pinto, Hawken High School; Katie Xu, Caroline Wilkowski, David Xiong, Kala Hurst, Dustin DeMeo, Bryan Carroll, Department of Dermatology, University Hospitals Cleveland, Case Western Reserve University

Background:
Digital image correlation (DIC) measures 3D deformation and strain over an object's surface, the DIC is commonly used with randomized speckle patterns. The software is able to take a picture of the surface and recognize areas of deformation/displacement on the speckle's surface.

Goals:
The overall goal of this project is to use speckle patterns measured with DIC to test the deformation in different length-to-width ratios of elliptical closure. The results will demonstrate how much deformation each suture caused concluding that the suture is ideal for the least defects. My part in the project is creating an optimal speckle pattern for both 2D surfaces with paper and 3D surfaces with pig skin, this allows for the project as a whole to have the best results.

Material and Methods:
My team used a VIVOHOME 110-120V Professional Airbrushing Paint System, after filling the airbrush tool with Createx water-based opaque airbrush color to spray a randomized speckling pattern on paper for a 2D model and pig skin as a 3D surface. Pictures are then taken of both models using my phone (iPhone 12), and the images are saved and uploaded to the program GOM Correlate where they are analyzed. GOM correlates rates of each speckle pattern with a score allowing for a comparison of what is considered an optimal speckle of 2D pattern versus the 3D patterns.

Results:
For data comparison, a percent was calculated for the quality of the speckle patterns. The average for 10 psi on paper is 83.07% (Standard deviation 0.19, 95% confidence interval 83.01% - 83.13%) and 99.47% pig skin (Standard deviation 0.03, 95% confidence interval 99.46% - 99.48%). When the air pressure was 20 psi the result on paper was 94.33% (Standard deviation 0.11, 95% confidence interval 94.03% - 94.63%) and 99.98% (Standard deviation 0.001, 95% confidence interval 99.9797% - 99.9803%) on pig skin. The results of 30 psi are 93.01% (Standard deviation 0.1, 95% confidence interval 92.98% - 93.04%) on paper and 97.84% (Standard deviation 0.06, 95% confidence interval 97.82% - 97.86%).

Conclusions:
The 240 samples obtained show that while there is a slight change in the quality of speckle pattern from air pressure the main difference is in the speckle pattern surface, whether it's 2D or 3D. The reason for this can be due to the thickness of each surface. A 3D surface such as pig skin is much thicker so as paint splatters the character is able to take in the pressure, while a 2D surface like paper does not have the thickness to be able to hold against the pressure. Instead, the paint bounces off the paper and splatters, creating a less optimal speckle pattern. For ideal results when creating a speckle pattern, it is best to use a 3D surface that has a thicker surface to withstand the pressure from the airbrush. While preparing to transition from 2D to 3D surfaces, one should expect the quality of the pattern to increase. After figuring out what variables help to make the speckle pattern optimal the following steps are speckling pig skin, suturing up the skin, then using DIC to test the deformation caused by the suture.

ABSTRACT #59

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

Alaina Pizarro, Hawken School; Dennis Gruszka, Fabio Cominelli, Division of Gastroenterology and Liver Disease, Department of Medicine, Case Western Reserve University

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. Individuals with inflammatory bowel disease have an increased chance of developing colorectal cancer. Genetic predisposition is also a known risk factor. Our laboratory is currently investigating the effects of chronic stress on tumor associated colon cancer using the Winnie mouse model of colitis-associated cancer (CAC). Our results show that chronic restrain stress increased colitis severity and tumor formation in Winnie mice.

Goals:
To determine the role of pro-inflammatory and anti-inflammatory cytokines in colonic tumorigenesis following chronic restrain stress.

Materials & Methods:
Gene expression of the following cytokines was evaluated by qPCR in the colons of stressed and unstressed Winnie mice: IL-17, IL-10, TNF, IL1alpha IL1beta, IL-6, IL-13, Slpi, IL-33, TLIA.

Results:
Preliminary results show a significant increase in the expression of colonic TNF, IL-1beta and IL-17 while no differences were observed for IL-10 and IL-33. My next experiments are designed to complete the analysis of the other cytokines and perform an unbiased RNAseq analysis of colonic tissues obtained from stressed and unstressed Winnie mice.

Conclusions:
Specific pro-inflammatory cytokines appear to be important mediators of stress-induced colonic inflammation and tumorigenesis. These results may help in elucidating the mechanisms of stress induced CAC and lead to the development of novel therapeutic modalities for this condition.

ABSTRACT #60

The impact of human patient mutations in UPF1 on Nonsense mediated mRNA decay while using a budding yeast model

Sofia Poindexter, Cleveland School of Science and Medicine; Sarah Nock, Kristian E Baker, Department of Genetics and Genomic Sciences, Case Western Reserve University

Background:
Nonsense mediated mRNA decay (NMD) is a process that recognizes and degrades mRNAs that have premature stop codons (PTCs). Three proteins; UPF1, UPF2 and UPF3 are required for NMD to occur within cells. Recently a patient with intellectual disability was found to have a mutation in his UPF1 gene. We hypothesize that this mutation impairs NMD and contributes to the patient's disability.

Goals:
Our goal is to test whether the patient mutation in UPF1 impacts NMD using a yeast model. We will perform a protein alignment analysis, in order to identify conserved amino acids between the human and yeast UPF1 protein. Also identify the conserved residue(s) in yeast UPF1 (yUPF1) and site-directed mutagenesis (SDM) to introduce the mutation in a plasmid-encoded gene of yUPF1. We will express the mutant UPF1 protein and appraise the effect of this mutation on NMD using the budding yeast model system.

Materials and Methods:
We have performed the human/yeast UPF1 protein sequence by using a multitude of alignment programs including Emboss, Expasy and NCBI blast. We will design and order DNA oligos which will be used in site-directed mutagenesis reactions (SDM), a Polymerase Chain Reaction (PCR)is a based technique used to introduce specific mutations to the DNA of a certain gene. Northern blot analysis will then be used to assay NMD efficiency in yeast.

Results:
Multiple protein alignments were performed and showed strong conservation between the human and yeast UPF1 proteins, including the position of a mutation in UPF1 identified in the male patient with intellectual disability. We have designed oligos to introduce the mutation into yeast UPF1 then performed SDM. With plasmid-encoded yUPF1; these experiments are still ongoing. Upon successful completion we will introduce mutant yUPF1 into yeast cells and perform Northern blot analysis to measure the effect of mutant yUPF1 on NMD.

ABSTRACT #61

In vitro Efficacy of an Enfumafungin Derivative Antifungal SCY-247 Against *Candida auris*

Samara Rivchun, Laurel School; Rachael Gowen, Mahmoud Ghannoum, Departments of Dermatology and Pathology, Case Western Reserve University

Background:
Candida auris **is a multi-drug resistant pathogenic fungus that has been affecting patients in hospital settings and has emerged as a public health threat.** ***C. auris*** **is resistant to commonly prescribed antifungals due to a high mutation rate. This multi-drug resistance presents challenges in treatment and is associated with higher patient mortality rates. A new enfumafungin derivative antifungal, SCY-247, targets the β-(1,3)-D-glucan cell wall enzyme of** ***C. auris*****, inhibiting the synthesis of glucan, a structural unit of the cell wall. SCY-247 provides a new treatment possibility for strains of** ***C. auris*** **that are resistant to other antifungals.**

Goals:
The goal of this study is to provide more clinical options for treating ***C. auris.*** **This study will address** ***C. auris*** **antifungal resistance and assess SCY-247** ***in vitro*** **for antifungal activity.**

Materials and Methods:
Scanning Electron Microscopy: ***C. auris*** **was standardized via nephelometer to 1.5 x 10^8 CFU/mL and incubated for 24 hours in the presence of SCY-247 at double the MIC_{50} (0.25 ug/mL). Following the 24h incubation, 1 mL of 2% glutaraldehyde was added and the mixture was chilled at 4℃. A 1% osmium tetroxide solution was added, then incubated at 4°C for 1h in the dark. The** ***C. auris*** **cultures were added to glass cover slips that were then sputter coated with Palladium for 60 seconds.** ***C. auris*** **cultures were then visualized using a ThermoFisher Apreo 2S Scanning Electron Microscope. Time Kill:** ***C. auris*** **was suspended in 10 mL RPMI media at a concentration of 1x 10^5 cells/mL. SCY-247 was added at 0.5, 1, 2, and 4 g/mL, respectively. Cell suspensions were incubated for 1, 4, 8, 24, and 48 hours. At the end of each time point, 100 uL of the cell suspension was diluted in media 1:4. 30 uL of the diluted suspension was plated onto PDA media plates. Culture plates were incubated for 48 hours at 37°C. Following incubation, colonies were counted and representative graphs prepared.**

Conclusions:
When treated with SCY-247, ***C. auris*** **showed changes in cell morphology, growth inhibition, and cell death. SCY-247 provides a possible new treatment alternative for strains of** ***C. auris*** **that are resistant to other antifungals.**

ABSTRACT #62

Impact of Gut Microbiome on Sex-Based Differences of Immune Profiles

Lilly Russo, Gilmour Academy; Hannah L. Wargo, Joseph Williams, Theresa T. Pizarro, Department of Pathology, Case Western Reserve University School of Medicine

Background:
Crohn's disease (CD), one of two major forms of inflammatory bowel disease (IBD), is a chronic, relapsing inflammatory disorder affecting the gastrointestinal tract. Epidemiology studies in Western cohorts indicate that the risk for developing CD has a female sex bias, particularly during adult life stages. Although it is well established that the gut microbiome plays an important role in the pathogenesis of IBD, its precise impact on sex-based differences is currently unknown. Work performed last summer confirmed sex-based differences in a well characterized model of CD-like ileitis, i.e., SAMP1/YitFc (SAMP) strain, showing an earlier onset and more severe disease in SAMP females (SAMP-F) vs. age-matched SAMP-M. Importantly, these differences were abolished in SAMP raised under germ-free (GF) conditions.

Goals:
To follow up on our prior findings, the aim of the present study was to determine potential mechanism(s) of microbiome-dependent sex-based differences in the pathogenesis of ileitis-prone SAMP mice by evaluating cytokine immune profiles.

Materials and Methods:
10- and 20-wk-old SAMP-M and -F mice raised under either specific pathogen-free (SPF) or GF conditions were sacrificed and ilea harvested for histological evaluation of disease severity by H&E staining and use of an established scoring system, and for cytokine immune profiling by RNA extraction followed by reverse transcription (RT)-quantitative (q)PCR. Multiplex immunoassays were performed using the Luminex instrument platform for protein quantification of Th1, Th2 and Th17 cytokines from isolated cells of draining mesenteric lymph node (MLN) from 20-wk-old SPF- and GF-SAMP that have been activated by anti-CD3/anti-CD28.

Results:
We confirmed our earlier results that SAMP mice show a clear female sex bias over their male counterparts in regards to onset (early) and severity of ileitis, and that these differences are dependent on the gut microbiome. Several cytokines were increased in SPF- vs. GF-SAMP, but particularly those with a Th17 type profile. Specifically, IL-17A protein levels were greater in SPF- vs. GF-SAMP, with increased expression in SPF-SAMP-F vs. -M mice. These sex-based differences were not present in GF-SAMP. Interestingly, no significant differences were found in Il17a mRNA expression levels. In addition, another Th17 type cytokine, IL-22, was increased in SPF- vs. GF-SAMP, which was confirmed at the mRNA level. However, despite the lack of differences in Il22, significant sex-based differences were found in IL-22 protein, with higher levels in SPF-SAMP-F vs. -M, which was not found in GF-SAMP.

Conclusions:
Taken together, our findings suggest that microbiome-driven sex-based differences in ileitis-prone SAMP mice may be attributed to Th17 type immune responses, which appear to be more robust in females compared to their male counterparts. These differences may have important implications for the pathogenesis and treatment of IBD patients based on sex, and lays the foundation for sex-based precision medicine approaches.

ABSTRACT #63

Multi-Parametric Magnetic Resonance Imaging to Detect and Characterize Chronic Kidney Disease in Children with Youth-Onset Type-2 Diabetes (DetectKID2)

Hamza Said, Westlake High School; Madison E. Kretzler, Katherine Kutney, University Hospitals Cleveland Medical Center; Chris A. Flask, Department of Radiology, Case Western Reserve University

Background:
Because of the increase in childhood obesity, Type 2 Diabetes (T2D) is now becoming more prevalent in school age children. In addition to other complications, children with Type 2 Diabetes (T2D) are also at higher risk to develop chronic kidney disease (CKD) at earlier ages. As they grow older, CKD can progress to end stage kidney disease (ESKD) requiring either kidney transplant or dialysis. Unfortunately, little is known about the actual incidence of CKD in children with T2D and the specific impact of obesity. In this study, we are using multiple Magnetic Resonance Imaging (MRI) methods to comprehensively assess kidney structure, function, and composition in cohorts of obese children with and without youth-onset T2D.

Goal: To use multi-modal MRI methods to determine the extent of early / moderate CKD in obese children with and without youth-onset T2D.

Methods: Obese children (age range = 14-19 years) and BMI > 95 percentile were recruited from the pediatric practices at Rainbow Babies and Children's Hospital according to an approved Institutional Review Board protocol at University Hospitals - Cleveland Medical Center. The children were stratified into two groups with (n=9) and without (n=15) T2D for at least 1-2 years. All subjects were scanned in the supine position without sedation and no injectable contrast on a Siemens Vida 3T MRI scanner. The approximately 30-minute MRI scanning protocol consisted of five parts: 1) localizer scans for kidney slice positioning; 2) MR Fingerprinting (kidney tissue composition); 3) Arterial Spin Labeling MRI (ASL, cortical perfusion in ml/min/100g); 4) Blood Oxygen Level Dependent MRI (BOLD, medullary oxygenation in 1/ms); 5) Diffusion Tensor MRI (DTI, medullary microstructure). A region-of-interest (ROI) analysis was used to calculate each MRI metric for each imaging slice of the left and right kidneys, and the results were averaged across all slices and both kidneys to calculate overall assessments for each subject. All MRI measures were compared between the two groups and with established normative values in healthy adult subjects using Student's t-tests. A p-value < 0.05 was considered significant.

Results: Clinical assessments have shown that a portion of the cohort without T2D have reduced kidney function (reduced eGFR) in comparison to the cohort with T2D. These findings are consistent with the MRI assessments of cortical perfusion. Further, the MR Fingerprinting assessments are showing significantly increased kidney T1 values for all of the obese subjects in comparison to healthy adult control subjects that may be suggestive of kidney hyperfiltration in early CKD. Corresponding microstructural (DTI) and medullary oxygenation (BOLD) MRI assessments are pending.

Conclusion: Multi-parametric MRI has the potential to assist clinicians in the understanding and eventually treatment of the impact of obesity and T2D on kidney structure and function.

ABSTRACT #64

The angiotensin receptor blocker, Losartan, is effective in maintaining reduced fibrosis using a model of DexM-induced remission in Crohn's Disease-prone SAMP mice

Anna V. Saline, Gilmour Academy; Joseph Williams, Carlo De Salvo, Stefania De Santis, Theresa T. Pizarro, Department of Pathology, Case Western Reserve University

Background:
Patients with Crohn's disease (CD) have an increased risk of developing fibrosis, which can result in stricture formation, stenosis, and potentially, the development of fistulae formation. Unfortunately, the only available treatment for fibrostenotic CD is surgery with a high recurrence rate. Thus, other non-surgical therapeutic options should be investigated, with the aim of both reducing the incidence, as well as decreasing the rate of recurrence, of fibrosis in patients with CD. Angiotensin receptor blockers (ARBs), also known as angiotensin II (AT2) antagonists, are best known as a treatment for patients with high blood pressure and heart failure. However, we recently showed that the ARB, Losartan, was efficacious in treating fibrosis in a mouse model of experimental Crohn's disease (*i.e.*, SAMP1/YitFc or SAMP strain).

Goals:
As a logical extension of this work, the aim of the present study was to test the ability of Losartan to either arrest or decrease inflammation-driven fibrosis in a maintenance of remission model, using ileitis/fibrosis-prone SAMP mice.

Materials and Methods:
20-wk-old SAMP mice with the established disease were administered dexamethasone (DexM) (1.0mg/kg, i.p., daily for 1 wk) to induce remission, and subsequently treated with/without Losartan (0.6 g/L in drinking water for the following 5 wks) in an attempt to maintain remission and potentially reduce gut inflammation and/or fibrosis. Mice were euthanized after the experimental period (6 wks total), and ileal tissues were harvested for evaluation of inflammation and fibrosis by H&E and Masson's trichrome staining, respectively, using established scoring systems. In addition, AT2 receptor expression was assessed in experimental mice by immunohistochemistry (IHC).

Results:
Our results showed the presence of AT2 receptors in ilea from SAMP mice that were increased in inflamed, fibrotic lesions compared to areas of healthy tissues. While treatment of SAMP with DexM displayed short-term beneficial effects by decreasing both inflammation and fibrosis, which slowly rebounded over a six-week period, back to the baseline of untreated control mice, maintenance of reduced fibrosis was extended after administration of Losartan vs. vehicle, independent of the degree of inflammation, in DexM-treated SAMP mice.

Conclusions:
These results suggest that administration of ARBs during periods of remission in patients with fibrostenotic CD may be effective in specifically decreasing and/or blocking the perpetuation of intestinal fibrosis, but may not help in reducing gut inflammation. Further studies are warranted to investigate optimal combination therapies to target both inflammation and fibrosis in this important patient population.

ABSTRACT #65

The Role of Macrophage-KLF6 in Stent-Induced Arterial Injury

Soham Shah, St. Ignatius High School; Ganapati Mahabaleshwar, Department of Pathology, Case Western Reserve University

Background:
Atherosclerosis is a major contributor to cardiovascular disease, characterized by plaque formation in arterial walls. Stenting, a common intervention for arterial blockages, can induce vascular injury and trigger smooth muscle cell accumulation. The role of KLF6, a transcription factor involved in cellular proliferation and differentiation, in regulating smooth muscle cell response to injury remains poorly understood.

Goals:
This study aims to investigate the impact of macrophage-KLF6 on inflammatory gene expression and arterial stenosis in the context of atherosclerosis.

Materials and Methods:
Two types of mice were used in this experiment, Wild Type (WT) and KLF6 Knockout (KO). The two types of mice were split into control mice (CC/CA) and wire induced injury mice (WIA/LC). The WIA mice had a wire pass through their carotid artery to induce injury. After 28 days the mice were euthanized and their carotid arteries were harvested. Arteries from male and female mice were tested alongside each other for each quantification. Smooth Muscle Cell Number, Smooth Muscle Cell Area, Macrophage Number and Macrophage Area were quantified using immunostaining techniques and ImageJ software. Luminal Area, Arterial Occlusion, Neo-intimal Area, and medial area were quantified using a modified Verhoeff Van Gieson Elastin staining kit to stain the arteries. Then, the internal elastic lamina (IEL) and the external elastic lamina (EEL) were measured by tracing the luminal surface. These measurements were used to calculate the luminal area, Neo-intimal area, arterial occlusion and medial area.

Results:
There was no significant difference in the gender of mice in any of the experiments. WIA WT mice showed a significant increase in Smooth muscle cell number, smooth muscle cell area, macrophage number, macrophage area, arterial occlusion, neo-intimal area, and medial area as opposed to their counterpart, WIA KLF6 KO. This in turn produced a significantly lower Luminal area for WIA WT mice.

Conclusions:
This study displays that KLF6 has a direct impact on wire induced injury through raising the count of macrophages and smooth muscle cells causing a decrease in luminal area and in increase in arterial occlusion.

ABSTRACT #66

The effects of mutations G350D and R710G on dynamin-related protein 1

Tasneema Shaik, Cleveland School of Science and Medicine; Anelise Hutson, Brianna Bauer, Jason Mears, Department of Pharmacology, Case Western Reserve University

Background:
Dynamin-related protein 1 (Drp1) is a key regulator of mitochondrial fission, the division of a mitochondrion into two or more. During mitochondrial fission, the role of Drp1 is to form helices and constrict the mitochondrial membrane upon GTP hydrolysis, eventually leading to mitochondrial fission. Mutations in Drp1 can cause structural and biochemical changes in the protein, leading to impaired mitochondrial fission. These mutations can also cause neurodevelopmental diseases in children, although the mechanism by which the mutations progress to the diseases is unknown. In this study, the effects of the mutations G350D and R710G on Drp1 are examined to analyze how specific mutations in Drp1 affect protein assembly and function.

Goals:
By examining the G350D and R710G mutations, our goal is to learn about the effects of these mutations on Drp1 biochemical and structural function and to gain insight into the mechanisms of how mutations in Drp1 can lead to neurodevelopmental diseases in children.

Materials and Methods:
In this study, mutations G350D and R710G were introduced into bacterial expression constructs through site-directed mutagenesis that allowed the Drp1 protein to be isolated. To functionally characterize Drp1, GTPase assays and negative stain electron microscopy (EM) were performed on WT (wild type) Drp1 protein, and similar procedures will be performed with the mutants once isolated. These activity assays and images will define differences between the normal (WT) and mutant (G350D & R710G) proteins by studying biochemical and structural functions.

Results:
The WT Drp1 protein was able to form spiral structures that were observed using a negative stain EM. We expect that the G350D mutation will cause an assembly defect as the mutation is located in the MD of the protein, so spirals would not be observed. We expect the R710G mutation to impair GTPase activity as the mutation is located in the BSE, adjacent to the GTPase domain.

Conclusions:
By analyzing the effects of specific mutations such as G350D and R710G on Drp1's assembly and function, we can understand the fundamental mechanisms by which neurodevelopmental diseases can arise, allowing us to gain invaluable knowledge on potential treatments for these diseases. Continuing to research mitochondrial dynamics is vital to fully understanding the role that mitochondria have in our body and improving human health.

ABSTRACT #67

The impact of social vulnerability index influx on overall and race-specific prostate cancer one-year survival over a 20-year period (2000-2020)

Anshul Sharma, University School; Weichuan Dong, Frederick R. Schumacher, Department of Population and Quantitative Health Sciences, Case Comprehensive Cancer Center, Case Western Reserve University

Background:
The Social Vulnerability Index (SVI) is a compilation of factors that represent the overall vulnerability of an individual's health based on their geospatial location and environment. These factors are key as they can impact cancer risks. Previous studies reported associations between SVI and cancer incidence and mortality rates, however these studies only examined one point in time.

Goals:
We examine changes in county-specific SVI values from 2000-2020 on changes in prostate cancer (PrCa) one-year survival for the overall population and by self-reported race.

Methods:
SVI county level data from 2000 and 2020 and Surveillance, Epidemiology, and End Results (SEER) patient level cancer data from 2000 and 2019 were utilized. For SVI and SEER datasets, all counties present in both data resources were included. SEER data was limited to all PrCa diagnoses over the age of 40, except for counties with less than 10 PrCa cases or no change in one-year PrCa survival. Chi-squared tests were performed for overall populations, stratified by race, and then stratified to only include SVI changes greater than 10% and less than -10%. An alpha level of 0.05 was applied to determine statistical significance and all analyses were performed in R 4.3.1.

Results:
Out of the 1006 total counties available in SEER, 590 were usable for the overall population, 397 for White PrCa, and 97 for Black PrCa. Overall, PrCa survival rates ranged from -25% to 22.6% and SVI changes ranged from -61% to 87%. A marginally statistically significant association between SVI changes and one-year PrCa survival was observed in the overall population (*p-value* =0.08). SVI changes greater than 10% or less than -10% resulted in a statistically significant association between SVI and one-year PrCa survival rates (*p-value* =0.02). This association was also observed when limiting the analysis to only White PrCa cases, (*p-value* =0.02). Our stratified analyses limiting to one-year PrCa survival rates for Black PrCa cases failed to reach statistical significance when examining any SVI change (*p-value* =0.62) or greater than 10% or less than -10% change (*p-value* =0.80). Overall, we observed positively correlated associations between increases of SVI (*i.e.* a decrease in social vulnerability) with one-year PrCa survival. These associations were statistically significant when SVI change was limited to a 10% change in either direction, thus indicating a threshold effect of SVI changes on cancer characteristics. These results were only replicated, however, when one-year PrCa survival rates were limited to White PrCa cases.

Conclusions:
The findings suggest a threshold effect of SVI changes on PrCa survival, emphasizing the role of social vulnerability in cancer prognosis. Our study is the first to establish the impact of SVI county changes across a twenty-year period with cancer survival, but additional research is still needed to determine the generalizability of these findings across other cancers, cancer stages, and with other self-reported racial groups. This study examines the impact of the Social Vulnerability Index (SVI) changes from 2000-2020 on one-year prostate cancer (PrCa) survival— for the overall population and stratified by race. Using SVI county data and Surveillance, Epidemiology, and End Results (SEER) patient data, we found a marginally significant correlation between SVI changes and PrCa survival in the overall population (p=0.08), reaching significance when SVI changes were greater than 10% or less than -10% (p=0.02). This pattern was replicated for White PrCa cases, but not for Black PrCa cases. Further research is needed to examine this association across other cancers, stages, and racial groups.

ABSTRACT #68

Association of MR image quality measures with diagnostic accuracy and inter-reader agreement of PI-RADS v2.1 for detection of Clinically-significant prostate cancer

Pranav Sompalle, Mayfield High School; Rakesh Shiradkar, Emory University; Satish E. Viswanath, Department of Biomedical Engineering, Case Western Reserve University

Background:
Prostate imaging reporting and data system (PI-RADS) guidelines have been established to standardize radiologists' interpretation of prostate cancer (PCa) on multi-parametric MRI (mpMRI) (ADC and T2W scans). PI-RADS scores (range 1-5) reflect the probability of PCa lesions being clinically-significant (csPCa) defined as International Society of Urologic Pathology Grade Group (IGG) > 1 on biopsy. PI-RADS is influenced by several factors including variable image quality limiting its usage for confirmatory non-invasive PCa diagnosis. Quantitative metrics derived from computational image processing can provide an objective means of assessing MRI quality.

Goals:
Use the open-source tool MRQy to derive quantitative image quality metrics of prostate bpMRI and evaluate their association with (a) accuracy of PI-RADS in detecting csPCa and (b) inter-reader agreement between PI-RADS scores.

Methods:
Multi-parametric MRI scans of N=99 patients from the ProstateX Challenge dataset were used in this study. IGG estimated from targeted biopsies were used to determine csPCa (IGG > 1). Four experienced radiologists (R_1-R_4) assigned PI-RADS v2.1 scores to each lesion using mpMRI. We derived image quality measurements of the T2W and ADC sequences using MRQy and rank-ordered them by their coefficients of variation. Metrics with the largest variation were SNR1 and SNR2 (signal-to-noise ratios). We computed median SNR1 and SNR2 values over the entire dataset individually for T2W and ADC and used them as thresholds to partition the dataset into four groups (G_{LL}, G_{LH}, G_{HL}, G_{HH}), subscripts representing low and high values for T2W and ADC, respectively. In a separate experiment, patients were sorted into Peripheral Zone (PZ) and Transition Zone (TZ) lesion groups and partitions were completed separately. Accuracy of PI-RADS within each of the four groups and for each reader (R_1-R_4) were computed using the area under the receiver operating characteristics curve (AUC). Fleiss' Kappa (κ) was used to determine inter-reader agreement of PI-RADS within each group. (Languages: Python, MATLAB)

Results:
Median thresholds of SNR1 and SNR2 quality metrics for T2W were 10.6, 9.1 and 35.7, while those for ADC were 12.1, 16.9 and 50.0, respectively. Mean AUC of PI-RADS assigned by four radiologists within G_{LL}, G_{LH}, G_{HL}, and G_{HH} groups based on SNR1 were 0.54 ± 0.08, 0.58 ± 0.17, 0.57 ± 0.09, and 0.63 ± 0.11. For SNR2, they were 0.57 ± 0.08, 0.64 ± 0.11, 0.49 ± 0.13, and 0.66 ± 0.14, respectively. Fleiss' Kappa (κ) of PI-RADS scores between the readers for G_{LL}, G_{LH}, G_{HL}, and G_{HH} groups based on SNR1 were 0.31, 0.21, 0.20, and 0.15. For SNR2, they were 0.32, 0.24, 0.20, and 0.12, respectively. For both PZ and TZ lesions, ADC SNR1/SNR2 impacted agreement and performance the most (G_{LH}).

Conclusions:
Quantitative metrics of image quality can be used to distinguish between low- and high-quality prostate MRI. Accuracy of radiological assessment of clinically-significant prostate cancer in terms of PI-RADS is significantly higher in patients with higher quality MRI, resulting in improved non-invasive prostate cancer diagnosis.

ABSTRACT #69

Long-term Androgen depletion in mice is linked with cognitive impairment

Diya Swain, Shaker Heights High School; Shiv Verma, Eswar Shankar, Sanjay Gupta, Department of Urology, Case Western Reserve University

Background:
Androgens play a neuroprotective role in maintaining the normal physiological functions of the brain. It also plays a pivotal role in prostate cancer development and progression. Current prostate cancer treatment is majorly based on androgen deprivation therapy (ADT) that blocks male hormone testosterone. More so, prostate cancer patients that undergo ADT have been shown to develop neuropathological conditions such as loss of memory, learning, reasoning, and decision making. Several studies have shown a positive association between ADT and risk of cognitive impairment. Currently there are no clinical markers to identify patients susceptible to ADT-mediated cognition. This demands a need for biomarkers that can help distinguish the vulnerability of patients toward cognitive impairment undergoing ADT. We utilized a mouse model to study the impact of ADT in different regions of the brain and to identify biomarkers of ADT.

Materials and Methods:
Sixteen-week-old BALB/c mice were gavage 50 mg/kg of enzalutamide (mimicking ADT) per day for 5 days per week (0.2 ml of vehicle consisting of 0.5% methyl cellulose and 0.025% Tween 20) for a total of 8 weeks. The control group of animals received 0.2 ml vehicle per day for the same time period. Mice were observed for behavioral changes post enzalutamide treatment. The experiment was terminated, brain was excised for cortex, cerebellum, and hippocampus and mass spectroscopy was performed. Differentially expressed proteins were identified and validated using quantitative real-time polymerase chain reaction (qRT-PCR) in the mice blood.

Results:
Enzalutamide treatment to mice for 8 weeks resulted in a modest weight gain and lack of attention and letharginess in these mice. Examination of H&E sections of the mice brain from the control group by light microscopy showed a normal morphology of neurons in the cortex. Enzalutamide treatment showed lower neuron density and signs of neuron injury, as well as cytoplasmic swelling of the astrocytes. Mass spectrometry analysis identified a number of differentially expressed proteins that were validated in the blood. These molecules include ABCB10, CAB, DAZAP1, DCU, DERL1, FBXO, MBNL, PUM2, SERL1, SLC8A3, SLC9A, TCF20, VIM, and ZYXIN. Among them the expression of SLC8A3, PUM2, and SERL1, were significantly higher compared to others in the enzalutamide treated group.

Conclusions:
Our findings demonstrate that enzalutamide treatment in mice demonstrate cognitive impairment similar to that observed in men on ADT protocol. Our study highlights that blood-based markers can be developed for ADT-mediated cognition that can lead to identification of new strategies for prevention and early intervention to improve quality-of-life for prostate cancer survivors.

ABSTRACT #70

The Impact of Covid-19 on Cancer (2019 - 2020)

Christopher Swetel, Campus International High School; Fangzhou Liu, Weichuan Dong, Siran Koroukian, Department of Population and Quantitative Health Sciences, Case Western Reserve University

Background:
Cancer diagnosed in an early stage is more likely to be treated successfully. Thus we aim to diagnose everyone at an earlier stage of cancer. With the Covid-19 pandemic hitting in 2020, we hypothesize that there will be a notable increase in late-stage cases due to a lower availability of doctors and screening equipment.

Goals:
This project aims to pinpoint what counties in Ohio had a change in specifically late-stage cancer results between 2019 (pre-covid) and 2020 (covid) and look for patterns and observations. Understanding what certain counties accomplished by not falling behind due to the Covid-19 pandemic can be critical in improving earlier diagnosis results on a county-wide level.

Methods and Materials:
The project included all 88 counties in Ohio. It focused on the four most common screenable cancers according to Surveillance, Epidemiology, and End Results Program (SEER) data: breast, prostate, lung and bronchus, and colorectal. All cancer-related data was pulled from the Ohio Cancer Incidence Surveillance System's (OCISS) Cancer Incident Data. Using the Python programming language and the open-source graphing library Plotly, we created choropleth maps, histograms, and bar charts to plot and visualize data from 2019 and 2020.

Results:
From analyzing a choropleth map of Ohio based on the case percentage difference from 2019 to 2020, we can observe that some counties had a percentage difference as low as -7.6% to as high as 7.5%. As we strive for more early-stage diagnosis results, the lower the percentage difference, the more positive a change occurs in the county as we want to lower late-stage diagnosis results. With our hypothesis expecting a drastic negative change between the two years, the average change of the 88 Ohio counties was only 1.5%. This small percentage change is excellent, as there was such a small difference during a global pandemic. When we look at the county types (Metro, Non-Metro, and Appalachian), we can see that Ohio's Appalachian counties contain some of the most negatively impacted counties, such as a 14.3% increase (the most significant increase among individual cancers) in late-stage Lung and Bronchus cancer in Hocking County. With Ohio's Appalachian counties having the most consistent counties with increases in late-stage cancers, the average change in percentage in the counties between the four cancers was only a 0.12% increase.

Conclusions:
Even with some counties' cancer results being impacted severely, our state-average case percentage difference was only 1.5%, giving us hope that even with an event as big as Covid-19, our cancer diagnosis will remain the same and even progressively get better over time.

ABSTRACT #71

Aggregation and cellular localization properties of human and mouse M- cone opsin

Maya Tang, Hathaway Brown; Sreelakshmi Vasudevan, Paul Park, Department of Ophthalmology and Visual Sciences, Case Western Reserve University

Background:
Cone opsins are light receptors located on the cone outer segments, and mutations in cone opsins are linked to defects in color vision. The C203R mutation of M cone opsin (MOP) in humans causes blue cone monochromacy, and the mouse ortholog of this point mutation is C198R. Properly folded MOP should oligomerize, and in cone photoreceptor cells, they traffic to disc membranes. In HEK293 cells, they traffic to the plasma membrane (PM). Misfolding and aggregation of cone opsins are thought to lead to protein retention in the endoplasmic reticulum (ER) and cone cell degeneration.

Goals:
The goal of this study is to characterize the aggregation properties and cellular localization of human and mouse M Opsin and their mutants *in vitro,* and to analyze the phenotype of C198R in a mouse model.

Materials and Methods:
DNA constructs coding for wild type (WT) human MOP, WT mouse MOP, human C203R, mouse C198R, each tagged with either yellow fluorescent protein (YFP) or mTurquoise2 (mTq2), were generated. HEK293T/17 cells were transiently transfected with a range of ratios of MOP vectors. Aggregation properties were determined by Förster resonance energy transfer (FRET) obtained from untreated cells and cells treated with n-dodecyl-B-D-maltoside (DM) followed by SDS detergent. FRET curves for Total FRET, DM-sensitive FRET (originating from oligomers), and DM-insensitive FRET (originating from aggregates) were generated. For the confocal microscopy analysis, HEK293T/17 cells were transiently transfected with the MOP vectors, and cells were subsequently treated with 15 μM 9-*cis* retinal. 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.

Results:
FRET analysis showed differential oligomerization properties of wild type human and mouse MOP. WT Human MOP showed higher DM-sensitive FRET, indicating that it existed as a mixture of oligomers and aggregates. WT Mouse MOP showed more DM-insensitive FRET, indicating that it misfolded and formed aggregates. Both human and mouse mutants displayed more DM-insensitive FRET, indicative of misfolding and aggregation. Confocal imaging confirmed the FRET data, with WT human MOP trafficking properly to the PM, and WT mouse MOP and both mutants trafficking to the ER. Treatment with 9-*cis* retinal allowed the mouse WT MOP, but not the mutant C198R MOP, to traffic to the PM.

Conclusions:
WT human and mouse M cone opsins differ in their aggregation properties *in vitro*. As a mixture of oligomers and aggregates, WT human MOP is more stable than WT murine MOP, which exists mainly as aggregates. Rhodopsin, the light receptor in rods, exists mainly as oligomers. Rhodopsin is more stable than both human and murine MOP. Both human C203R and mouse C198R mutants aggregate, which may underlie retinal cone cell degeneration. C198R could not be rescued by treatment with 9-*cis* retinal. Retinoid treatment is not predicted to be a valid therapeutic strategy.

ABSTRACT #72

The Effect of the Promyelocytic Leukemia Protein (PML) on Cancer Cell Glycolysis

Mythili Ungarala, Shaker Heights High School; Wilt Cao, Helena Zhao, Zixi Yun, Han Wang, Hung-Ying Kao, Department of Biochemistry, Case Western Reserve University

Background:
The Promyelocytic leukemia protein (PML) is a protein product of the PML gene. The PML nuclear body is a proteinaceous subcellular organelle assembled by different proteins that play substantial roles inside the nucleus. PML is thought to be a tumor suppressor protein. It is involved in many cellular processes and has proved to be vital in cancer research. Pyruvate kinase (PKM) is an enzyme involved in the last step of glycolysis, the first stage of cellular respiration, that converts phosphoenolpyruvate to pyruvate and produces energy, specifically adenosine triphosphate (ATP).

Goals:
This project aims to investigate PML's effect on cancer cell glycolysis, specifically the glycolytic enzyme, and see how the overexpression of the PML isoform affects the expression of PKM. We also looked for the localization of the exogenous protein HA-PML.

Materials and Methods:
The methods used for this experiment were the Immunofluorescence and Western Blotting techniques. Immunofluorescence is a technique that allows for visualization of different components in a given tissue or cell type, using a fluorescence microscope. Immunofluorescence (IF) can also tell the localization and the abundance of the protein of interest. Still, it could only give us a general idea of it and would not be as quantitative as Western blotting. Western Blotting is a technique used to detect a specific protein using antibodies specific to the protein. It uses gel electrophoresis to separate the sample's proteins and then transfer them out of the gel to the surface of a membrane, where Western blotting is performed. Western Blot allows for quantitative results to be found.

Results:
The results were found to conclude that PML 1 positively regulates the PKM. The overexpression of PML 1 causes the PKM to increase. When the PML 2 increases, the PKM decreases.

Conclusions:
The transfection technique is involved in overexpressing some particular types of PML isoform in order to know how one type of isoform could regulate the PKM by observing the degree of PKM expression inside the cancer cell through IF and Western Blot. The *PML* gene, as an oncogene, can facilitate vital cellular processes inside the cancer cells. Specifically, from this experiment, the amount of PKM increases as the amount of PML 1 increases indicating that PML could speed up the process of glycolysis and produce energy in the cell. In turn, the production of energy will favor a lot of activity of cancer cells, such as proliferation, survival under stress and harsh environment, and metastasis. On the other hand, PML2, which can negatively regulate the expression of PKM in cancer cells, plays the opposite role as PML 1 does. However, based on the previous studies, although isoforms other than PML1 have the totally opposite function as PML1, PML is still an oncogene since it consists of 70% of PML1 isoform.

ABSTRACT #73

Cloning the Human Beta-Actin Gene

Mythreyi Ungarala, Shaker Heights High School; Jessica Miley, Can Shi, Department of Medicine, Case Western Reserve University

Background:
The human beta-actin gene (ACTB) is a housekeeping gene that is transcribed continually and is required for maintenance of basal cellular function. It is one of the actin isoforms, meaning it is a protein that deals with cell motility and structure.

Goals:
The overall goal of this project is to successfully clone the ACTB gene through the pGEM T Easy Vector method. We hope to create multiple copies of the gene through PCR then go through ligation, transformation, digestion and finally sequencing to create an exact clone of the original gene.

Materials and Methods:
We first started with the polymerase chain reaction (PCR) testing to amplify the gene. To do this we used ddH_2O, 5x Taq buffer, 25Mqecl2, dNTP mix, primers: AETB-L27 and AETB-R215, T8, and GoTaq polymerase. Put into a 1% agarose gel with a 1kb+ ladder. To go through the cloning vector we used a ligation buffer, vector, the PCR product, T4 ligase and ddH_2O. For transformation we combined 3 microliters of the PCR DNA and 5 microliters of bacteria and let it sit for 30 minutes. We then went through a mini-prep to isolate and collect the plasmids. We digested twice using different enzymes. Digest No. 1 used a cutsmart buffer, ddH_2O, enzymes: Bsal1 and Sal1 and DNA from the blue and white colonies collected. They were put in 37 degrees celsius for 3 hours. Digest No. 2 contained the EcoR1 buffer, ddH_2O, enzyme: EcoR1 and DNA from the blue and white colonies collected from the transformation. They were then put into a 2% agarose gel with a 1kb+ ladder. To finish; the samples were sent in for sequencing.

Results:
The sequence came back, informing us that the cloning was successful.The three white colony vectors were successful while the singular blue colony vector was empty. This was to be expected because the blue colonies could not consume the plasmid- meaning there was no chance of cloning, while the white colonies successfully consumed the plasmid, in turn, successfully cloning the ACTB gene.

Conclusions:
My research has concluded that through the vector method, the human beta-actin gene can be cloned.

ABSTRACT #74

Malassezia Fungus Promotes Carcinogenesis of Hepatocarcinoma

Sahishnu Vallabhajoysula, Avon High School; Filip Sagl, Véronique Roche, Mei Zhang, Department of Biomedical Engineering, Case Western Reserve University

Background:

Hepatocarcinoma (Liver cancer) is a leading cause of cancer deaths worldwide, accounting for more than 700,000 deaths each year. In fact, even with modern therapies, the combined 5-year prognosis of liver cancer patients sits at a meager 17% compared to the national average of 67%. Recently researchers have attributed the potency of hepatocarcinoma to its ability to interact and manipulate its microenvironment. The tumor microenvironment (TME) is a collection of blood vessels, immune cells, signaling molecules, extracellular matrix, bacteria, and other biological factors that surround a tumor. Recently, researchers have uncovered multiple connections between the specific TME factors and carcinogenesis. One of these specific factors is the microbiome, a combination of bacteria, archaea, viruses, fungi, and protozoa present in the skin, oral cavity, and GI tract. In this study we evaluate a specific microbiota, Malassezia globosa (*M.gl*). Researchers have observed this fungus to translocate or migrate to the primary cancer site before disease progression in liver cancer patients. However, the mechanism at which M.gl influences cancer progression remains unknown. Previous studies, such as the one by Aykut Berk, have shown that some microbiome species promote carcinogenesis while others promote tumor suppression. Still, no studies have discerned the direct relationship between M.gl and liver cancer.

Goals:

This study aims to uncover whether M.gl has carcinogenic or tumor suppressive properties in Hepatocarcinoma as well as the effect of heat and time on these properties.

Materials and Methods:

First, HEPA cells were cultured in flasks (expanded/split as necessary) while a suspension of *M.gl* was created from colonies of fungus grown on agar plates. While the fungal suspension was shaking for 48hrs, a constant of 250K HEPA cells were plated into each of the 6 wells. Next, some suspensions of *M.gl* were heated to 90 degrees Celsius and were inoculated with fungus at HEPA:*M.gl* ratios of 2:1, 20:1, and 100:1 for both unheated and heated treatments. Duplicate plates were created with one plate co-culturing for 24hrs while the other for 48hrs. The negative control of HEPA only was cultured on a separate plate for both timepoints. Exact ratios were created through counting HEPA cells with an automatic counter; *M.gl* was counted manually with a hemocytometer. Immediately after inoculation microscopic pictures were taken of all conditions to analyze morphology changes. After each co-culture was finished, the cells were harvested to undergo RNA extraction and RT. The resulting cDNA was frozen and underwent SYBR qPCR the following day. Apoptosis genes include BAX, BAK & Caspase 1/11 and proliferation genes include BCL2, AhR, & HiLPDA; β-Actin and TBP were used for housekeeping. Lastly, ddCT analysis was performed to analyze genomic expression.

Results:

First, due to low RNA counts, we only were able to do qPCR on the 48hrs condition. Additionally, BAX, BAK, and HiLPDA were not expressed at all. For AhR we found that HEPA KO had a higher expression in the unheated condition than the heated condition. Furthermore, HEPA KO had a higher expression than HEPA WT. Both the pictures and qPCR showed this trend. More importantly, we found that lower amounts of *M.gl* resulted in decreased AhR expression and thus less proliferation in both KO and WT. In other words, higher amounts of *M.gl* may increase proliferation and carcinogenesis. For Caspase-1, there was a difference between HEPA KO and HEPA WT in the 100:1 unheated & heated condition. In line with AhR data we found that less *M.gl* increases apoptosis in HEPA KO, but not in HEPA WT. This means that higher amounts of *M.gl* reduces apoptosis, resulting in carcinogenesis once again. For Caspase-11, we generally found that HEPA WT had higher expression than KO and heated conditions

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were overexpressed compared to the unheated condition. Notably, we found that HEPA KO had less apoptosis expression as *M.gl* concentration increased, indicating carcinogenesis once again. Lastly, in BCL2 we found that all the conditions were underexpressed compared to the control, indicating less apoptosis expression in general. Furthermore, in HEPA WT apoptosis expression increases as *M.gl* concentration fell promoting carcinogenesis.

Conclusion:

Overall, we found that higher concentrations of *M.gl* resulted in proliferation and downregulated apoptosis, ultimately promoting the carcinogenesis of Hepatocarcinoma. Furthermore, *M.gl* had a greater effect on HEPA KO than HEPA WT. However, without the 24-hour time point, we cannot be fully confident. For future studies, we believe increasing the amount of initial mammalian cells to 500K instead of 250K will resolve the low RNA counts for 24 hours. In the end, understanding the role *M.gl* and the microbiome plays in hepatocarcinoma carcinogenesis will create new therapeutic targets for this deadly disease.

ABSTRACT #75

Evaluating Combination Treatment on Diffuse Intrinsic Pontine Glioma (DIPG) with CDDO-2P-Im Drug and Radiotherapy

Samuel Wales-McGrath, Twinsburg High School; Bhavya Sharma, Stevie Rieger, John Letterio, Department of Pediatrics, Case Western Reserve University School of Medicine

Background:
Pediatric cancers, particularly central nervous system (CNS) tumors, represent a significant cause of mortality among children in developed nations. Within this context, pediatric high-grade gliomas (pHGG) pose a formidable challenge. Diffuse intrinsic pontine glioma (DIPG), an aggressive and rare form of pHGG, primarily affects children ages five to ten and manifests in the ventral pons region of the brain. Treatment options for DIPG remain limited, with radiation therapy serving as the primary therapeutic modality. However, the efficacy of radiation therapy is hampered by adverse effects and the emergence of treatment resistance. To address these concerns, radiosensitizers such as CDDO-2P-Im assume a pivotal role. Acting as an enhancer of radiation therapy, CDDO-2P-Im augments its effectiveness by permitting the utilization of reduced radiation doses, thereby minimizing the potential cognitive consequences observed in pediatric patients. Additionally, manipulating the signaling pathway of the chemokine CCL2/MCP-1 offers a promising avenue for impeding glioma progression and augmenting immunotherapeutic responses. Synthetic oleanane triterpenoids, including CDDO-2P-Im, are currently being explored as potential inhibitors of CCL2/MCP-1, with researchers aiming to optimize the therapeutic outcomes of radiation therapy in DIPG while concurrently mitigating treatment-related toxicities.

Goals: Through rigorous research, our lab sought to test the efficacy of CDDO-2P-Im as a radiosensitizer through the use of combination therapy with radiation in a colony-forming assay. The hope was that the data would demonstrate statistical significance through a decrease in cell count with higher doses, which would illustrate an enhancement of the treatment.

Materials and Methods: To pursue the effects of CDDO-2P-Im in combination with radiation, cell harvesting of DIPG cell lines took place involving trypsinization; cells were detached from the culture and resuspended in a trypsin-inhibiting medium. Accurate cell counting was crucial for precise plating efficiency and survival calculations. Exponentially growing cells were plated into two new 12-well plates, incubated for adherence, and checked through imaging. Subsequently, cells were subjected to varying combinations of CDDO-2P-Im and radiation treatments (50nM, 1G, 50nM + 1G, 2G, and 50nM + 2G) or no CDDO-2P-Im treatment as a control group. The plates, including controls with no drug, were placed in a controlled incubator environment of 37℃ and 5% CO_2 humidity. After colony formation, cells were rinsed with PBS, stained with a glutaraldehyde-crystal violet mixture, and air-dried at room temperature. Following staining, cells could then be counted and statistically analyzed using imaging software.

Results: The results of the colony-forming assay showed a statistically significant decrease in both cell count and colony number in the radiation doses for which CDDO-2P-Im had been administered, indicating enhanced radiosensitivity of DIPG cells when subjected to the combination of CDDO-2P-Im and radiation therapy. This suggests that CDDO-2P-Im acted as a radiosensitizer, augmenting the effects of radiation treatment and leading to a significant reduction in cell viability and colony formation.

Conclusions: Future objectives include conducting in vivo studies using animal models to determine optimal dosages and safety profiles, paving the way for potential clinical trials. Also, through exploring relevant biomarkers, research can lead to personalized treatment strategies, improving outcomes for pediatric DIPG patients and potentially revolutionizing pediatric cancer care and offering new avenues for combating this aggressive disease.

ABSTRACT #76

Integrin Beta3-Mediated Cell Senescence and Colonic Abnormalities in Alzheimer's Disease: Insights from Bioinformatics Analysis

Evan J. Wang, Beachwood High School; Zhenxiang Gao, Rong Xu, Center for Artificial Intelligence in Drug Discovery, School of Medicine, Case Western Reserve University

Background:
Alzheimer's disease (AD) is a neurodegenerative disorder that ultimately leads to dementia. Currently, 50 million people worldwide suffer from AD, and the pathogenesis underlying AD pathology is unknown. While AD is primarily a neurological disease of the brain, individuals with AD often experience gut disorders, and gut abnormalities have been implicated as a major risk factor in the development of AD and relevant dementia. However, the mechanisms that mediate gut injury in AD remain unknown.

Goals:
In this project, we aim to identify key proteins and pathways involved in the gut injury of AD mice by bioinformatic approaches.

Methods:
Bioinformatics analysis was first conducted on the proteomics database of variously aged AD mouse gut tissues. An advanced artificial intelligence (AI)-based prediction system was then used to predict whether the genes identified by the bioinformatics are associated with AD phenotypes. In addition, an immunohistochemistry study was performed to validate the changes of proteins of interest in AD mouse colonic tissues.

Results:
Bioinformatic study found that levels of integrin beta-3 and beta-Galactosidase (beta-Gal), two markers of cellular senescence, increased with age in the colonic tissue of mice with AD, concomitant with the immune system disruption. Moreover, the advanced AI-based prediction of AD risk demonstrated the association between integrin beta-3 and beta-Gal and AD phenotypes. In addition, immunohistochemistry analysis validated the elevated levels of integrin beta-3 and cellular senescence in the colonic tissue of AD mice.

Conclusions:
The study provides a new bioinformatic understanding of tissue damage and cellular degeneration in AD and suggests that integrin beta-3-associated cellular senescence may function as a novel target mediating gut abnormalities during AD development.

ABSTRACT #77

GLP-1RA and gynecologic cancer risk in drug-naïve patients with type 2 diabetes: A nationwide retrospective cohort study in the US

Lindsey Wang, Orange High School; Rong Xu, Center for Artificial Intelligence in Drug Discovery; Nathan A. Berger, MD, Center For Science, Health and Society, Case Western Reserve University

Background:
Glucagon-like peptide-1 receptor agonists (GLP-1RA) are an FDA-approved medication for treating type 2 diabetes mellitus (T2DM). GLP-1RA has pleiotropic effects on lowering plasma glucose, inducing weight loss, and modulating the immune system. Since T2DM and overweight/obesity are risk factors for gynecologic cancers (GC), we investigated if GLP-1RA is associated with decreased risk of ovarian, endometrial, and cervical cancer. We compared GLP-1RA with 7 other anti-diabetic drug classes among drug-naïve patients with T2DM, including metformin and insulin, both suggested to impact GC risk.

Methods:
We used the TriNetX platform to access aggregated, de-identified electronic health records of nearly 96.7 million patients including 6.2 million with T2DM from 57 healthcare organizations in the US across 50 states, covering diverse age, race/ethnic, income, insurance groups and clinical settings. TriNetX built-in analytic functions allow for patient-level analyses, while only reporting population-level data.

The study population comprised 1,402,233 drug-naïve female T2DM patients prescribed anti-diabetic medication in 2005–2019, with no prior anti-diabetic prescription or GC diagnosis. GLP-1RA was compared to insulin, metformin, alpha-glucosidase inhibitors (AGI), dipeptidyl-peptidase-4 inhibitors (DPP-4), sodium-glucose cotransporter-2 inhibitors (SGLT2), sulfonylureas (SU), and thiazolidinediones (TZD). The time window of 2005–2019 was chosen due to GLP-1RA's approval in 2005.

Cohorts were propensity-score matched for demographics, adverse socioeconomic determinants of health, pre-existing medical conditions, genetic susceptibility to cancers, family history of cancers, and lifestyle factors. The outcome was the first instance of ovarian, endometrial, or cervical cancer within the 15-year time window starting from the first occurrence of the index event (prescription of GLP-1RA or other anti-diabetics) and was compared between matched cohorts.

Results:
GLP-1RA was associated with significantly decreased risk for ovarian cancer compared with insulin (HR: 0.48, 95% CI: 0.38–0.61), DPP-4 (HR: 0.78, 95% CI: 0.67–0.91), and TZD (HR: 0.75, 95% CI: 0.62–0.92). Lower but not significant risk was found when comparing GLP-1RA with metformin, AGI, SGLT2, and SU. For endometrial cancer, GLP-1RA was associated with significantly decreased risk compared with insulin (HR: 0.79, 95% CI: 0.67–0.92) and SU (HR: 0.86, 95% CI: 0.77–0.96). Lower but not significant risk was found when comparing GLP-1RA with metformin and SGLT2. For cervical cancer, GLP-1RA was associated with significantly decreased risk compared with insulin (HR: 0.35, 95% CI: 0.26–0.47), metformin (HR: 0.74, 95% CI: 0.56–0.98), SU (HR: 0.74, 95% CI: 0.61–0.90), and TZD (HR: 0.75, 95% CI: 0.60–0.94).

Discussion:
GLP-1RA was associated with a reduced risk of GC in drug-naïve T2DM patients compared to other anti-diabetic drugs, including insulin and metformin. Study limitations include potential biases due to the observational and retrospective nature of electronic health record analyses and uncontrolled confounders. Further research is warranted to investigate effects in patients with prior anti-diabetic treatments, different demographic groups, and the impact on obesity-associated cancers.

ABSTRACT #78

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

William Wang, Orange High School; Nora D.Volkow, National Institute Drug Abuse; David C.Kaelber, Rong Xu, Center for Artificial Intelligence in Drug Discovery; Nathan A. Berger, MD, Center For Science, Health and Society, Case Western Reserve University

Background:
Suicide was among the top 10 leading causes of death in the US. Anecdotal reports in people treated with semaglutide, a popular medication for weight management, describe reduced desire to smoking, alcohol drinking and other substance addictions, all of which are significant risk factors for suicides and suicide attempts. However most recently, cases of suicidal ideations have been reported in people treated with semaglutide. Currently it remains unknown of the net benefit and risk of semaglutide on suicidal thoughts.

Objectives:
To compare the risk of developing new diagnosis of suicidal ideations in patients with obesity and no prior history of suicidal ideation between those were prescribed semaglutide (Wegovy), vs other anti-obesity medications; (2) To compare risk for subsequent medical encounter for suicidal ideation diagnosis in patients with obesity and prior history of suicidal ideation between those who were prescribed semaglutide vs other non-GLP-1 RA anti-obesity mediations; (3) Similar analyses were performed in patients with type 2 diabetes who were prescribed semaglutide (Ozempic) vs other non-GLP-1RA anti-diabetic medications.

Design, Setting, and Participants:
Retrospective cohort study based on a multicenter and nationwide database of electronic health records (EHRs) in the US. There are 4 study populations to examine the preventive and treatment effects on suicidal ideations in patients with obesity and in patients with type 2 diabetes: (1) 206,910 patients with obesity and no prior suicidal ideations who were prescribed semaglutide or other anti-obesity medications during 6/2021-12/2022, (2) 1,450,586 patients with type 2 diabetes and no prior suicidal ideations who were prescribed semaglutide or other anti-diabetic medications during 12/2017-5/2021, (3) 7,164 patients with obesity and a prior diagnosis of suicidal ideations who were prescribed semaglutide or other anti-obesity medications during 6/2021-12/2022, (4) 15,601 patients with type 2 diabetes and a prior diagnosis of suicidal ideations who were prescribed semaglutide or other anti-diabetic medications during 12/2017-5/2021. Similar analyses were performed in study populations stratified by gender, age groups (<= 45 and >45 years old) and race (Black and White).

Exposures:
Semaglutide, other non-GLP-1RA anti-obesity medications, other non-GLP-1RA anti-diabetic medications

Main Outcomes and Measures:
Diagnosis of suicidal ideations and prescriptions of medications related to suicidal ideations pharmacotherapy. Hazard ratio (HR) and 95% confidence interval (CI) of outcomes within 6 month time frame after the exposure by comparing propensity-score matched cohorts using Kaplan-Meier survival analysis.

Results:
Semaglutide was associated with significant preventive effects in patients without a prior diagnosis of suicidal ideations: compared with other anti-obesity medications semaglutide was associated with significantly lower risk for first-time diagnosis of suicidal ideations in patients with obesity (0.13% vs 0.40%; HR: 0.32, 95% CI: 0.24-0.42). Similarly, semaglutide compared with other anti-diabetic medications was associated with significantly lower risk for first-time diagnosis of suicidal ideations

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in patients with type 2 diabetes (0.13% vs 0.44%; HR: 0.28, 95% CI: 0.19-0.42). Consistent reductions were seen in patients stratified by gender, age groups, and race. Semaglutide was associated with significant treatment benefits in patients with a prior diagnosis of suicidal ideations: compared with other anti-obesity medications semaglutide in patients with obesity was associated with significantly lower risk for follow-up medical encounter for suicidal ideation diagnosis (7.4% vs 14.9%; HR: 0.48, 95% CI: 0.35-0.65) and related medication prescriptions (70.2% vs 96.4%, HR: 0.31, 95% CI: 0.28-0.35). Consistent treatment benefits on suicidal ideation and in patients stratified by gender and age groups.

Conclusions:
Semaglutide was associated with significant lower risk for both first-time diagnosis of suicidal ideations and subsequent follow-up medical encounter for suicidal ideations and related medication prescriptions in patients with obesity and patients with type 2 diabetes, suggesting both its prevenative and therapeutic benefits on suicidal ideations. These findings are relevant to the development of guidelines for medication selections for weight and diabetic management in patients with prior history or at high risk for suicidal ideations and also inform future medication development for suicidal thoughts and behavior that minimizes risks while maximizing benefits.

ABSTRACT #79

Genotyping floxed mouse models to create conditional knockouts for cancer studies

Mya Williams, Charles F. Brush High School; Sanford Markowitz, Erika Cordova, Steven Fink, Department of Medicine, Case Comprehensive Cancer Center, Case Western Reserve University

Background:

Colorectal cancer (CRC) is the third most diagnosed cancer and the second most lethal type of cancer worldwide. The research focus of the Markowitz lab is to better understand the cause of CRC development with the hopes of discovering new therapeutic targets for disease treatment. Previously, the Markowitz lab has demonstrated that the prostaglandin-degrading enzyme 15-Hydroxyprostaglandin dehydrogenase (15-PGDH) acts as a tumor suppressor gene and expression is significantly downregulated in colorectal cancer tissues. In turn, suppression of 15-PGDH leads to upregulation of the prostaglandin PGE2, an important mediator of carcinogenesis Due to the link between loss of 15-PGDH expression and CRC development, the Markowitz lab seeks to elucidate the role of loss of 15-PGDH in CRC. The Markowitz lab also focuses on better understanding the carcinogenesis how a very rare form of CRC, Signet ring carcinoma CRC (SRCRC). SRCRC, is a highly malignant and aggressive subtype of CRC and patients with the disease have a very poor prognosis. After genetic analysis of SRCRC patient tumor samples, the Markowitz lab found inactivating mutations in the integrin alpha chain V(ITGAV) gene leading to speculation that ITGAV loss of function may be a key player in SRCRC development. Given the significant links between 15-PGDH and ITGAV in different subtypes, the Markowitz lab is working on creating conditional 15-PGDH and ITGAV knockout mouse strains by utilizing the Cre-loxP system. By creating these knockouts may allow the Markowitz lab to have further knowledge on the role of 15-PGDH and ITGAV in cancer and potentially other targeted disorders.

Goals:

The goal of this project is to help genotype mice strains used to create conditional 15-PGDH and ITGAV knockout mouse models. These knockout mice will be used for future studies of gastrointestinal cancers and other diseases.

Methods and Materials:

Tissue samples were collected using an ear or tail snip from 3-4 week old mice, were digested using NaOH and incubated at 95C for 90 minutes to isolate genomic DNA for genotyping. The tissue samples were then neutralized by adding 1M Tris (pH 7.5). The samples were then centrifuged and vortexed to get rid of any debris that are present.PCR genotyping reactions specific for each target gene mice were then setup using the FastStart Taq DNA Polymerase, dNTP Pack (Roche) and cycling conditions were run based on the corresponding protocol. After the PCR, the results are visualized using gel electrophoresis which results in clear pictures that let me find the different sample genotypes by analyzing the sizes of the different genetic bands present for each sample.

Results

The results found from the PCR samples collected from 15-PDGH floxed mice being backcrossed onto a C57BL/6J background revealed that there are several heterozygous offsprings (flox/+) that can be set up to use for the next generation of breeding cages. The mice have to first be backcrossed for 10 generations for studying purposes because mice with different backgrounds respond differently to certain cancers. The results from the ITGAV/Villin Cre PCR reveal that several mice heterozygous for the ITGAV floxed allele (flox/+) are now expressing the transgenic Cre gene (Villin Cre/+) needed to eventually inactivate ITGAV in the colon.

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Conclusions

Mice from two different mouse strains were successfully genotyped using three different PCR reactions, each one specific for a target gene. The 15-PGDH Flox/+ mice obtained from the F3 generation can now be used to establish F4 breeding cages by crossing them with wildtype mice to generate F5 litters. These mice will continue to be genotyped andcrossed until generation F10, at which time floxed heterozygous mice will be paired to generate 15-PGDH flox/flox mouse that will be bred with Cre specific mice to generate conditional knockouts in select tissue or cell types. As for the ITGAV/Villin Cre mice, the genotyping results reveal several mice expressing the Villin Cre transgene can now be used to set up additional breeding needed to potentially knockout ITGAV in the colon. Creating these conditional knockout models for 15-PGDH and ITGAV will allow the Markowitz lab to further explore the role of 15-PGDH and ITGAV in disease development and hopefully lead to future therapeutic practices for Colorectal Cancer (CRC) and Signet ring cell carcinoma (SRCC).

ABSTRACT #80

The Impact of SLX4IP on cell growth of HER2+ Breast Cancer

George Zaky, St. Ignatius High School; Deepak Babu, William Schiemann, Department of Biochemistry, Case Comprehensive Cancer Center, Case Western Reserve University

Background:
HER2+ breast cancers (BC) exhibit high aggressiveness and pose significant therapeutic challenges. Telomere maintenance mechanism (TMM) plays a crucial role in enabling the repeated proliferation of cancer cells, leading to their "immortality." TERT, a key component of TMM, has been identified as a potential target to eliminate cellular immortality. Eventually, an alternative mechanism known as Alternative Lengthening of Telomeres (ALT) can also cause replicative immortality in 15% of cancers. SLX4IP is identified as a key regulator in TMM in ALT-active cancer cells.

Goals:
This research aimed to investigate the effect of SLX4IP in cell proliferation and growth of HER2+ breast cancers.

Methods:
To evaluate the function of SLX4IP, we genetically engineered SLX4IP expression in SKBR3 and HCC1954 HER2+ BC cells by a shSRNA-based approach (shScram/shSLX4IP). SLX4IP knockdown was validated by qPCR and Western blotting. Multiple growth assays were conducted to assess the impact of SLX4IP in SLX4IP knockdown SKBR3 and HCC1954 HER2+ BC cells. We also performed qPCR and Western blotting to study the molecular mechanism of SLX4IP in SLX4IP-inhibited HER2+ BCs.

Results:
Our findings demonstrated that SLX4IP knockdown in SKBR3 and HCC1954 cell lines reduced proliferation and growth of spheroid when propagated in a 3D cell growth environment. Notably, colony assays indicated SLX4IP knockdown in SKBR3 cells nearly abolished cell colony formation, with minimal colonies observed, in contrast to approximately 250 colonies in SKBR3 cells without SLX4IP knockdown (shScram). Similar results were observed in HCC1954 cells. Our qPCR and western blot results showed inhibited GLI1 expression in SLX4IP deficient SKBR3 and HCC1954 cells. These results underscore the critical role of SLX4IP in cell proliferation and cell growth by affecting GLI1 in HER2+ BCs.

Conclusions:
This research provides valuable insights into the significance of SLX4IP in tumorigenesis of HER2+ BCs. The elucidation of SLX4IP's involvement as a tumor promoter by inhibiting GLI1, a key regulator of Hedgehog signaling in HER2+ BCs offers opportunities for novel therapeutic interventions.

ABSTRACT #81

Investigating the role of C1 esterase inhibitor in regulating thrombosis

Amy Zhou, Beachwood High School; Alvin Schmaier, Departments of Medicine and Pathology, Case Western Reserve University

Background:

This research is focused on the thrombosis-related phenotype of C1 esterase inhibitor (C1INH), a serine protease inhibitor that helps regulate the complement cascade, contact (intrinsic) pathway of coagulation, and the kallikrein kinin pathway. These pathways are important for physiologic inflammatory response and blood coagulation. In a hereditary angioedema (HAE) model, it is shown that the deficiency of C1 inhibitor is associated with increased susceptibility to vasodilation and increased vascular permeability due to the uncontrolled activation of these systems.

Goals:

The research goal is building upon previous research on the role of C1INH deficiency in the pathogenesis of HAE and to determine its potential impact on thrombotic risk. In the present experiment, we hypothesize that the absence of C1INH in the intravascular compartment will cause a disruption of physiological balance leading to a prothrombotic phenotype.

Materials and Methods:

Mice of two groups, wild type and *C1INH*$^{-/-}$, were anesthetized using a sodium pentobarbital solution intraperitoneally injected 5x the weight of the mouse in grams. Upon exposing the right common carotid artery of the mouse, a piece of filter paper soaked with a range of concentrations of 2-8% ferric chloride ($FeCl_3$) solution was placed on it. We studied the influence of the size of the filter paper being added to induce the thrombosis, ultimately deciding on 2 mm x 1 mm in size. At that site of the vessel wall, reactive oxygen species are liberated causing injury to the vessel wall by oxidizing the tissues on the artery. We serially check blood flow to the injured artery, and the time to vessel occlusion is noted. Another 20 minutes is monitored afterwards to establish its stability. 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 for each experiment. The data are presently being analyzed for differences between the two treatment groups.

Conclusions:

The conclusions as to whether the *C1INH*$^{-/-}$ mice are prothrombotic are in progress.

ABSTRACT #82

MFN2 a Potential Therapeutic Target for Alzheimer's disease

Julia Zhu, Hathaway Brown; Fanpeng Zhao, Wenzhang Wang, Department of Pathology, Case Western Reserve University

Alzheimer's disease (AD) is the most common age-related neurodegenerative disease that affects memory and learning. Mitochondria are critical to neuronal function in the brain, and brain mitochondrial deficits have long been documented before the clinical onset of AD, suggesting mitochondria dysfunction may play an important role in the pathogenesis of AD. Recent data suggest mitochondrial fragmentation in AD likely underlies impaired mitochondrial homeostasis and function in AD. Among the protein regulators of mitochondrial fusion and fission dynamics, mitofusin 2 (MFN2), a mitochondria fusion protein, is significantly downregulated in the brains of AD patients. This could be the reason for mitochondrial fragmentation in AD. In this study, we investigated the effects of MFN2 expression induced by BAY injections, an MFN2 inducer, in 5xFAD mice, an AD mouse model. We explored if BAY could rescue mitochondrial deficits in AD and whether mitochondrial rescue will alleviate other AD-related deficits. Currently, we are still investigating and conducting experiments. Overall, we hope to determine if MFN2 is a potential therapeutic target for AD.