University of Arizona Undergraduate Biology Research Program

30th Annual Conference

January 26, 2019 | 10:00AM - 3:00PM

Environment and Natural Resources 2 Building

UBRP.ARIZONA.EDU

The 30th Annual University of Arizona

UNDERGRADUATE BIOLOGY RESEARCH PROGRAM CONFERENCE

January 26, 2019
Environment & Natural Resources 2 Building

UBRP is made possible by support from the University of Arizona Office of the Provost, Office of Research, Discovery & Innovation, the BIO5 Institute, and the Deans of the Colleges of Science, Medicine, Agriculture & Life Sciences, Pharmacy, and the Mel and Enid Zuckerman College of Public Health.

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WELCOME

Dear Students, Faculty, Friends, Family, and Visitors:

Welcome to the 30th Annual UBRP Conference! In reflecting upon the activities, events, and most importantly, the people of UBRP at this milestone anniversary, I'm reminded of the things which make UBRP unique and special, and thought it would be fun to share some interesting UBRP facts with you.

Fact #1: UBRP was started because of a student. Back in 1988, an undergraduate named Teri Suzuki asked University of Arizona Professor Michael Wells a simple question: "Is it possible for a student to work in a real research lab?" Dr. Wells created an opportunity for Teri to work in his laboratory, and soon had additional undergraduate student scientists. Seeing the need to educate and support students in the conduct of scientific research, Dr. Wells invited Carol Bender to coordinate a formal research education program, and UBRP was born with 19 students and 13 faculty in its starting class. Three decades later, UBRP is running strong with approximately 2,500 alumni and continues to train and support around 100 undergraduate researchers each year.

Fact #2: People truly care about supporting college students through UBRP. Ever since the program's inception, the students in UBRP have been paid wages to enable them to offset college costs. These wages come from faculty mentors, committed units and colleges at the University of Arizona, grants, and private donors, including alumni, mentors, parents, and staff, who all value supporting UBRP students.

Fact #3: Lots of people enjoy learning science from UBRP students. Today's audience might be the most diverse audience to whom UBRP students will ever present! This afternoon, students may find themselves presenting to scientists, but also family members, representatives from industry, elected officials, UA administration, K-12 students and teachers, curious kids, fellow students, friends, the media, mentors, and visitors from the community.

Fact #4: UBRP has a big family. Interestingly enough, we have some *literal* family involvement in UBRP. Siblings have participated in the program, several UBRP mentors' children have been UBRP students, some UBRP alumni have actually returned to UA as faculty and now serve as UBRP mentors themselves, and even significant others have met in UBRP. (I have not yet met a current UBRP student whose parent was also a UBRP participant, but I suspect I will soon… and I look forward to the day I can add that to our list of UBRP family members!) However, our family also includes amazing volunteers like our Small Group Co-Leaders who help to train our students, Bridgitte Thum at KXCI Community Radio, who untiringly produces our weekly "Thesis Thursday" radio show, the faculty volunteers who educate students at our annual Ethics Retreat, established UBRP alumni who donate both time and money to support the next generation of UBRPers, and others. We are grateful for all of you!

I hope today's event gives you pause to reflect on the people for whom you are grateful, and that you enjoy the Conference, both as a celebration of scientific work and as an expression of gratitude for all who have made UBRP the excellent program that it is over the past thirty years.

Enjoy the conference!

Jennifer Cubeta
UBRP Director

30TH ANNUAL UBRP CONFERENCE AGENDA

ENVIRONMENT & NATURAL RESOURCES 2 BUILDING, 1064 E. LOWELL STREET

9:00am – 10:00am **CHECK IN**

GROUND AND SECOND FLOORS

- Check in at the Registration Table
- Preview students' posters (second floor)
- Meet & network with UBRP students, faculty mentors, alumni, and guests

10:00am – 11:00am **KEYNOTE ADDRESS**

ROOM N120, GROUND FLOOR

- Welcome by Jennifer Cubeta, UBRP Director
- UBRP Student Highlight Video
- Endowment Announcement and Acknowledgement of Donors by Dr. John Szivek, UBRP External Advisory Board Chairman
- Introduction of Keynote Speaker by Dr. William Montfort
- Keynote Address: "Never Tell Me the Odds: The Drug Discovery Process" by Dr. Teri Suzuki, UBRP Alumna and Senior Consultant for Therapeutics at Reglagene
- Poster Session Logistics by Jennifer Cubeta

11:00am – 2:00pm **UBRP POSTER SESSION & ACTIVITIES**

POSTER SESSION ON SECOND FLOOR IN ROOMS S215, S225, & S230

- Odd numbered posters present from 11:00am – 12:30pm
- Even numbered posters present from 12:30pm – 2:00pm

SCIENCE ACTIVITIES ON GROUND FLOOR

- Symbiosis: An Exhibit of Biological Art – Room S107
- Arthropod Diversity – Courtyard
- Shark Anatomy – Courtyard
- Science in Color - Courtyard

VIDEO BOOTH: SHOUT-OUTS OF GRATITUDE, RM. 120A (CANYON CAFÉ)

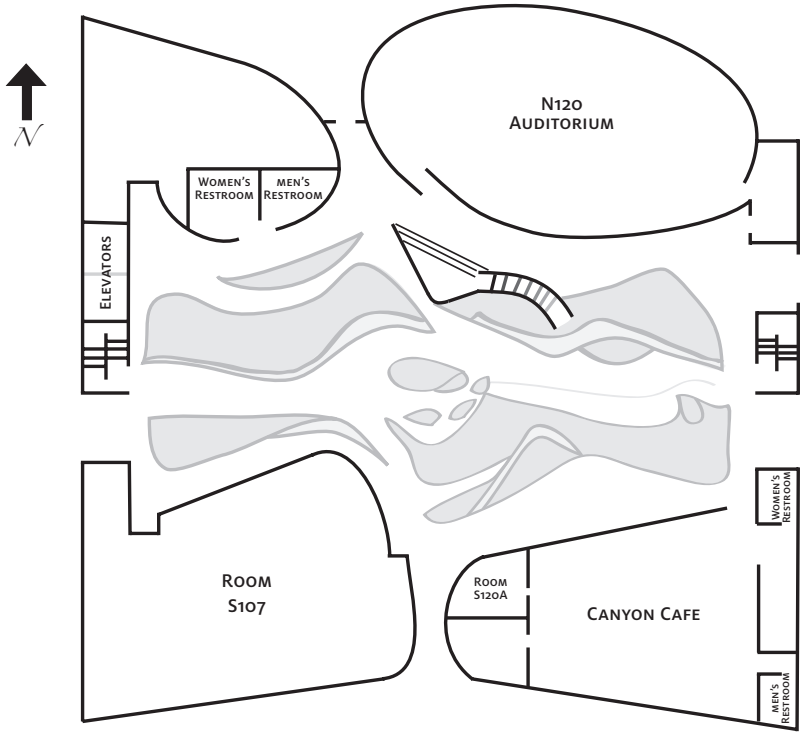
- Give someone the thanks they deserve!

2:00pm – 3:00pm **CLOSING: AWARDS PRESENTATION & DOOR PRIZES**

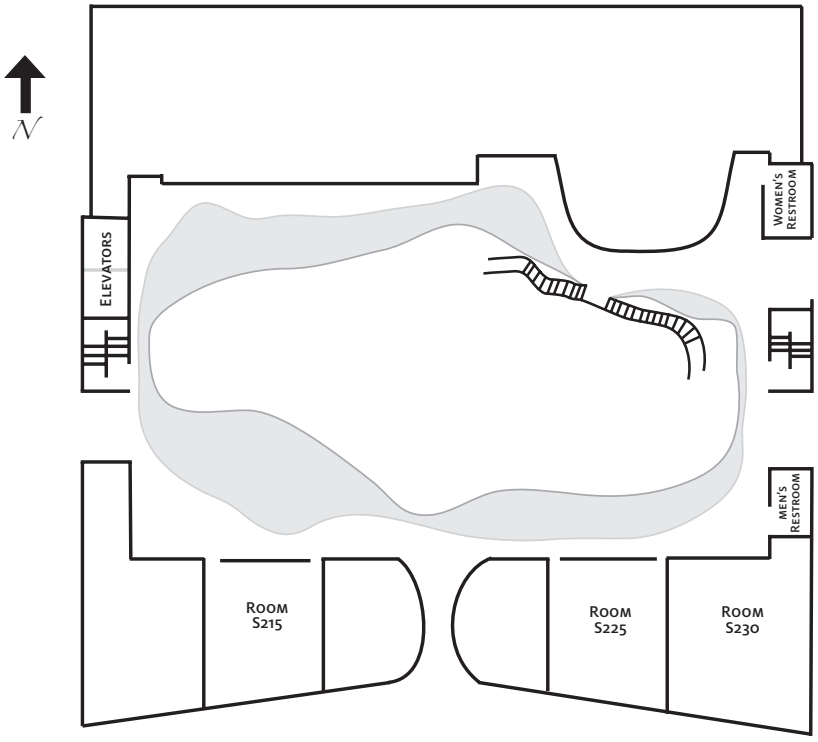
ROOM N120, GROUND FLOOR

- Outstanding Graduate Student Mentor Award
- Outstanding Faculty Mentor Award
- Recognition of UBRP Ambassadors
- Door Prizes
- Recognition of UBRP Poster Presenters

MAP OF VENUE:
ENVIRONMENT AND NATURAL RESOURCES 2 BUILDING



GROUND FLOOR



SECOND FLOOR

TODAY'S ACTIVITIES

10:00am – 11:00am ✹ KEYNOTE ADDRESS

"Never Tell Me the Odds: The Drug Discovery Process" by Teri Suzkui, PhD
UBRP Alumna and Senior Consultant for Therapeutics, Reglagene

INTRODUCTION OF KEYNOTE SPEAKER
BY DR. BILL MONTFORT, PROFESSOR, DEPARTMENT OF CHEMISTRY AND BIOCHEMISTRY

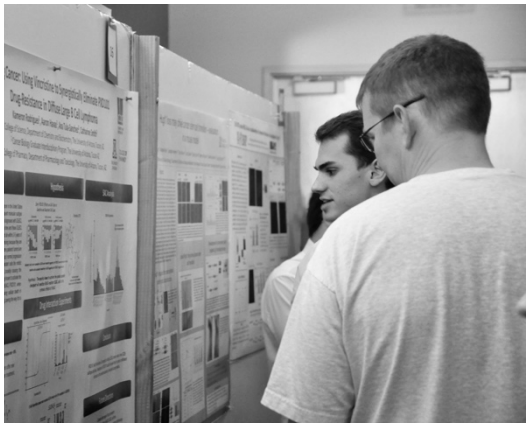
Teri Suzuki has more than 20 years of Pharmaceutical R&D experience. She began her career at Selectide (later Sanofi) where she led pharmaceutical Lead Discovery Projects which culminated in multiple advanced lead compounds, international patents and clinical candidate compounds. She forged and led several innovative collaborations with academic groups, biotech companies and larger partners, based on the vision of mutual benefit. Her areas of expertise are the identification of drug leads and lead compound progression. She holds undergraduate degrees in chemistry and biochemistry and a Ph.D. in biochemistry (University of Arizona). She is an Angel Investor with Tucson's Desert Angels and serves on the External Advocacy Board for the University of Arizona's Mathematics Department and proudly serves on the External Advisory Board for the University of Arizona's Undergraduate Biology Research Program.

11:00am – 2:00pm ✹ POSTER SESSIONS AND ACTIVITIES

STUDENT POSTER SESSIONS

SECOND FLOOR

If you have not been to a scientific poster session before, we invite our visitors to simply be curious and to ask question, such as "*Can you walk me through your poster? How did you get involved in research? What excites you about doing research? What is the 'take home' message from your project?"* Our students will be happy to share their research experiences with you! You can use the Topical Guide to UBRP Conference Posters and the List of Abstracts located in this booklet to help you identify posters of interest.



To give our own students a chance to see each other's work:

- Odd-numbered posters will be presented from 11:00am - 12:30pm.
- Even-numbered posters will be presented from 12:30pm – 2:00pm.

SCIENCE ACTIVITIES

GROUND FLOOR

- **Symbiosis: An Exhibit of Biological Art**, Ground Floor, Room S107. This event showcases the aesthetic appeal of the life sciences and celebrates the fusion of science and art. Symbiosis is hosted by the Neuroscience and Cognitive Science (NSCS) Ambassadors with support from the School of Mind, Brain and Behavior.
- **Arthropod Diversity**, Ground Floor, Courtyard. See arachnids, giant centipedes, and stinging insects! Hosted by Dr. Justin Schmidt, winner of the IgNoble Award and author of *The Sting of the Wild.*
- **Shark Anatomy**, Ground Floor, Courtyard. Learn the anatomy of sharks and how they play an important role in our ocean. Hosted by Marine Awareness and Conservation Society (MACS).
- **Science in Color**, Ground Floor, Courtyard. Explore scientific concepts with colorful experiments. Hosted by the Biochemistry Club.

ONE-MINUTE SHOUT-OUTS OF GRATITUDE!

GROUND FLOOR, ROOM S120A (entrance inside Canyon Café)

Our video booth is open to all conference visitors! Simply select a prompt and we'll film your response. We'll share your "gratitude videos" throughout the year on the UBRP website, Facebook, and Twitter.

REFRESHMENTS

GROUND FLOOR, CANYON CAFÉ

2:00PM – 3:00PM ✹ AWARDS PRESENTATION AND DOOR PRIZES

UBRP MENTOR AWARDS

Each year, we celebrate UA's supportive culture for undergraduate research and the outstanding mentorship UBRP students enjoy by granting the Outstanding UBRP Graduate Student, Postdoctoral Fellow, or Research Specialist Mentor and the Outstanding UBRP Faculty Mentor Awards. Candidates are nominated by current UBRP students and UBRP alumni. A committee composed of UBRP students and alumni reviews the nominees and selects the finalists.

2018 Outstanding UBRP Graduate Student Mentor Awardee:

Kristiane Torgeson Pelletier
Doctoral Student, Biochemistry
Nominated by Emilie Cuevas

Nominees: Katie Chenard (Doctoral Student, Ecology & Evolutionary Biology), Anna Figueroa (Research Technician, Ophthalmology & Vision Science), and Costanza LoCascio (Graduate Student, Barrow Neurological Institute).

2018 Outstanding UBRP Faculty Mentor Awardee:

Dr. Helena Morrison
Assistant Professor, Nursing
Nominated by Rebeca Gardner and Ayumi Pottenger

Nominees: Janis Burt (Professor, Physiology), John Jewett (Associate Professor, Chemistry & Biochemistry), Brian McKay (Associate Professor, Ophthalmology), and Rebecca Page (Professor, Chemistry & Biochemistry).

UBRP AMBASSADORS

UBRP Ambassadors, the reincarnation of the UBRP Undergraduate Student Advisory Group (USAG), is charged with the responsibility of helping to create community among undergraduate researchers by organizing social activities, providing feedback to the program director, and representing UBRP in speaking to on- and off-campus groups. We thank our 2018-2019 UBRP Ambassador officers for their service!

Tiffany Cho
President

Lauren Wilson
Vice President

Andrew Alamban
Secretary

Jason Juang
Treasurer

Allison Eby
Volunteer Chair

DOOR PRIZES

UBRP thanks the following organizations and companies for donating door prizes:

Chocolate Iguana 4th Espresso Bar Cafe Sweet Shop

Tohono Chul Gardens • Galleries • Bistro

Flandrau Science Center & Planetarium

Antigone Books

Tucson Botanical Gardens

KXCI Community Radio 91.3 FM Tucson

Biosphere 2 Where science lives.

ARIZONA ATHLETICS

SUPPORTING UBRP

THE NEW UBRP ENDOWMENT!

In the fall of 1988, undergraduate Teri Suzuki asked Professor Michael Wells a simple question: "Is it possible for a student to work in a real research lab?" Dr. Wells created an opportunity for Teri to work in his laboratory, and soon had additional undergraduate student scientists. Seeing the need to educate students in the conduct of scientific research, Dr. Wells invited Carol Bender to coordinate a formal research education program, and UBRP was born! Three decades later, UBRP is running strong with over 2,500 alumni and continues to train and support approximately 100 undergraduate researchers each year.

As UBRP celebrates its 30th anniversary, we are excited to announce that a generous UBRP alumna, Ms. Carol Arakaki, has initiated an endowment with the goal of making UBRP available to University of Arizona students *forever*!

The UBRP Endowment will be fully established in 2021 when an initial balance of $25,000 is reached and will provide steady funds equivalent to 4% of the endowment's balance on a yearly basis to support UBRP participants. As the endowment grows, we will be able to provide paid research positions for a growing number of UBRPers, regardless of changes in internal funding, the tenuous availability of external grants, and fluctuations in annual donor giving.

In celebration of UBRP's 30th anniversary, please consider giving to support UBRP students in one of the following ways:

Sustain UBRP for future students, via the new UBRP Endowment. Join our founding group and give to grow the endowment fund. The more quickly the endowment grows, the sooner UBRP will be able receive funds to support students!

Help our current students by making a contribution to the UBRP Fund. Contributions to this fund will continue to support our students with financial need by funding research positions for them throughout the academic year.

HOW TO GIVE TO UBRP

As always, contributions of any amount are greatly appreciated. We thank you for your support!

Each year, donors contributing $250 or more to either the UBRP Endowment or the UBRP Fund will become members of *Friends of UBRP*. These donors receive a yearly student highlight publication and have access to UBRP student hosts and reserved seating for the keynote talk at the annual UBRP Conference.

The University of Arizona Foundation is a tax-exempt 501(c)3 organization and your gift is tax-deductible.

To Give By Check:
Please make checks out to "The University of Arizona Foundation," and include one of the following notes on the memo line:

- UBRP Endowment, #20-10-2852
- UBRP Fund, #20-10-0426

You may drop off your check at the registration table during the conference, or you can mail it to UBRP, University of Arizona, P.O. Box 210106, Tucson, AZ 85721.

To Donate by Credit Card:
Donations can be made online at **http://ubrp.arizona.edu/donate**, or you may visit the registration desk during the Conference to contribute via credit card.

If you have any questions regarding a donation to UBRP or the new UBRP endowment, please contact Jennifer Cubeta, UBRP Director, at (520) 621-9348 or cubeta@email.arizona.edu.

THANK YOU TO OUR UBRP DONORS!

FRIENDS OF UBRP

Anonymous
Ms. Carol Arakaki
Dr. Craig Aspinwall
Dr. David Bellows
Dr. Sajiv Boggavarapu
Drs. Margaret Briehl and Dennis Ray
Drs. Gail Burd and John Hildebrand
Dr. Susheela Carroll
Ms. Roxie Catts
Mrs. Jennifer Cubeta
Mr. Richard Edelman
Dr. John Enemark
Dr. Brenda Gardner
Dr. Wulfila Gronenberg
Dr. Marilyn Halonen
(in memory of Michael Cusanovich)
Dr. Ronald Hammer
Dr. James Hazzard
Dr. David Johnson
Dr. Henry Johnson
Dr. Paul Klekotka
Dr. Megan O'Meara and Mr. Brian Massey
Dr. Janna Mundt
Mr. Robert and Mrs. Kim Nelson
Dr. Elena Plante
Mr. Robert Smith
Mr. Norman Soloway and Ms. Kay Ransdell
Dr. John Szivek
Ms. Samantha Szuter
Dr. Ronald Teed
Dr. Kenneth Teter
Dr. Allison Titcomb
Dr. Ilya Vilinsky
Mrs. Andrea and Mr. Doug Wellington
Dr. Jessica Yingling and Mr. Christopher Mahoney

Additionally, these individuals and entities have donated in 2018. We are grateful for your support!

The American Online Giving Foundation
Mr. Matthew Chuang
Ms. Monica Chaung
Ms. E.A. Coffman
Eli Lilly and Company Foundation
Dr. Jeffrey Frelinger
Mr. Mario Gastelum
Dr. A. Teresa Isaiass
Mr. David Gonzales
Dr. Xi He
Mr. Rohith Jayaram
Dr. Christina Kochel
Dr. Michael Kuhns
Ms. Rosalind Longmire
Mr. Clinton Musil (in honor of Carol Bender)
Dr. Daryn Stover
Ms. Cathy Tran
Dr. Elizabeth Vierling (in honor of Carol Bender)
Dr. Guang Yao

ACKNOWLEDGEMENTS

UBRP ADVISORY BOARD MEMBERS

John Szivek, Chair
Teri Suzuki
Nathan Ellis
Samantha Szuter
Kenneth Wertman
Henry Johnson
Sheldon Trubatch

Emeriti Board Members:
Carol Bender
John Enemark

SUMMER 2018 SMALL GROUP CO-LEADERS

UBRP students meet in small groups every other week during the summer to discuss their research with their peers. Faculty, postdocs, graduate students, and advanced undergraduates volunteer their time to facilitate these groups and to mentor undergraduate researchers.

We feel incredibly fortunate that these individuals volunteered their time and talents to serving as small group leaders in Summer 2018! We deeply appreciate their contributions to enriching UBRP students' experiences.

Tiffani Begay
Program Coordinator, Senior
NACP

Alura Benally
Graduate Student Assistant
NACP

Margaret Briehl
Professor
Pathology

Lindsey Crown
Doctoral Student
Psychology

Randall Eck
Beckman Scholar

Nichole Eshleman
Doctoral Student
Molecular & Cellular Biology

Lindsay Guzman
Doctoral Student
Chemistry

Ernesto Manzo
Doctoral Studen
Molecular & Cellular Biology

Stephanie Matijevic
Doctoral Student
Psychology

Arun Sambamurthy
Postdoctoral Research Associate
BIO5

Yannick Schreiber
Beckman Scholar

2018-2019 PEN PALS

During the 2008-2009 academic year, UBRPer Misha Pangasa, in conjunction with sixth grade teacher Patricia Robles-Medina at Mansfeld Middle School, initiated the UBRP Pen Pals Project. UBRPers volunteer to correspond with sixth grade students throughout the course of the year. Every May and December, UBRP students host their sixth-grade Pen Pals in a morning of science activities on campus. We thank everyone who participated in the program this year!

Rachel Bear
Pen Pals Coordinator

Ms. Susan Sumner
Mansfeld Middle School Pen Pals Teacher

Pen Pals:
Andrew Alamban
Alexis Anderson
Haley Arnold
Rachel Bear
Anne-Laure Blanche
Kiera Blawn
Casey Calderon
Swati Chandra
Randall Eck
Margret Fye
Emma Harrell
Jason Juang
Heber Lara
Samantha Macklin-Isquierdo
Caroline Plecki
Ayumi Pottenger
Shelby Rheinschmidt
Rachel Sadler
Matthew Scandura
Maria Catherine Schoelen
Dakotah Schreiner
Karen Serrano
Erica Spence
Sneha Srinivasan
Lauren Wilson

2018-2019 PARTICIPANTS AND FACULTY MENTORS

OVERVIEW

The programs housed within the Undergraduate Biology Research Program (UBRP) are designed to teach students science by involving them in biologically related research. Students are paid for their time doing research where they develop an understanding of the scientific method and receive a realistic view of research. They also participate in professional development workshops, scientific seminars, and supplementary activities to acquire the tools necessary to be successful in post-graduate studies should they choose careers related to biology or biomedical research and join a community of scholars as undergraduate researchers.

UNDERGRADUATE BIOLOGY RESEARCH PROGRAM (UBRP)

Funding for UBRP is provided by the UA Office of the Provost, Office of Research, Discovery & Innovation (RDI Research Fellows), the BIO5 Institute, and the deans of the Colleges of Science, Medicine, Agriculture and Life Sciences, Pharmacy, and the Mel and Enid Zuckerman College of Public Health. Additional funding is provided by private donors and the Western Alliance to Expand Student Opportunities (WAESO). We gratefully acknowledge this support!

Student	Mentor
Andrew Alamban	Janis Burt
Alexis Anderson (RDI Research Fellow)	Renee Duckworth
Haley Arnold	Mary Alt
Esther Bae	Todd Vanderah
Kayenat Aryeh (RDI Research Fellow)	Andrew Paek
Rachel Bear	Daniela Zarnescu
Shreya Bellampalli	Rajesh Khanna
Gabriel Birchak	Daniela Zarnescu
Anne-Laure Blanche	Renee Duckworth
Kiera Blawn	Tally Largent-Milnes
Kylie Calderon (RDI Research Fellow)	Kristian Doyle
Tiffany Cho	Haijiang Cai
Dez Coleman	Todd Vanderah
Angelina Condarcure	Craig Aspinwall
Emilie Cuevas (RDI Research Fellow)	Rebecca Page
Victoria Damore	Catharine Smith
Brandon David (RDI Research Fellow)	Mark Beilstein
Samantha Davidson (RDI Research Fellow)	Timothy Bolger
Lillian Delacruz (RDI Research Fellow)	Michael Riehle
Allison Eby	Stephen Cowen
Jordan Fink (RDI Research Fellow)	Oliver Monti
Makayla Freitas (RDI Research Fellow)	Rebecca Page
Steven Fried	Michael Brown
Margret Fye	Janis Burt
Maria Catherine Schoelen (RDI Research Fellow)	Jamie Edgin
Emily Galloway	Megha Padi
Marissa Giunta	Rajesh Khanna
Sarah Hancock	Ravishankar Palanivelu
Emma Harrell	Rebecca Mosher
Destiny Hodges (RDI Research Fellow)	Ramin Yadegari
Calvin Holst	Jean-Marc Fellous
Gregory Howard	Ravishankar Palanivelu

Student	Mentor
Victoria Howard (RDI Research Fellow)	A. Betsy Arnold
Jason Juang	Daniela Zarnescu
Caleb Kim	John Streicher
John Kim	Tally Largent-Milnes
Konner Kirwan	Lalitha Madhavan
Sakthi Kumar	Anita Koshy
James Lacey	John Allen
Maxwell Lagas	Ross Buchan
David Lasansky (RDI Research Fellow)	Indraneel Ghosh
Joo Ryung "Ray" Lee	Craig Aspinwall
Samantha Macklin-Isquierdo (RDI Research Fellow)	Daniela Zarnescu
Erin Mamaril	Stephen Cowen
Jacob Mapp (RDI Research Fellow)	Craig Aspinwall
Brenna McIntyre	Brian Enquist
Caitlin Moffett	Heddwen Brooks
Alexis Morrison	Aneta Kielar
Jibriel Noun	Michael Marty
Victor "Blue" Paat	Anna Dornhaus
Caroline Plecki	Mark Beilstein & A. Betsy Arnold
Shelby Rheinschmidt	Jian Gu & Jared Churko
Rachel Sadler	Wulfila Gronenberg
Estevan Sandoval (RDI Research Fellow)	Scott Boitano
Matthew Scandura	Daniela Zarnescu
Johnny Schmidt	George Sutphin
Dakotah Shreiner	Daniela Zarnescu
Sara Sillik (RDI Research Fellow)	Brian McKay
Saskia Smidt	Torsten Falk
Julian Somers (RDI Research Fellow)	Mark Beilstein
Madeline Souder	Jean-Marc Fellous
Erica Spence	George Sutphin
Sneha Srinivasan	Shwetal Mehta & Andrew Paek
Jack Stearns	Mark Beilstein
Arjun Syal	Lalitha Madhavan
Emily Turner	George Sutphin
Noelle Van Linden	Pelagie Beeson
Lauren Wilson (RDI Research Fellow)	Ross Buchan
Juliana Young (RDI Research Fellow)	Nam Lee & May Khanna

THE BECKMAN SCHOLARS PROGRAM

The Beckman Scholars Program is designed to help stimulate, encourage and support research activities by exceptionally talented undergraduate students at our nation's universities and colleges. The Beckman Scholarship at the University of Arizona provides funding for students to conduct in-depth research with one of 15 stellar research mentors in UA's College of Science. Funding for this program is provided by the Arnold and Mabel Beckman Foundation.

Student	Mentor
Randall Eck	Daniela Zarnescu
Yannick Schreiber	John Jewett
Amanda Warner	Ross Buchan

AMERICAN SOCIETY FOR PHARMACOLOGY AND EXPERIMENTAL THERAPEUTICS SUMMER UNDERGRADUATE RESEARCH PROGRAM (ASPET SURF)

The ASPET SURF Program, funded by a grant from the American Society for Pharmacology and Experimental Therapeutics, supports five undergraduate students per year who work under the mentorship of ASPET members. The program goal is to introduce undergraduate students to pharmacology research, using authentic, mentored research experiences to heighten student interest in careers in research and related health care disciplines.

Student	Mentor
Michael Gee	Ronald Lukas
Corwyn Krassy	Frank Porreca
Dominique Lund	Todd Vanderah
Angela Smith	Todd Vanderah
Carolyn Stine	John Streicher

ENVIRONMENTAL HEALTH SCIENCES: TRANSFORMATIVE RESEARCH UNDERGRADUATE EXPERIENCE (EHS-TRUE)

EHS-TRUE, funded by the National Institute of Environmental Health Sciences grant #1-R25-ES025494 under Dr. Walt Klimecki, provides classroom training, two years of paid training and research experience in an environmental health sciences research laboratory, and funds for tutoring and travel to scientific meetings. The program targets students from STEM-underrepresented backgrounds. The goal of EHS-TRUE is to enhance the competitiveness of our undergraduates for post-baccalaureate education in the environmental health sciences. Additional individual student support is provided by WAESO.

Student	Mentor
Casey Calderon	Nathan Cherrington
Adam Carl	Mary O'Rourke
Rebeca Gardner	Helena Morrison
Cheyenne Grabiec	Marti Lindsey
Christian Jennings	Jeong-Yeol Yoon
Ricardo Lira Jr.	Walt Klimecki
Juliana Ordine	Shane Snyder
Ayumi Pottenger	Helena Morrison
Karen Serrano	Julie Neilson
Ashley Tolton	Julie Ledford

PARTNERSHIP FOR NATIVE AMERICAN CANCER PREVENTION (NACP)

The Partnership for Native American Cancer Prevention **(**NACP**)** is a collaboration between Northern Arizona University and the University of Arizona's Cancer Center. The mission of the NACP is to alleviate the unequal burden of cancer among Native Americans of the Southwest through research, training and community outreach programs in collaboration with the communities they serve. The Training Core of NACP at the University of Arizona is led by Dr. Margaret Briehl, and funding for NACP is provided by the National Cancer Institute grant #2U54CA143924; additional individual student support is provided by WAESO.

Student	Mentor
Brenn Belone	Daniela Zarnescu
LeCario Benashley	Mary Koithan & Jared Churko
Alyssa Little	Robin Harris
Shanoa Nez	Ronald Heimark
Nancy Pham	Rajesh Khanna
Roxanne Vann	H-H. Sherry Chow & Heidi Hamann

TOPICAL GUIDE TO CONFERENCE POSTERS

BIOMEDICAL ENGINEERING

Presenter	Title of Poster	Poster	Room
Angelina Condarcure	OPTIMIZATION OF FIBER OPTIC ALIGNED CAPILLARY ZONE ELECTROPHORESIS WITH LASER INDUCED FLUORESCENCE	15	S230
Alana Gonzales	PAPER-BASED VERTICAL ASSAY FOR DETECTION OF METASTATIC BREAST CIRCULATING TUMOR CELLS	34	S225
Marianne Madias	A CLOSED-LOOP SYSTEM FOR JUXTACELLULAR PIPETTE CONTROL	54	S225
Jacob Mapp	DEVELOPING MORE COST-EFFECTIVE AND MOBILE CAPILLARY ELECTROPHORESIS INSTRUMENTATION THROUGH 3D PRINTING	56	S225
Frank Servin	ASSESSMENT OF PULMONARY ARTERIAL STRUCTURE AND ITS ASSOCIATION WITH RIGHT VENTRICULAR FUNCTION IN PULMONARY ARTERIAL HYPERTENSION	76	S215

CANCER

Presenter	Title of Poster	Poster	Room
Andrew Alamban	A TRUNCATED, 13KDA ISOFORM OF CX37 DOES NOT SUPPRESS PROLIFERATION OF RAT INSULINOMA CELLS	1	S230
Kayenat Aryeh	FOXO1 RESPONSE TO MTOR INHIBITORS IN SINGLE CANCER CELLS	2	S230
Haley Ciccone	CHRONIC ADMINISTRATION OF MORPHINE LEADS TO INCREASED BONE LOSS AND PROLONGED NEUROPATHIC PAIN IN A MURINE METASTATIC BREAST CANCER MODEL	13	S230
Alana Gonzales	PAPER-BASED VERTICAL ASSAY FOR DETECTION OF METASTATIC BREAST CIRCULATING TUMOR CELLS	34	S225
Emily Koons	EVALUATION OF A HUMANIZED SINGLE CHAIN VARIABLE FRAGMENT (SCFV) SPECIFIC TO PROSTATE STEM CELL ANTIGEN (PSCA)	47	S225
Heber Lara	THE ROLE OF NITRIC OXIDE IN CELL QUIESCENCE	50	S225
Angela Smith	MECHANISMS OF OPIOID-INDUCED TLR4 SIGNALING	80	S215
Sneha Srinivasan	CRISPR MEDIATED TAGGING OF ENDOGENOUS CELL FATE MARKERS	84	S215
Roxanne Vann	FORMATIVE QUALITATIVE RESEARCH TO INFORM A COMMUNITY NAVIGATION PROGRAM THAT SUPPORTS CANCER SURVIVORSHIP	90	S215

GENETICS

Presenter	Title of Poster	Poster	Room
Andrew Alamban	A TRUNCATED, 13KDA ISOFORM OF CX37 DOES NOT SUPPRESS PROLIFERATION OF RAT INSULINOMA CELLS	1	S230
Gabriel Birchak	UTILIZING CRISPR-CAS9 TO GENERATE A TRANSLATIONAL FUSION OF THE GENE ENCODING PHOSPHOFRUCTOKINASE WITH ENHANCED GREEN FLUORESCENT PROTEIN	6	S230
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A TRUNCATED, 13KDA ISOFORM OF CX37 DOES NOT SUPPRESS PROLIFERATION OF RAT INSULINOMA CELLS

***ANDREW ALAMBAN*, TASHA K. PONTIFEX, JANIS M. BURT**

Connexins (Cx) are important proteins that allow direct cell-cell communication via gap junction channels or permit cell-environment exchange of material via hemichannels. Benefits of these types of communication can be observed in Cx37, which is expressed in the arterial endothelium and suppresses proliferation during laminar flow but promotes proliferation in its absence. Our lab has shown that Cx37 expressed in rat insulinoma (Rin) cells limits the cells ability to multiply. The sequence of the Cx37 gene reveals an internal start codon analogous to that found in Cx43, which, if active, would produce a 13 kDa truncated isoform (13k) consisting of a fraction of the fourth transmembrane domain and the entire carboxyl terminus (CT). It is unknown whether growth suppression of Rin cells would be observed if only the 13k were present. In this study, we monitored the growth of Rin cells expressing 13k (iRin13k), Cx37 (iRin37), or neither (iRin) throughout the course of 21 days. Our results indicate that iRin13k cells proliferated comparably to iRin cells, whilst iRin37 cell proliferation was significantly less. This suggests that the 13k alone is insufficient to induce growth arrest in Rin cells. Since Cx37 mediated growth suppression depends on the phosphorylation state of the protein, we compared phosphorylation of Cx37 and 13kCx37 using mass spectrometry. No obvious differences were detected between growth arresting Cx37 and non-growth arresting 13kCx37, suggesting phosphorylation differences between the 13k and Cx37 protein are unlikely to explain differential growth effects. Previous work has shown that Cx43 interacts with its internally translated isoform (20kCx43). Their interaction enhances trafficking of Cx43 channels to the membrane. Moving forward, we will determine whether or not Cx37 and the 13k have similar interactions within the context of growth phenotype. Elucidating the mechanism by which Cx37 regulates growth might offer insight for novel therapeutic targets that can aid with either tumor suppression or wound-healing. This work was funded by the National Institutes of Health grant HL 122443, 1R01HL131712; and in part by the University of Arizona Undergraduate Biology Research Program with funds from the College of Medicine and private donors.

THE EFFECT OF WORD GENERATION ON THE RETENTION OF NOVEL WORDS IN CHILDREN WITH DEVELOPMENTAL LANGUAGE DISORDER

***HALEY ARNOLD*, LUCIA SWEENEY, ELENA PLANTE, MARY ALT, REBECCA GOMEZ**

Developmental Language Disorder (DLD) affects nearly 10% of the population and is characterized by persistent speech, language, and communication problems that are not accompanied by outside cognitive or intelligence impairments. Considering that children with DLD often struggle with learning and retaining vocabulary, we examined whether having a child with DLD generate a novel word out loud increases their ability to accurately recall and identify that same word. We taught nineteen monolingual four-year-old and five-year-old children (5 girls, 14 boys) six novel words over three sessions, half of which they generated twice per session, followed up with two tests to assess their retention of the words 48 hours and 3 weeks after the last session administered. Overall, no differences were found between retention of generated versus non-generated words at either the 48 hour or 3-week testing period, although we are continuing to examine the individual differences that may be present. This research indicates that although previous studies with typical language children showed better retention with word generation, that this may not be the case for children with DLD. This project is supported by the National Institutes of Health grant R01DC015642, the Undergraduate Biology Research Program with funds from the College of Science and Office of the Provost, as well as through the generous donations from Cecile Moore.

FOXO1 RESPONSE TO MTOR INHIBITORS IN SINGLE CANCER CELLS

***KAYENAT ARYEH*, JULIE HUYNH, ANDREW PAEK**

One of the biggest advancements in cancer treatment has been the development of targeted therapy. Unlike standard chemotherapy, targeted therapies go after specific alterations in cancer cells, minimizing the side effects in patients. However, many targeted therapies are not maximally effective because not all cancer cells die in response to the treatment. FOXO1 is a transcription factor that controls whether cells live or die in response to several different targeted therapies including mTOR inhibitors. We have tagged FOXO1 in lung cancer cells using CRISPR/Cas9. We are using these tagged lines to follow the FOXO1 dynamics of single cancer cells in response to the mTOR inhibitors to better identify patterns associated with cell death. This project is supported in part by the Undergraduate Biology Research Program with funds from the Office of Research, Discovery & Innovation, and private donors.

ENDOGENOUS PEPTIDE, ANGIOTENSIN (1-7), CONTAINS NEUROINFLAMMATION AND RESCUES COGNITIVE DECLINE AND NEURONAL LOSS FOLLOWING TRAUMATIC BRAIN INJURY (TBI)

***ESTHER BAE*, MICHAEL GAUB, RYAN P. BRUHNS, RACHEL B. DAVIDSON KNAPP, ANNA R. LARSON, ANGELA SMITH, DEZ COLEMAN, WILLIAM D. STAATZ, ALEXANDER J. SANDWEISS, BELLAL JOSEPH, MEREDITH HAY, TALLY M. LARGENT-MILNES, TODD W. VANDERAH**

Traumatic brain injury (TBI) is a leading cause of death in the U.S., accounting for 30% of all injury deaths. Nearly three million TBI-related emergency visits, hospitalizations, and death occur yearly. Falls, motor vehicle crashes, contact sports, and incident by being struck, are all leading causes of TBI - with these namely affecting children and the elderly. Non-fatal TBI ranges in severity from mild (i.e. concussions) to severe (long-term memory loss). In this area of study thus far, there is limited research in mitigating the post-inflammatory effects of non-fatal traumatic brain injury. Most recently, Angiotensin (Ang) 1-7, an endogenous peptide that acts on the MAS receptor, has shown to moderate heart failure. In the context of cardiac function, it is known to be anti-inflammatory, anti-oxidative, and vasodilatory. In addition to being cardioprotective, Ang 1-7 attenuates pain in cancer-induced bone pain models. Here, we asked the question of whether Ang 1-7 plays a key role in modulating neuroinflammation as an endogenous neuroprotective agent following mild TBI (mTBI). Administration of Ang 1-7 treatment following mTBI in mice resulted in significantly reduced expression of GFAP and phosphorylated Tau (inflammatory markers) in cortical and hippocampal tissue compared to that of saline-treated mice, suggesting containment of widespread inflammation through Ang 1-7 molecular intervention. Following Western blot analysis, cytokine dot blot screening was used to compare levels of proinflammatory mediators in mice serum between groups. Notably, novel objection recognition (NOR) served as our behavioral assay in measuring cognition following mTBI for treatment versus saline groups, where in which we found that the Ang 1-7 treated group had significantly higher NOR performance. Lastly, H&E staining and analysis (NIH ImageJ) of cortical and hippocampal tissue showed that Ang 1-7 treated mice had significantly reduced neuronal loss than their control counterpart structural histology confirming the biochemical workings of Ang 1-7. Together, the data and pathophysiology of Angiotensin 1-7 puts forth the induction of this novel therapeutic as an anti-inflammatory, anti-oxidative agent against secondary intrinsic injury following extrinsic mTBI. Supported by funding from the Undergraduate Biology Research Program with funds from the College of Medicine and private donors, and grants from the National Institute of Neurological Disorders and Stroke (R01NS099292), and the U.S. Army Research Laboratory and Defense Advanced Research Projects Agency (W911NF-15-1-0093).

FTIR BASED IMAGING METHOD FOR LOCOMOTOR FUNCTION ANALYSIS IN A *DROSOPHILA* MODEL OF ALS

***BRENN BELONE*, VINCENT BAI, MATTHEW SCANDURA, DIANA FERRO, DANIELA C. ZARNESCU**

ALS (amyotrophic lateral sclerosis) is a progressive neurodegenerative disease affecting the motor neurons of an individual. TDP-43, or TAR DNA binding protein 43 kDA, has been identified as a major disease protein within ALS. TDP-43 is hypothesized to regulate mRNA localization and translation in motor neurons. Therefore, mutations in the protein cause mRNAs associated with TDP-43 aggregation to forgo translation, creating dysfunction in the motor neurons. Through expressing human TDP-43 in a *Drosophila melanogaster* model, we are able to reproduce ALS phenotypes, specifically locomotion. Previously, to test locomotion, larvae turning assays have been the novel method. However, in attempt to reduce the variation often exemplified in this method, the goal of this project is to develop an automated system called FIM as a reliable and effective tool to test larvae locomotive function. Our recent data has replicated results from larvae turning and transitioning to the FIM system has been promising. Funding for this project has been made possible by the National Institutes of Health, the Muscular Dystrophy Association, the Partnership for Native American Cancer Prevention (NACP) through the National Cancer Institute Grant #2U54CA143924, and the Western Alliance to Expand Student Opportunities (WAESO) Louis Stokes Alliance for Minority Participation (LSAMP) National Science Foundation (NSF) Cooperative Agreement No. HRD-1101728.

UTILIZING CRISPR-CAS9 TO GENERATE A TRANSLATIONAL FUSION OF THE GENE ENCODING PHOSPHOFRUCTOKINASE WITH ENHANCED GREEN FLUORESCENT PROTEIN

***GABRIEL BIRCHAK*, ERNESTO MANZO, DANIELA C. ZARNESCU**

Amyotrophic lateral sclerosis (ALS) is a progressive neurodegenerative disease affecting motor neurons, and it typically results in patient death within three to five years of clinical diagnosis. To date, work in our laboratory has shown glycolytic upregulation in the motor neurons of a *Drosophila* ALS model, which is based on motor neuron-specific TDP-43 expression, and patient-derived tissue. Interestingly, in *S. cerevisiae* and at the synapses of *C. elegans* under hypoxic stress—a crude method to upregulate glycolysis by inhibiting oxidative phosphorylation—aggregates of several glycolytic enzymes, referred to as G bodies, have been observed. An especially notable enzyme found in G bodies is phosphofructokinase (PFK), which controls glycolysis' rate-limiting step. Given our findings that glycolysis is upregulated in motor neurons in a *Drosophila* model of ALS based on TDP-43 and the reports of pfk's association with G bodies, we hypothesized that aggregates localize to synapses in *D. melanogaster* expressing TDP-43 in motor neurons. To test this hypothesis, a translational gene fusion of PFK with enhanced green fluorescent protein (eGFP) was created using the adapted type-II CRISPR-Cas system. By implementing a custom gene-editing design strategy and co-injecting plasmids carrying the donor DNA and the genes encoding gRNAs into *D. melanogaster* embryos expressing Cas9 fused to nanos' promoter and 3' untranslated region, homology-directed repair (HDR) efficiency of approximately 30% was achieved—quantified based on eGFP expression in day-one pupae. The research was made possible by funding from the Bio5 Institute, the Muscular Dystrophy Association (grant #: MDA 418515), the National Institute of Health (grant #: R01 NS091299), and the HHMI Gilliam Fellowship.

INFLUENCE OF SOCIAL CONTEXT ON EXPRESSION OF AGGRESSION IN THE ZEBRA FINCH

***ANNE-LAURE BLANCHE*, KATHRYN CHENARD, RENÉE A. DUCKWORTH**

By definition, social behaviors are always expressed in the context of other individuals. However, this makes measuring them in a standardized fashion difficult because measurements outside the normal social context may not reflect the true measure of behavior. Here, we assess the importance of social context in the expression of aggression in zebra finches, a social species in which aggression is important in establishment of dominance hierarchies and resource acquisition. Aggression was measured repeatedly in twenty-two individuals in a flock context and was measured once for each individual in isolation. Birds in a flock were recorded at a treat feeder, and the number of aggressive interactions as well as their dominance position in the flock

were assessed. In isolation, aggressive response to individuals own reflection in a mirror was scored. Preliminary results indicate that aggression and dominance are highly repeatable in the flock context and are positively correlated with one another. These flock measures will be compared to measures of aggression from a solo mirror test, in which the bird's response to an equal intruder is measured. Given that most studies use the solo mirror test to measure aggression in this species, it will be important to determine whether it correlates with variation in aggression that is expressed in more naturally occurring flock contexts. This project is supported in part by the Undergraduate Biology Research Program with funds from the BIO5 Institute and the College of Agriculture and Life Sciences.

EXPLORING THE SEX DIFFERENCES OF OATP1A2 AND ITS IMPLICATIONS IN MIGRAINES

KIERA BLAWN, **TALLY LARGENT-MILNES, ERIKA LIKTOR-BUSA, AND VANI VERKHOVSKY**

Migraines affect around a billion people worldwide, and two-thirds of those afflicted are women. Cortical spreading depression (CSD) has been implicated in aura, a stage in migraines characterized by disturbances in sensory and motor functions. CSD is observed in the brain as a wave of hyperactivity and then inhibition. During CSD, changes in the permeability of the Blood Brian Barrier (BBB) have been found. Transcellular changes to the BBB suggest alteration of membrane transporters. A transporter called OATP1A2, found in the capillary endothelial cells of the BBB, uptakes anti-migraine agents into the central nervous system, and its expression levels have been observed to increase during migraines. The upregulation of OATP1A2 could result in a change in the uptake of migraine drugs and needs further study. Due to the discrepancy between male and female migraine rates, it is important to determine if there is a relationship with sex hormones and the proteins that are thought to play a role in migraines. This project established a baseline for OATP1A2 in naive female and male rats to see if there was a difference in expression based on sex and to find the standard level of protein expression to compare in future experiments that will induce CSD in rats and measure the changes in OATP1A2 and anti-migraine agents' uptake. Using Western Blots, it was found that there is no significant difference in the expression level of OATP1A2 between male and female rats, but this project has laid the groundwork for further experiments regarding OATP1A2 and its role in migraines. This project is supported in part by the Undergraduate Biology Research Program with funds from the BIO5 Institute.

MRP2 ALTERATIONS IN NASH/NAFLD LIVERS TREATED WITH SORAFENIB

CASEY CALDERON**, ERICA TOTH, NATHAN J. CHERRINGTON**

Sorafenib is a platinum-based chemotherapeutic approved for the treatment of renal cell, hepatocellular, and iodine resistant thyroid carcinomas. The disposition and metabolism of environmental toxicants and pharmacological agents, such as sorafenib, can be summarized in 4 processes: absorption, distribution, metabolism, and excretion. The liver is the primary organ for ADME processes in the body. As a result of ADME processes in the liver, sorafenib undergoes glucuronidation and is metabolized to sorafenib-glucuronide. One current theory in liver detoxification from sorafenib is that of hepatocyte shuffling, in which sorafenib is brought into hepatocytes via organic anion transporting polypeptides (OATPs) and converted into its metabolite form, sorafenib-glucuronide. Some of the sorafenib-glucuronide exits the hepatocyte into the bile via other transporters known as Multidrug resistance-associated protein 2 (MRP2), and some ends up back into circulation via Multidrug resistance-associated protein 3 (MRP3) transporters. The remaining circulatory sorafenib-glucuronide then enters the next hepatocyte again via OATP transporters, and so forth. This ensures efficient biliary excretion and proper hepatocyte detoxification Liver diseases, such as Nonalcoholic Steatohepatitis (NASH) can alter the functions of transporters, such as Multidrug resistance-associated protein 2 (MRP2), that are responsible for the excretion of sorafenib-glucuronide. NASH is the most advanced form of nonalcoholic fatty liver disease (NAFLD), and is marked by scarring, inflammation, and irreversible liver cell damage. NAFLD/NASH are thought to be the hepatic manifestations of metabolic syndrome, which is a cluster of symptoms such as obesity, hyperinsulinemia, and hypertension that is associated with increased cardiovascular risk. It is currently estimated that up to 30-50% of the American adult population has NAFLD, and 5-15% have NASH. Given the high incidence of the disease in the United States, it is likely that some of the patient population with NAFLD/NASH will be given sorafenib as a chemotherapeutic. We have found via western blots that NASH livers show some alterations in the expression of MRP2

compared with healthy livers. Finally, NASH should be considered as a source of inter-individual variation in the response to environmental exposures. The research is supported by funding from the Environmental Health Sciences – Transformative Research Undergraduate Experience (EHS-TRUE) through the National Institute of Environmental Health Sciences Grant #1-R25-ES025494.

CYCLODEXTRIN DECREASES IMMUNE CELL INFILTRATION IN CHRONIC STROKE INFARCTS IN A MOUSE MODEL OF STROKE

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Ischemic stroke occurs when an artery that supplies blood to the brain is blocked, thereby depriving tissues of oxygen and nutrients. In response to ischemia, damaged tissue in the brain undergoes liquefactive necrosis, a process through which tissue degrades and is transformed into a liquefactive mass. We have shown that stroke infarcts in the stage of liquefactive necrosis are sites of chronic inflammation, which we suspect prolongs the healing process and causes secondary neurodegeneration. In a mouse model of stroke, we previously found a second wave of inflammation between four and eight weeks post-stroke, as demonstrated by elevated cytokine and chemokine expression and which coincided with an accumulation of cholesterol crystals within the infarct. Because of the association between cholesterol crystal accumulation and chronic inflammation, the goal of the current study was to determine if stroke recovery in mice can be improved by preventing cholesterol overloading within phagocytic cells through treatment with cyclodextrin, an FDA-approved drug shown to increase cholesterol solubility, promote removal of cholesterol from foamy macrophages, and initiate anti-inflammatory mechanisms. To accomplish this goal, we used immunostaining to compare the chronic inflammatory responses of cyclodextrin-treated and saline-treated mice to stroke. Although we found no evidence of less cholesterol accumulation or less neuronal death in cyclodextrin-treated mice than in saline-treated mice, we did find evidence that cyclodextrin-treated mice experienced less of an immune response to stroke than saline-treated mice. Specifically, at seven weeks post-stroke, we found a smaller infiltrate of IgA+ and CD138+ plasma cells, B220+ B-lymphocytes, and CD3e+ T-lymphocytes in the chronic stroke infarct of cyclodextrin-treated mice when compared with that of saline-treated mice. Because matrix metalloproteases are expressed by immune cells and cause the fragmentation of tight junctions that compose the blood brain barrier (BBB), we suspect that by reducing the immune cell infiltrate in the infarct, cyclodextrin could help preserve the BBB following stroke. Possible future studies will use immunostaining, multiplex immunoassays, and behavioral testing to further investigate the effectiveness of cyclodextrin treatment, both alone and when used in combination with a liver X receptor (LXR) reverse cholesterol transport agonist, on improving stroke recovery in mice. This work was supported by the Undergraduate Biology Research Program with funds from the Office of Research, Discovery & Innovation, and the Office of the Provost; and the Western Alliance to Expand Student Opportunities (WAESO) Louis Stokes Alliance for Minority Participation (LSAMP) National Science Foundation (NSF) Cooperative Agreement No. HRD-1101728.

RETURNING STUDY MEASUREMENTS TO PARTICIPANTS OF THE HOPI ENVIRONMENTAL HEALTH PROJECT

***ADAM CARL*, MARY KAY O'ROURKE, ROBIN HARRIS**

The Hopi Environmental Health Project (HEHP) measures PM2.5, NO, NO_2, CO, CO_2, SO_2, temperature, humidity, CH_2O, radon, gamma radiation, arsenic exposure, household moisture, and metals in both the heating and non-heating season. Health assessments include spirometry, Fractional Exhaled Nitric Oxide (FeNO), height, weight, blood pressure, heart rate, and dietary intake. Returning of study results to the Hopi Community, along with other Native American communities, is an emerging issue for researchers due to cultural sensitivities. Our study seeks to understand how to return environmental health results while respecting cultural and religious values. A template for returning and reporting study results was created to provide participants with clear understanding of study results. This template incorporated traditional features such as the Hopi

traditional home, colors, and vocabulary. The template identifies likely sources of contaminants, recommends approaches participants may take to eliminate or reduce their exposure to sources, and describes potential health effects. We spent about one and a half hours at each home returning results and answering any questions the participants may have regarding the content of their results package. The participant and I independently completed an evaluation at the end of each visit. Participants were asked about the information they valued most, which included the clarity of presentation (everything was clear 71%), whether they would like additional information (50%), what to change (nothing 85%), and whether they would be willing to participate in another study (100%). Some participants (15%) recommended we include their dietary intake during the health assessment. Based on the return strategy implemented in this study, the participants were given the opportunity to review the results with qualified staff and were able to ask any questions they had regarding the content of their results package. This strategy ensured participants understanding of information and provided the opportunity for them to provide valuable feedback regarding the delivery and interpretation of the results. The implemented approach for delivering study results to participants enhanced health literacy, empowered individuals to take action to address potential environmental health issues and contributed to improving the way information is presented to the community. Funding by the Environmental Health Sciences – Transformative Research Undergraduate Experience (EHS-TRUE) through the National Institute of Environmental Health Sciences Grant #1-R25-ES025494.

CHRONIC ADMINISTRATION OF MORPHINE LEADS TO INCREASED BONE LOSS AND PROLONGED NEUROPATHIC PAIN IN A MURINE METASTATIC BREAST CANCER MODEL

***HALEY CICCONE*, AUSTEN L. THOMPSON, ANGELA SMITH, DIETER MOHTY, TODD W. VANDERAH, TALLY LARGENT-MILNES**

According to the CDC, breast cancer is the most common cancer found in women of all races, and commonly metastasizes to bone as the disease progresses, which leads to intractable pain. Cancer-induced bone pain following tumor proliferation is commonly attenuated with the administration of opioids, but previous studies have shown that chronic administration of these addictive analgesics may cause bone degradation due to interactions with receptors that mediate inflammation and bone remodeling. To date, the mechanism of opioid-induced bone loss is unknown, which presents a problem to physicians when prescribing analgesics to populations that are already at risk of bone fragility and fractures. Therefore, it is vital to investigate the interactions of opiates and pro-inflammatory pathways in addition to dose-dependent efficacy. In this study, we injected E0771 breast adenocarcinoma cancer cells or vehicle into the intramedullary space of the right hind femur of C57BL/6 mice and allowed the cancer cells to grow for one week. After seven days, we subcutaneously implanted minipumps to ensure a constant administration of morphine or vehicle and measured their subsequent pain behavior by quantifying flinching, guarding, and limb use. We also used Faxitron images and a bone lesion scoring procedure to quantify the loss of bone in the ipsilateral femur and found that although the cancer-morphine treated mice exhibited more pain relief than controls, they also displayed greater bone degradation. To further examine the mechanism by which morphine mediates osteoclast and osteoblast activity, we used cytokine assays and Western blots to probe for inflammatory cytokines and chemokines and developed an immune cell profile of the bone microenvironment in response to chronic administration of morphine (10 mg/kg/day). As the opiate epidemic grows more rampant, these data could positively influence how physicians utilize opiate-based therapies and investigation of novel non-opiate therapies, thus leading to improved outcome for patients.

MECHANISTIC ROLE OF ADENOSINE3-RECEPTOR IN HIV-INDUCED PERIPHERAL NEUROPATHY

***DEZ COLEMAN*, TALLY LARGENT-MILNES, TODD VANDERAH**

Patients living with human immunodeficiency virus (HIV) often experience chronic neuropathic pain caused by inflammation in the brain and spinal cord. Opioids are commonly prescribed to manage this pain; however, this treatment is inadequate due to chronic opioid usage exacerbating pain by causing opioid-induced hyperalgesia. Our research focuses on determining the mechanistic role of HIV-induced peripheral neuropathy, as well as further understanding the increased neuropathic pain seen in HIV patients using chronic opioid treatment. Protein expression was analyzed in tissue samples taken from animals treated with gp120, the glycoprotein on the HIV envelope that allows viral entry. In addition, these animals were observed over 35 days to

monitor the progression of neuropathic pain post-gp120 treatment. Our preliminary data demonstrate that gp120 treatment decreases the CD39 and CD73 enzymes, which play a crucial role in ATP producing a pro-inflammatory response by increasing intercellular adenosine. In addition, our preliminary data suggest that opioid treatment increases the expression of adenosine kinase, an enzyme that removes extracellular adenosine. This prevents the activation of the adenosine3-receptor, which activates anti-inflammatory responses. These data suggest the pro-inflammatory response caused by gp120 treatment contributes to neuropathic pain in patients living with HIV. This pain is further exacerbated by opioid treatment decreasing anti-inflammatory responses. Further understanding of the mechanism behind HIV-induced peripheral neuropathy may provide insight into developing novel pain-relieving compounds for these patients. This project is supported in part by the Undergraduate Biology Research Program with funds from the BIO5 Institute.

OPTIMIZATION OF FIBER OPTIC ALIGNED CAPILLARY ZONE ELECTROPHORESIS WITH LASER INDUCED FLUORESCENCE

***ANGELINA CONDARCURE*, KENDALL E. SANDY, CRAIG A. ASPINWALL**

Capillary electrophoresis, as an analytical separation technique, has many advantages over methods such as HPLC, and CLC, including the cheap and uncomplicated equipment required. However, alignment of the light source on the capillary and the emission to the detector can be cumbersome and difficult. We have developed a new CZE instrumental design that eliminates the need for alignment and can be adapted to many different analytical needs. Using fiber optic cables and a custom designed holder, we have been able to detect 50 nM fluorescein, as well as separated NDA-labelled amino acids. This project is supported in part by the Undergraduate Biology Research Program with funds from the Office of the Provost.

AN INHIBITORY TAIL: LYP IS AUTOINHIBITED BY ITS INTRINSICALLY DISORDERED DOMAIN

***EMILIE CUEVAS*, KRISTIANE TORGESON PELLETIER, REBECCA PAGE**

A protein's three-dimensional structure determines its function and leads to molecular insights into the breadth of its role(s) in biology. My research is focused on understanding how enzymes control a key post-translational modification in the cell: phosphorylation. Specifically, I study the protein tyrosine phosphatase, lymphoid tyrosine phosphatase (Lyp). This enzyme prevents spontaneous T-cell activation by dephosphorylating its substrates, including kinases (LcK, FAK, PYK2) and regulators of cell motility (WASP, p190RhoGAP, RhoGDI), among others. Mutations in Lyp are also highly associated with autoimmune disorders. To understand endogenous Lyp activity in detail, I explored an area of the protein that has not been previously studied; namely, the intrinsically disordered region (IDR) between its catalytic domain and its four SH3-binding domains. Using purified protein (cloning, E. coli expression, purification) coupled with biochemical phosphatase activity assays (pNPP assay), I unexpectedly discovered that the IDR inhibits endogenous Lyp activity. I am now using molecular methods (NMR spectroscopy/X-ray crystallography) to determine how, at a molecular level, this is achieved. This project is supported in part by the Undergraduate Biology Research Program with funds from the Office of Research, Discovery & Innovation, and private donors, and the Western Alliance to Expand Student Opportunities (WAESO) Louis Stokes Alliance for Minority Participation (LSAMP) National Science Foundation (NSF) Cooperative Agreement No. HRD-1101728.

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NEURON COUNT IN ANT BRAINS

***JORDAN DASEN*, WULFILA GRONENBERG**

Intelligence is widely defined as mental flexibility, behavioral flexibility, and problem-solving skills, manifesting in the ability to find novel solutions and entailing forms of associative learning and memory formation, behavioral flexibility and innovation rate, and abilities requiring abstract thinking, concept formation, and insight. Many anatomical and physiological properties have been proposed as quantitative predictors for intelligence, such as absolute brain size, encephalization, and properties relevant to information processing capacity, such as the number of neurons and axonal conduction velocity. Brain size seems to be unrelated to intelligence: for instance, whales and elephants have larger brains than humans, observations that fail to align with what is understood about each species intelligence. The encephalization hypothesis faces similar problems: research has shown that while humans and dolphins have relative brain sizes that correspond with expected values, capuchins have relatively high encephalization quotients and whales, chimpanzees, and gorillas have relatively low encephalization quotients, again contrasting with intelligence observations. Neuron count appears to be a better predictor: elephants and false killer whales have larger brains than humans but fewer cortical neurons at about 11 and 10.5 billion respectively compared to the human 15. Less research has been performed on insects: while the correlation between brain and body mass is well documented in ants, the variation in their neuron counts and the way they compare with other insects is not well understood. Here I count neurons from various ant species differing in brain and body size using sectioned brain tissues and compare those neuronal estimations with counts based on the isotropic fractionator method, in which whole brains are homogenized and neuron numbers are estimated similarly to how blood cells are counted the medical field. Several staining methods - hematoxylin, cresyl violet, and the nuclear stain DAPI have resulted in difficulty with the Kenyon cells of mushroom bodies, which failed to show compact, easily countable nuclei. My preliminary work suggests that block staining with silver nitrate is the best suited method. While my method is more time consuming, unlike the isotropic fractionator, it allows comparing neuron numbers of particular brain components. Funding: National Institutes of Health Maximizing Access to Research Careers Training Grant T34 GM08718.

THE ROLE OF POLYMERASE V IN RNA-DIRECTED DNA METHYLATION DURING BRASSICACEAE SEED DEVELOPMENT

***BRANDON DAVID*, KELLY DEW-BUDD, REBECCA MOSHER, MARK BEILSTEIN**

The process of DNA methylation is important for regulating transcription. In plants, DNA methylation is partially the result of the RNA-directed DNA Methylation (RdDM) pathway. The RdDM pathway utilizes small RNAs to bind RNA polymerase V transcripts resulting in the recruitment of methylation machinery to specific regions of DNA. RdDM is involved in the imprinting of genes during seed development. Imprinting is the silencing of genes inherited from one parent, or of paralogs from subgenomes in polyploid species. Understanding the role of RdDM could help increase seed productivity of important crop species. Previous experiments indicate that mutations in the RdDM pathway have different affects in different species. In *Brassica rapa*, an important commercial crop, mutations to the RdDM pathway resulted in plants with significantly smaller seed set and seed weight. In contrast, in *Arabidopsis thaliana*, there was only a small effect on seed weight. Two important genomic differences between these two species are genome copy number (ploidy) and breeding system (outcrossers vs. inbreeders). We believe these are important distinctions because of the potential role of RdDM in mediating conflicts among subgenomes and/or parental genome conflict. To explore how these genomic and breeding differences are important in seed development and the function of RdDM in other species of Brassicaceae, we are using CRISPR-Cas9 to knock out NRPE1, the largest subunit of RNA polymerase V, in three additional Brassicaceae species. These species differ in either breeding system (inbreeder vs. outcrosser), or ploidy (diploid vs. hexaploid). Currently, we have successfully generated nrpe1 knockout mutants in all three species and are in the process of determining if there are any significant differences in seed set, size, or weight in the mutants when compared with wild-type for each species. This work was supported by the National Science Foundation Award Number 1546825 to MAB and in part by the Undergraduate Biology Research Program with funds from the Office of Research, Discovery & Innovation.

MEASURING DED1 INTERACTIONS USING A SPLIT-LUCIFERASE ASSAY

***SAMANTHA DAVIDSON*, TELSA M. MITTELMEIER, TIMOTHY A. BOLGER**

A family of highly conserved RNA helicases, called DEAD-box proteins, help determine the secondary structure of RNA, and the proteins to which the RNA is bound. Ded1, an essential DEAD-box protein in yeast (with a conserved ortholog, DDX3, in humans), is required for translation initiation in the cell. Ded1 has been shown to interact with another translation initiation factor, eIF4G, by co-immunoprecipitation. It has also been demonstrated that in vitro, Ded1 oligomerizes, or self-binds, and that eIF4G1 interferes with Ded1 oligomerization. We are interested in determining whether Ded1 oligomerizes and/or binds with eIF4G in vivo and whether cellular conditions affect these interactions. To do this, we are developing a protein-fragment complementation assay, more specifically a split-luciferase assay, to measure Ded1 oligomerization and Ded1-eIF4G interaction in both un-stressed and stressed cells. To date, we have not detected luciferase activity resulting from a Ded1-Ded1 interaction in unstressed cells, relative to a positive control. Through Western blot analysis, we have observed that the level of the Ded1-Luciferase 2 (C-terminal two-thirds) protein is much greater than that of the Ded1-Luciferase 1 (N-terminal one-third) protein, which may explain the lack of Ded1-Ded1 signal. Alternatively, our data may suggest that under normal growth conditions, Ded1 only interacts with eIF4G1, and Ded1 oligomerization only occurs as a response to changing conditions such as cellular stress. To differentiate between these alternatives, we are building constructs to express eIF4G1-luciferase fusion proteins and developing fluorescence-based protocols to analyze Ded1-Ded1 interaction following cellular stress. Funding for this project has been provided by the Undergraduate Biology Research Program with funds from the Office of Research, Discovery, & Innovation, and from the MCB Faculty Innovator Award.

THE EFFECTS OF AMPK ACTIVATION IN *ANOPHELES STEPHENSI* MOSQUITOES

***LILLIAN DELACRUZ*, CHIOMA ORINGANJE, MICHAEL RIEHLE**

The AMP-dependent protein kinase (AMPK) pathway is highly conserved in eukaryotic organisms and regulates metabolic energy homeostasis. When AMPK is activated, it shuts down energy consuming pathways and stimulates energy producing pathways. It has also been shown to regulate aging by maintaining optimal mitochondrial quality in the cell. We investigated the role of increased AMPK activity in the *Anopheles stephensi* mosquito, a primary vector of the malaria parasite (Plasmodium falciparum), in regulating energy metabolism and mitochondrial activities. We fed a chemical activator of AMPK, 5-amino-4-imidazolecarboxamide riboside-1-β-D-ribofuranoside (AICAR) to wild type mosquitoes and measured its effects on macronutrients and mitochondrial proteins. Our results showed that increasing AMPK activity led to reduction in stored nutrients (glycogen and lipids) five hours post-blood feeding compared to the controls fed blood only. We also saw an increase in transcript expression of mitofusin and autophagy-related gene 6 one-hour post-feeding. Our findings highlight the importance of the AMPK pathway on nutrient metabolism and on key genes that influence a variety of physiological processes in the mosquito. This project is supported in part by the Undergraduate Biology Research Program with funds from the Office of Research, Discovery & Innovation and private donors, and the Western Alliance to Expand Student Opportunities (WAESO) Louis Stokes Alliance for Minority Participation (LSAMP) National Science Foundation (NSF) Cooperative Agreement No. HRD-1101728.

INVESTIGATING MOTOR LEARNING IN A LRRK2 MOUSE MODEL OF PARKINSON'S DISEASE

***ALLISON EBY*, LINDSEY M. CROWN, STEPHEN COWEN**

While most cases of Parkinson's disease are idiopathic, meaning of unknown origin, in 10% of cases, a genetic link has been identified. Of these, the most common is the G2019S mutation of the leucine-rich repeating kinase 2 (LRRK2) gene. Investigation into this mutation could prove useful not only for those with LRRK2 Parkinson's, but for idiopathic Parkinson's as well. Genetic mouse models of this mutation are important for translational research, but despite the increasingly large number of studies on these animals, few have identified a reliable phenotype. In this study, we measured the average latency to fall

during a rotarod-based motor-learning task conducted twice a week for two weeks with transgenic (Tg) and non-transgenic (NTg) mice 6-8 months old. During the second week, half the animals were given a LRRK2 inhibitor, MLi-2. Although we detected no effect of the drug, results have been mixed for overall motor performance with a trend towards LRRK2 Tg animals performing worse on the task. In this study, we examine whether LRRK2 Tg mice perform similarly to NTg mice for within-day learning, between-day learning, and overall latency to fall measures. Funding from Michael J. Fox Foundation and in part by the Undergraduate Biology Research Program with funds from the Office of the Provost and private donors.

DYNAMIC EXPRESSION OF RNA STRESS GRANULE COMPONENTS IN BEHAVIORALLY CHARACTERIZED YOUNG, MIDDLE AGED AND OLD RATS

***RANDALL ECK*, MONICA K. CHAWLA, BRITTANY WILLIAMS, BHAVANI BAGEVALU SIDDEGOWDA, NATALIE J. CAREY, MARC A. ZEMPARE, CHRISTIE J. NGUYEN, CAROL A. BARNES, AND DANIELA C. ZARNESCU**

RNA stress granules are dynamic cytoplasmic structures that assemble in response to various cellular insults. During this process, these non-membrane bound organelles sequester mRNAs and specific proteins causing inhibition of translation initiation, resulting in cell protection during times of stress. Upon stress removal, RNA stress granules disassemble, and translation is reinitiated. These changes in RNA stress granules have been linked mechanistically to age-related neurodegenerative disease suggesting that they may play a key role in the aging process. To further understand RNA stress granules role in aging and neurodegeneration, we investigated the expression of RNA stress granule-associated proteins including PABP, G3BP1, TIAR, and EIF2alpha. In rats, we found that there is a region-specific distribution across rat brains and that there are dynamic changes during aging in the transcript and protein levels of stress granules components in both flies and rats. Similar dynamic changes in rat brains were found for translation initiation factors EIF4G2, EIF4E-BP, EIF4A1 and EIF4E during aging. These molecular analyses were performed on brain regions isolated from young adults (6-8 mo), middle-aged (15-17 mo) and old (23-25 mo) rats that were previously assessed for their spatial and working memory using the Morris water maze. Male endogenously GFP tagged Rin *Drosophila* were also used. Confocal imaging of brains from mechanically stressed *Drosophila* show older *Drosophila* mount a reduced stress granule response to mechanical stress. The Morris water maze task revealed that aged rats were memory impaired compared to both middle-aged and young animals, and middle-aged rats were also memory impaired compared to young rats. When region-specific reverse transcription (RT) qPCR and western blot analyses were normalized for behavioral performance, regression models of protein or transcript level significantly predict the age of the rats. Future studies will examine the ability of aging *Drosophila* to assemble and disassemble stress granules in response to different stressors, examine protein expression levels in aging *Drosophila*, and determine the mRNAs and proteins that associate to stress granules across aging. This work was supported by the National Institutes of Health (R01 NS091299, ADC pilot (P30 AG019610 to DCZ), by the McKnight Brain Research Foundation (to CAB), University of Arizona Undergraduate Biology Research Program (UBRP), the Arnold and Mabel Beckman Foundation (4212940 to SY, RE), the Maximizing Access to Research Careers Program (to BW), and MCB Faculty Innovator funds (to DCZ).

THE SALT-ASSISTED CHEMICAL VAPOR DEPOSITION OF TRANSITION METAL DICHALCOGENIDES ON SI/SIO2

***JORDAN FINK*, SARA ZACHRITZ, OLIVER L.A. MONTI**

Transition Metal Dichalcogenides (TMDCs) have shown novel properties that make them applicable to photovoltaics and hydrogen evolution reactions. Yet, the growth processes to make these materials and as well as the materials intrinsic properties are not understood well. In an effort to expand this knowledge, we have investigated the growth process of MoS2 on Si/SiO2 juxtaposing the standard growth process with a salt-assisted (SA) growth process. Both models have identical reaction setups, but the amounts of reactants vary. Additionally, NaCl is added in the SA growth process which allows us to lower the growth time and temperature. Large monolayer crystals are obtained in each growth process, but there are clear differences in the nucleation due to different reaction mechanisms and increased mass flux. The SA process yields smooth, large-area growth

with fewer grain boundaries when compared to the standard process. Additionally, we have attempted to transfer these MoS2 crystals from the Si/SiO2 wafer to a template-stripped gold (TSG) wafer for future band structure measurement experiments. This project was funded by the Undergraduate Biology Research Program with funding from the Office of Research, Discovery & Innovation. Additional funding was obtained from Division of Materials Research Eager, and National Science Foundation Electrical, Communications and Cyber Systems.

ROLE OF SEX HORMONES IN MODULATING WEIGHT GAIN DUE TO SLEEP DISRUPTION

***ASHLEY FLORES*, JENNIFER A. TESKE**

Noise exposure is a concern causing insufficient sleep and risk for weight gain. Women have a higher prevalence of obesity, are more sensitive to noise, and have poorer sleep quality than men. The obesogenic food environment allows for easy access to a variety of palatable foods that stimulates calorie intake and weight gain in humans and animals. Like male rodents, exposure to chronic pre-recorded environmental noise causes sleep disruption (SD) and increases weight gain and calorie intake in females. Although weight gain in women is promoted by experimental sleep restriction, the underlying mechanisms are unknown. Therefore, we created a rodent model for women who gain weight with inadequate sleep. We hypothesized that access to the cafeteria-diet (CAF-D) together with SD would stimulate weight gain and calorie intake more so than access to the CAF-D alone, increase sensitivity to weight gain in female rats, and have no effect on the estrous cycle. To test this, we conducted a behavioral study using a rodent model. Twenty-eight male and female rats (11-weeks old) were fed a standard rodent diet (chow) and slept undisturbed during an 8d staging period. Then rats were randomized to either SD by exposure to noise (8h/d during light cycle) or sleep undisturbed, with access to the CAF-D and chow ad libitum for a 15d treatment period. Estrous cycle phase, food intake, and body weight were determined daily. Estrous cycle length was maintained during noise-induced SD. Weight gain was similar between CAF-D fed females and males. SD plus CAF-D stimulated weight gain and calorie intake in male rats only. In conclusion, females are more sensitive to the effects of the CAF-D in comparison to males, as SD did not further stimulate weight gain or calorie intake in combination with access to the CAF-D. This project was funded by the National Institutes of Health (NS099468-01A1 to JAT), the National Institutes of Health Maximizing Access to Research Careers Training Grant (T34 GM08718), and the US Department of Agriculture (ARZT-1370530-R23-156 to JAT).

G-PROTEIN-COUPLED RECEPTOR ACTIVATION IS COUPLED TO INTERNAL HYDRATION

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Rhodopsin is the G-protein-coupled receptor (GPCR) responsible for scotopic vision in the retina. Up to this point, the role of water in the activation of GPCRs has remained largely unknown. Recently, however, nanosecond molecular dynamics simulations have revealed an influx of bulk water into rhodopsin during activation [1]. Utilizing rhodopsin as a model GPCR, we tested the hypothesis that rhodopsin activation is hydration mediated using osmotic stress techniques. We subjected rhodopsin within its native lipid membranes to varying osmotic pressures induced by different-sized polyethylene glycol polymers. UV-Visible spectroscopy of the photoactivated rhodopsin system reveals the fraction of protein in the active metarhodopsin-II (MII) conformation, the receptor state capable of activating the G-protein. We discovered high-molecular weight osmolytes uniformly favored the closed, inactive metarhodopsin-I conformation by dehydration of the protein interior. By contrast, small osmolytes penetrated into the transducin binding cleft and stabilized the active MII conformation until a quantifiable saturation point. A universal osmotic response occurred in the limit of increasing osmolyte size and maximal polymer exclusion from rhodopsin. By measuring the thermodynamic dependence of the metarhodopsin equilibrium on osmotic pressure, we determined that rhodopsin activation is coupled to a bulk influx of 80-100 water molecules into the protein core with a substantial increase in compressibility. We propose a new model for the functional role of water in GPCR signal transduction, in which a wet-dry cycling mechanism amplifies the activation of G-proteins. Our results necessitate a new understanding of GPCR activation, in which the influx of water plays a critical role in establishing the active receptor conformation. This work was supported by the National Institutes of Health (EY026041 and EY012049), the National Science Foundation (MCB 1817862), and

in part by the Undergraduate Biology Research Program with funds from the BIO5 Institute. [1] N. Leioatts et al. (2014) Biochemistry 53, 376-385.

MUTATIONS OF CX37 THAT INDUCE CELL DEATH REQUIRE THE FULL-LENGTH PROTEIN, A TRUNCATED 13K ISOFORM IS INSUFFICIENT

***MARGRET FYE*, TASHA K. PONTIFEX, JANIS M. BURT**

Connexin (Cx) 37 is a transmembrane protein expressed by the endothelial cells of the arterial vasculature where it supports phenotypic switching between growth arrested (differentiated), proliferative, and death states; thus, contributing to the growth status of the vasculature. The possible mechanisms underlying this phenotypic switching include phosphorylation-dependent regulation of 1) intercellular and transmembrane exchange of signaling molecules and metabolites via gap junction channels and hemichannels, respectively, or 2) intracellular signaling via protein-protein interactions mediated by the carboxyl terminus (CT). The Cx37 mRNA has a potential internal ribosomal entry site (IRES) available at methionine 213, which could support translation of a truncated 13 kDa (13k) piece that contains the entire CT with all its putative phosphorylation sites, and a portion of the 4th transmembrane domain, which would tend to anchor the protein at the membrane. M213 of the Cx37 transcript is homologous M213 in Cx43, which supports translation of a truncated 20k piece essential for Cx43 protein trafficking. As the point mutations S321D or S275D in the full-length protein induce death, we sought to determine whether these mutations in the 13k form would 1) induce cell death or 2) alter the trafficking of the full-length form. We hypothesized that expression of Cx37-13k-S321D or Cx37-13k-S275D would be sufficient to induce cell death and regulate trafficking, channel functions, and growth phenotype of Rin cells. We transfected naïve rat insulinoma (Rin) cells with inducible i13k-S321D or -S275D; proliferation assays and immunocytochemistry indicated that i13k-S321D did not induce cell death nor alter the proliferative properties of Rin cells. Preliminary data suggest i13k-S275D also does not induce cell death. In addition, i13k-S321D co-localizes with endoplasmic reticulum and Golgi apparatus markers. The data suggest that i13k-S321D does not form functional channels and does not alter the growth phenotype of Rin cells. Future transfection of i13k-S321D or S275D into Cx37-expressing Rin cells may reveal a regulatory role for the truncated protein. This project is supported in part by the Undergraduate Biology Research Program with funds from the College of Medicine.

INVESTIGATING HORMONAL REGULATION OF MOLECULAR PATHWAYS IN MIGRAINE THROUGH NETWORK ANALYSIS

***EMILY GALLOWAY*, ERIKA LIKTOR-BUSA, KIERA BLAWN, KATHRYN KELLOHEN, TODD VANDERAH, TALLY LARGENT-MILNES, MEGHA PADI**

Migraine is the most common neurological disorder, affecting approximately 11% of the world population. Because women comprise over 75% of the migraineur population, female reproductive hormones, namely estrogen, are thought to play a crucial role in this debilitating disease. Preclinical studies have demonstrated that estrogen increases susceptibility to an electrical phenomenon in the brain called cortical spreading depression (CSD), which is theorized to be associated with migraine with aura; however, its mechanism is unknown. Dysregulation of pH in the brain is also known to occur in CSD and potentially aura, however it is unknown if estrogen influences brain pH. NHE1 is a ubiquitously expressed Na+/H+ exchanger involved in maintaining cellular pH. Both increases and decreases in NHE1 expression may affect neuronal excitability and meningeal nociception, which have implications in migraine. In preliminary studies, NHE1 expression was significantly lower in female rats than in males. This observation was coupled with an increase in measured craniofacial sensitivity in females. Blots showed that estrogen decreases NHE1 expression in rat brain endothelial cells in a concentration-dependent manner. To elucidate how estrogen regulates NHE1 expression, cells were treated with both estrogen and a selective ERβ antagonist, PHTPP. The estrogen-dependent decrease of NHE1 was reversed, indicating that ERβ is part of the estrogen-NHE1 regulatory pathway. To analyze estrogen-related molecular pathways with a wider lens, computational approaches were used. RNA-Seq values from 100 individual brain cortex samples were obtained from the publicly-available Genotype-Tissue Expression (GTEx) dataset.

Subjects had no underlying pathology and were split by sex. Data was normalized and randomized, then differential expression values were calculated. Differential expression values underwent gene set enrichment analysis (GSEA) and outputted several significant gene ontology (GO) terms associated with ion transport and others my lab hypothesizes correlate with migraine. Using computational methods called PANDA and ALPACA, networks of genes and transcription factors were created to better understand how genetic factors in brain tissues interact to produce conditions ideal for migraine development. Through this project, we have identified specific genes that may correspond with estrogen's effect on migraine susceptibility. This project is supported in part by the Undergraduate Biology Research Program with funds from the College of Science.

DISTINGUISHING BETWEEN MICROGLIA AND SYSTEMIC MACROPHAGES IN POST-STROKE BRAIN INJURY

***REBECA GARDNER*, KIMBERLY F. YOUNG, AND HELENA W. MORRISON**

Ischemic stroke is an acquired brain injury that elicits a robust immune response. Macrophage responses are necessary for debris clearance and wound healing but are potentially detrimental in excess. As of yet, the ability to distinguish between populations of resident versus systemic macrophages (microglia versus macrophage) in the 24hr post-stroke has been difficult. Therefore, our knowledge in neuroinflammatory mechanisms of post-stroke injury or repair is unclear and limits the development of microglia/macrophage-based therapeutics. Based on previous investigations, we hypothesized the majority of responding cells in the ipsilateral hemisphere to stroke are microglia whereas the cells abutting the infarct injury to be systemic infiltrating cells. Brain tissue was collected for immunohistochemical staining or western blot methods. Microglia were visualized using antibodies against ionized calcium-binding adapter molecule (Iba1) and transmembrane protein 119 (TMEM119). Iba1 is non-specific to both microglia and infiltrating macrophages whereas TMEM119 is said to be specific to microglia. Using these two markers, we aimed to distinguish between macrophage and microglia populations in an injury model. Immunofluorescent cells were imaged using confocal microscopy (40x objective) in four regions for morphometric analysis: sham, ipsilateral regions distal (ID), proximal (IP) and the region abutting the infarcted area (IN). Cell morphology was analyzed using skeleton and fractal analysis, an ImageJ platform. The percent area of TMEM119+ immunoreactivity per Iba1+ cell was calculated using a consistent imageJ thresholding protocol. All evaluators were blinded to experimental conditions, with data tested using ANOVA with Bonferroni post-hoc. Additional tissue (fresh frozen) included 1mm tissue punches in sham, ipsilateral distal and proximal regions for western blot methods. Similar to our previous studies, we show that microglia become significantly de-ramified as proximity to the infarcted tissue decreases ($p < 0.0001$). Using fractal analysis, we show that the de-ramified cells abutting the infarcted tissue were elongated ($p < 0.0001$), suggestive of either a different microglia function in this region or that these cells might be infiltrating macrophages. Although all cells imaged in the ipsilateral hemisphere were ramified to some extent, TMEM119 immunohistochemistry analysis revealed that the percent area of TMEM119+ immunoreactivity per Iba1+ cell was decreased proximal to the infarcted tissue ($p < 0.02$). These data are suggestive that infiltrating macrophages are extensively present in the ipsilateral hemisphere. The stability of TMEM119 immunohistochemistry with gross injury has yet to be tested, therefore we aimed to validate these data using western blot methods. Contrary to our IHC data, we found that TMEM119 protein expression was similar across regions ($p = 0.73$). These contrasting data suggest that additional studies are necessary to both validate the stability of TMEM119 immunoreactivity using immunohistochemistry methods to distinguish among microglia versus systemic macrophages. This project is supported in part by the Environmental Health Sciences – Transformative Research Undergraduate Experience (EHS-TRUE) through the National Institute of Environmental Health Sciences Grant #1-R25-ES025494.

AMYLOID-BETA (Aβ) DIFFERENTIALLY MODULATES α7* NACHRS EXPRESSED IN VITRO

***MICHAEL GEE*, LINDA M. LUCERO, ANDREW A. GEORGE, RONALD J. LUKAS, PAUL WHITEAKER**

Alzheimer's disease (AD), a progressive neurodegenerative disorder, is one of the most common causes of mental deterioration in the elderly. Hallmarks of AD pathology include alterations in brain regions associated with higher cognitive functions. Several studies have correlated the severity of cognitive decline in AD with a loss of basal forebrain cholinergic neurons (BFCNs).

Mechanisms underlying cholinergic neurodegeneration and subsequent memory impairments remain unknown. However, interactions between amyloid-β (Aβ), a suspected etiopathogenic agent in AD, with a nicotinic acetylcholine receptor subtype containing α7 subunits (α7*-nAChR) can trigger neuronal homeostatic instability. To understand the interaction between Aβ and α7*-nAChRs, nAChR DNA constructs were generated with fixed subunit stoichiometries to study how the positional effects of α7 and β2 subunits confer the sensitivity and functional modulation seen with Aβ. These DNA constructs were transfected into SH-EPI cells where the DNA is transcribed into RNA and subsequently into functional receptors. To help visualize these receptors expressed in SH-EPI cells, nAChR constructs were designed to coexpress mCherry, a fluorescent marker used to validate the expression of α7 and α7β2-containing nAChR in vitro. To facilitate cell-surface expression, we engineered a fluorescently tagged nAChR chaperone, NACHO, which guides nAChRs to the plasma membrane and, therefore, increases the total number of cell-surface nAChRs. To elucidate the precise interaction between α7-containing nAChRs and Aβ, we used single-channel electrophysiology to investigate the functional interaction between Aβ and α7 and α7β2- containing nAChRs. We demonstrate that oligomeric Aβ activates both α7 and α7β2 nAChRs and enhances α7β2 nAChR single-channel open-dwell times. Single-channel activation of both nAChR subtypes can be inhibited with the known α7 antagonist mecamylamine. These interactions may be uniquely specific to certain cholinergic circuits within the basal forebrain and suggest novel and potentially productive therapeutic strategies to combat neurodegeneration in a brain region affected early in AD. This work was supported by an American Society for Pharmacology & Experimental Therapeutics Summer Undergraduate Research Fellows (ASPET/SURF) grant to the University of Arizona and funds from the University of Arizona College of Medicine.

EXPLORATORY BEHAVIORAL EFFECTS OF INHIBITING CRMP2 SUMOYLATION IN TRANSGENIC MICE

***MARISSA GIUNTA*, KEVIN HURTADO, AUDE CHEFDEVILLE, AUBIN MOUTAL, AND RAJESH KHANNA**

There has been an increase in prescribing opioids for chronic pain sufferers in the U.S. since the 1980s, resulting in a nationwide opioid epidemic. Chronic pain is caused by over firing of neurons. Targeting the ions that produce action potentials can be an alternative treatment to opioids. Particularly, the NaV1.7 channel is dysregulated in cases of chronic pain. Collapsin response mediator protein (CRMP2) interacts with NaV1.7 and posttranslational modifications, such as phosphorylation and SUMOylation of CRMP2, regulates NaV1.7 activity. In a previous study, we used viral injections to mutate CRMP2 to inhibit SUMOylation resulting in decreased NaV1.7 channel excitability. In this study, we created a transgenic mouse line bearing a genetic mutation preventing SUMOylation. We assessed pain perception in these transgenic mice by performing hot plate and tail flick tests. Complete CRMP2-KO in the brain can alter hippocampal morphology, reduce memory, and produce schizophrenia-like behavior in mice. We explored the potential off-target effects of preventing CRMP2 SUMOylation. To assess anxiety, we performed marble burying tests (MBT), nestlet shredding tests (NST), and novel object recognition tests (NOR). We conducted an anosmia test because NaV1.7 is also crucial for olfaction. In this study, we showed that preventing CRMP2 SUMOylation can affect nociception. Overall, we found that male and female transgenic mice had decreased pain sensitivity in the hot plate and tail flick experiments. Only the male homozygous mice had a statistically significant ($p < 0.001$) increase in their time response compared to the wild type during the hot plate test. This result indicates a higher pain threshold. In the experiments that assessed anxiety, the transgenic mice did not have statistically significant differences compared to the wild type. There was not a statistically significant difference in olfaction compared to the wild type in the anosmia test. In the future, we aim to study other dysregulated ion channels that interact with CRMP2 in hopes of finding an alternative treatment for chronic pain. Funding for this research was provided in part by the Undergraduate Biology Research Program with funds from the BIO5 Institute to MG.

PAPER-BASED VERTICAL ASSAY FOR DETECTION OF METASTATIC BREAST CIRCULATING TUMOR CELLS

***ALANA GONZALES*, TIFFANY-HEATHER ULEP, RYAN ZENHAUSERN, JEONG-YEOL YOON**

Metastasis, the primary cause of death in cancer patients, occurs when secondary tumors arise from circulating tumor cells (CTCs), which are shed from the primary tumor and circulated through the bloodstream to other parts of the body. As an alternative to traditional tissue biopsy, current technologies seek to use liquid biopsy of the blood to detect and count CTCs as a method for measuring patient prognosis and determining the most effective treatment options. These technologies are often costly and require highly trained personnel and strict regulations. This project seeks to overcome these issues by using a low-cost, paper-based vertical flow immunoassay and a smartphone-based microscope as a novel biosensor for quantifying CTCs. Antibodies specific for protein expression markers of epithelial and mesenchymal cell morphology, respectively, were conjugated with 1.1 m fluorescent polystyrene particles, and these particles were mixed with both epithelial and mesenchymal breast cancer cell lines to model the diagnostic assay in suspension and on paper. The paper-based vertical assay device is designed to filter red blood cells and platelets, leaving white blood cells and CTCs on the paper before adding particles. Fluorescent microscope images were taken, and a MATLAB program was developed to detect the particles bound to CTCs, enabling the accurate counting of CTCs towards the single cell level. Imaging was repeated using a smartphone-based confocal microscope device. Results showed that epithelial-specific particles bound most frequently to epithelial cells, and mesenchymal-specific particles bound most frequently to mesenchymal cells. This trend was not statistically significant based on normal distribution ($p>0.05$), but it allowed us to conclude that specific binding of antibody-conjugated particles to their respective cell lines is observable, and there may be statistical significance when analyzing the data using additional methods. Future experiments aim to increase the accuracy of image processing and to re-analyze the data to look for significant trends. Successful detection of CTCs as epithelial or mesenchymal using this method will provide a cost-effective, less invasive way to assess metastasis and prognosis of cancer patients.

CONDUCTING RESEARCH IN COLLABORATION WITH TRIBAL COMMUNITIES: A RESEARCH FRAMEWORK

***CHEYENNE GRABIEC*, MARTI LINDSEY**

When conducting research in tribal communities it is important to understand that the research is not being done on the tribal community, but rather in collaboration with the tribal community. This framework seeks to outline the most important steps to be taken when conducting research in collaboration with tribal communities, which are used at the Southwest Environmental Health Sciences Center. It depicts the steps taken when working with a tribal community in Southern Arizona related to their concern for air pollution and a suspected high prevalence of asthma. The framework has four main aspects that are vital when conducting research in collaboration with tribal communities; Relationship Building, Project Planning, Project Execution, and Reflection. Relationship Building is a constant process that includes meeting frequently with tribal partners to develop a project and to build a trust relationship between the community and the researcher. With some tribal communities the Relationship Building may include the development of a Memorandum of Agreement and/or a Tribal Resolution between the tribe and the researcher. Project Planning occurs after a relationship has been developed and it is the collaboration between the tribal community and the researcher to identify an issue that the community faces to be researched and hopefully improved. Project Execution is the carrying out of the research determined in the planning process. When working with tribal communities this step includes training community members in the research collection process through what is known as citizen or community science. Reflection occurs iteratively during the project as well as summative once the project has been carried out. It includes reviewing the data collected and determining how that data can be used to address or improve the issue faced by the community. It also includes looking back on what went well in the project and what can be improved upon in the future. The future direction of this framework is to share it with all students and researchers that plan to work with tribal communities so that they can utilize best practices in their collaborative projects. This project is supported in part by the Environmental Health Sciences – Transformative Research Undergraduate Experience (EHS-TRUE) through the National Institute of Environmental Health Sciences Grant #1-R25-ES025494.

LORELEI AND ITS MOST CLOSELY RELATED PARALOG, LLG1, HAVE SHARED FUNCTION BUT DIFFERENT EXPRESSION PATTERNS

***SARAH HANCOCK*, JEN NOBLE, MARK BEILSTEIN, ALICE CHEUNG, RAVI PALANIVELU**

LLG1 (LORELEI-like GPI-Anchored Membrane Protein 1) is a closely related paralog to *LORELEI*, a GPI-anchored membrane protein required for pollen tube reception in fertilization of *Arabidopsis thaliana* plants. While LORELEI is expressed in in the reproductive tissues (specifically in the synergid cells of the ovule), LLG1 is expressed primarily in vegetative tissues and not in the reproductive tissues. We hypothesized that the differences in selective pressures between the paralogs was due to divergent expression patterns rather than function. In order to test this hypothesis, a phylogenetic tree was constructed for both *LRE* and *LLG1* using *Tarenaya hassleriana* and *Cleome violacea* (as members of a sister group to *Arabidopsis thaliana*) and *Carica papaya* (an outgroup). The phylogenetic analysis showed that post-gene duplication, *LRE* was subject to a significant degree of positive selection when compared to *LLG1*. In order to characterize their functional relationship to each other, we tested whether *LLG1* could complement a *lorelei* mutant when expressed in the synergid cells under the *LORELEI* promoter. Analysis of stable transgenic lines carrying LLG1 fused to citrine YFP showed that the LLG1-cYFP fusion protein localized to the filiform apparatus of the synergid cells, which is where native LORELEI also localizes. Furthermore, LLG1 was also able to complement the *lorelei* mutant phenotype of reduced seed set and pollen tube reception defects. Additionally, loss of LLG1 did not impact pollen tube reception. Our collaborator's lab is testing if Arabidopsis LRE can complement *llg1* defects in vegetative tissues. Together, these results suggest that *LRE* and *LLG1* have shared function, but different expression patterns due to divergent evolution. To further test this hypothesis, we are examining whether or not the functions of LLG1 and LRE arose prior to their divergence from their shared ancestor. For this, we are investigating whether the ancestral copy found in *Cleome violacea* can complement both the *lorelei* and *llg1* mutant phenotypes. This research was supported by the Undergraduate Biology Research Program with funds from the BIO5 Institute and private donors.

RNA-BINDING PROTEIN FUSED IN SARCOMA (FUS) ROLE IN RNAP2 AND T7 TRANSCRIPTION IN THE PRESENCE OF MOLECULAR CROWDING AGENTS

***EMMA HARRELL*, RACHEL VICTOR, DANIEL WEILAND, VALERY THOMPSON, J. C. SCHWARTZ**

Amyotrophic Lateral Sclerosis (ALS) is a neurodegenerative disease that causes a drastic breakdown of motor neurons, resulting in eventual death by respiratory failure. Fused in Sarcoma (FUS) is a nuclear RNA-binding protein that has been found to associate with the carboxy terminal domain (CTD) of human RNA polymerase II (RNAP2) and other transcription machinery to impact the process of transcription. In its mutated form, FUS has been implicated in ~5% of familial ALS cases, as well as in 1% of sporadic ALS cases. Although the mutated form of FUS has been implicated in the development of ALS, little is known about its native function. Specifically, evidence shows that FUS interacts with the CTD of RNA Pol II and other transcription machinery within the nuclei of cells; this suggests that FUS serves to influence the process of human transcription. Additionally, FUS has been shown to influence bacteriophage T7 transcription. How these interactions specifically affect the efficiency of transcription, however, is relatively uncharacterized. To determine how FUS affects the process of transcription, both T7 and HEK293 in vitro models of transcription were adopted. An in vitro transcription assay in which produced RNA is DNase treated, reverse transcribed, and analyzed through quantitative polymerase chain reaction (qPCR) in addition to UREA-PAGE analysis of RNA were used to determine transcriptional efficiency; the crowding conditions of the in vitro reaction are modified in order to test how transcriptional efficiency of several genes, including green fluorescent protein (GFP) and FLAG-FUS, is affected by the presence of FUS. Current experimental results suggest that the addition of FUS to the transcription assay affects transcriptional efficiency of the target gene. These results provide insight into the role of FUS in the process of transcription and help to illustrate the native function of FUS within the nuclei of cells. This project is supported in part by the Undergraduate Biology Research Program with funds from the BIO5 Institute and private donors.

ANALYSIS OF CRISPR-CAS9-GENERATED MUTANTS OF MRP-1 TRANSCRIPTION FACTOR GENE IN MAIZE

***DESTINY HODGES*, CHOONG-HWAN RYU, RAMIN YADEGARI**

The development of the nutrient-rich endosperm is regulated by a number of key transcription factors (TFs) including the MYBR-type MRP-1. MRP-1 is expressed at high levels and has been shown to regulate the expression of many genes in the basal endosperm transfer layer (BETL) during early kernel development. BETL mediates uptake of sugars and nutrients into the kernel and can affect the size and quality of the endosperm as a whole. We are using a reverse-genetics approach to better understand the function of MRP-1 in endosperm development. We used CRISPR-Cas9 to knock out MRP-1 using both single and double target sites in the gene sequence. The mutagenizing cassettes were transformed into maize embryos by the Iowa State University Plant Transformation Facility to generate multiple T0 lines. We used PCR-based approaches to confirm the Cas9-generated mutations in the genome. We will report on ongoing experiments to verify transmission of the targeted MRP-1 mutations to the T1 generation. Related genes from the MYBR family are also being analyzed in the same manner. These mutations, individually and in combinations, will be used to understand the function of MRP-1 and the related MYBR TFs in endosperm development. This project is supported in part by the Undergraduate Biology Research Program with funds from the Office of Research, Discovery & Innovation.

SUBCELLULAR LOCALIZATION OF LORELEI IN PLANT CELLS VIA GPI-ANCHORING

***GREGORY HOWARD*, YANBING WANG, XUNLIANG LIU, RAVISHANKAR PALANIVELU**

In plant reproduction, a pollen grain must sprout a tube that navigates its way down through the pistil of the flower and grows into an ovule to fertilize it. Using a series of chemical cues, the pollen tube reaches the filiform apparatus at the tip of the ovule; a cascade of protein signals then allows the pollen tube to enter through the membrane of the ovule. When inside, the cell wall of the pollen tube becomes degraded leading to its eventual burst releasing the haploid sperm. LORELEI is a membrane protein in the filiform apparatus that plays a role in the signal cascade that leads to this fertilization; without it, the success rate of fertilization is reduced by 75%. LORELEI is post-translationally modified after translation in the Endoplasmic Reticulum (ER) with the addition of a lipid anchor, known as a GPI-anchor, which enables it to be embedded in the lipid membrane of the plant cell. A transamidase complex in the ER binds with an anchor signal domain present in LORELEI and proteolytically cleaves the signal sequence attaching a GPI anchor allowing the anchored protein to be trafficked through the endomembrane system and finally into the outer cell membrane. LORELEI localization in the plasma membrane of cells can be easily observed by expressing fluorescently tagged LORELEI in either the leaf cells of stably transformed *Arabidopsis thaliana* or by expressing it transiently in *Nicotiana benthamiana* leaves under a laser confocal microscope. LORELEI localization in plasma membrane was confirmed in co-localization experiments with a known membrane protein. Additionally, if the LORELEIs GPI anchor signal sequence is substituted for a polypeptide transmembrane domain, the localization of this fusion protein is similar to that of wild type LORELEI with a GPI anchor signal sequence. Deleting either the GPI anchor signal sequence or the amino acid residue to which the GPI anchor is attached, altered its localization in the cell to varying degrees. These data suggest that LORELEI is a GPI-anchored protein that localizes to the plasma membrane and contains various domains that facilitates the post-translational modification of obtaining a GPI-anchor. Funding: The Undergraduate Biology Research Program with funds from the BIO5 Institute, and private donors.

MICROBIAL SYMBIONTS OF AN INVASIVE GRASS DIFFER IN URBAN AND EX-URBAN ENVIRONMENTS

***VICTORIA HOWARD*, MING-MIN LEE, JAMISON CAREY, A. ELIZABETH ARNOLD**

Biological invasions are costly both in ecological and economic terms. *Cenchrus ciliaris* (buffelgrass) is one of the most widespread invasive plants in the Sonoran Desert, where it establishes readily in both intact and degraded soils, weathers

drought, flourishes with fire, and alters native fire regimes. Together these factors make management of buffelgrass costly and labor-intensive. A complement to current management techniques is to evaluate the factors relevant to the establishment of *C. ciliaris*, including the potential for microbial symbionts to aid in growth or tolerance of stress. The goal of this project is to evaluate the abundance, diversity, and composition of fungal and bacterial microbiomes associated with *C. ciliaris* in urban and ex-urban environments. We collected buffelgrass at sites with native plant communities on the north and west sides of Tucson and compared their endophytic microbiota with those of buffelgrass collected in urban alleys and parking areas in nearby areas of the Tucson metropolitan zone. We predicted that endophyte communities in depauperate urban environments would be less abundant and less diverse than those in ex-urban areas, with richer soils and more natural plant communities. We surface-sterilized plant tissues and isolated fungi and bacteria from roots and shoots of each individual. Microbial isolates were characterized via DNA barcoding following restriction fragment length polymorphism (RFLP) analysis. Preliminary analyses indicate a significant difference in the abundance of endophytes in urban vs. ex-urban sites. Characterization of these endophyte communities reveals the relevance of tissue type and location in shaping the endophytic microbiota of buffelgrass. Future research will focus on identifying any plant-microbe interactions that may influence the fitness of *C. ciliaris* as an invasive plant. This research was sponsored by the Undergraduate Biology Research Program through the University of Arizona Office of Research, Discovery & Innovation, and private donors.

A BACTERIAL SURFACE PROTEIN PROTECTS *RICKETTSIA* FROM MULTIPLE HOST POLYUBIQUITYLATION MECHANISMS

***NADIA INGABIRE*, PATRIK ENGSTRÖM, MATTHEW WELCH**

Rickettsia parkeri, a bacterial pathogen and the causative agent of spotted fever disease, strictly replicates in the cytosol of eukaryotic host cells and subsequently uses actin-based motility to spread to neighboring uninfected cells. Other pathogens that replicate in the cytosol have evolved mechanisms to avoid recognition by the ubiquitin-machinery, which can label cytosolic bacteria with ubiquitin chains and acts as the first event in degradation by antibacterial autophagy. However, the mechanism by which *R. parkeri* avoids ubiquitylation is not known. Recent work in our lab has suggested that outer membrane protein B (OmpB) acts on the bacterial surface to block polyubiquitylation of multiple surface proteins including OmpA. To gain insights into the mechanisms of polyubiquitylation of the ompB mutant, we assessed what types of ubiquitin chains formed globally on the whole bacteria, and specifically on OmpA. Using anti-ubiquitin chain-specific antibodies in immunofluorescence microscopy and western blotting experiments, we observed that whole ompB mutant bacteria, but not wild type bacteria, were positive for K63, K48, and M1 ubiquitin chains. In addition, in pull-down experiments with mutated ubiquitin, it was observed that OmpA was mainly labeled with K63 ubiquitin chains. Interestingly, we also observed that K63 ubiquitin chains colocalized with wild type *Rickettsia* actin tails and host cell actin fibers, suggesting a potential role for K63 ubiquitin chains in regulating actin dynamics and actin-based motility. Together, our data suggest that OmpB protects whole bacteria from multiple polyubiquitylation mechanisms, and specifically protects OmpA from K63 ubiquitylation.

INVESTIGATING THE EFFECTS OF SMALL MOLECULES ON ALS PHENOTYPES IN A *DROSOPHILA* MODEL

***JASON JUANG*, ARIELLE TRAN, DANIELA C. ZARNESCU**

Amyotrophic Lateral Sclerosis (ALS) is a progressive neurodegenerative disorder that results in loss of motor function and death three to five years after diagnosis. At the moment, Radicava is the newest and second only FDA approved treatment for ALS that can slow decline and extend lifespan by a few months. There is still a big need for discovering new compounds that can prolong lifespan further and improve motor function. Several genes including C9ORF72, SOD1, FUS, and TDP-43 contribute to ALS pathology; however, cytoplasmic inclusions related to TDP-43 are identified in more than 95% of cases. To encompass these cases, we work with a *Drosophila* animal model expressing wild type or mutant TDP-43 that exhibits motor function and lifespan phenotypes. This model is utilized in screening candidate compounds to determine toxicity and potential ability to

rescue phenotypes. As of late, we have been focusing on three compounds that may have neuroprotective properties: tauroursodeoxychlic acid (TUDCA), 4-phenylbutyric acid (PBA), and AQU-118. A preliminary screen was conducted through larval turning, a behavioral assay used by our lab to measure changes in motor function. By timing how long treated larvae take to return ventral side down after being turned onto their backs, it is possible to evaluate the efficacy of compounds compared to ALS larvae. Our results show that after treatment, ALS larvae exhibit a rescue in larval turning times, implying these compounds may be promising candidates. We are currently running additional experiments to measure the effects on TDP-43 levels through western blotting and the effects on lifespan. The results will provide future strategies on how to proceed with future experiments in order to gain a better understanding of the mechanism of action for these compounds and their therapeutic potential in patients. Experiments funded by the Undergraduate Biology Research Program, University of Arizona Office of the Provost (to JJ), National Institutes of Health NS091299 and Aquilus (to DCZ).

PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN REDUCES OPIOID INDUCED βARRESTIN2 RECRUITMENT TO THE MU OPIOID RECEPTOR

***CALEB KIM*, JUSTIN LAVIGNE, KATIE EDWARDS, AND JOHN M. STREICHER**

Opioids have been a highly effective treatment for chronic pain but at a cost of serious side effects, including tolerance and addiction. Side effects are caused in part by desensitization and downregulation of activated mu opioid receptors (MOR) due to the recruitment of βarrestin2. βarrestin2 is recruited once the MOR is phosphorylated by the kinase GRK2. GRK2 is regulated by Phosphatidylethanolamine-Binding Protein (PEBP) through phosphorylation by Protein Kinase C (PKC). However, PEBP has not been investigated for its role in MOR signaling and opioid response and may regulate MOR desensitization and subsequent side effects. We first tested this using an in vitro model of βarrestin2 recruitment in MOR expressing U2OS cells. We found that by inhibiting PEBP through siRNA knockdown or the small molecule inhibitor locostatin, we could increase the recruitment of βarrestin2 to the MOR in two separate assays. Conversely, we found that activating PKC via phorbol myristate acetate (PMA) led to PEBP phosphorylation/activation, and a reduction in βarrestin2 recruitment to the MOR, which could be blocked by PEBP knockdown. We then tested the role of PEBP in vivo by injection of locostatin into the brain or spinal cord, or CRISPR editing of PEBP in the spinal cord. We found that blocking PEBP in vivo led to a strong reduction in morphine-induced tail flick anti-nociception in both the brain and spinal cord. Together, these results support the hypothesis that PEBP acts to sequester GRK2 and block βarrestin2 recruitment downstream of the MOR both in vivo and in vitro. These results also suggest that enhanced PKC/PEBP activation by opioid drugs could further reduce opioid side effects and enhance analgesic efficacy. This project is supported in part by the Undergraduate Biology Research Program with funds from the College of Medicine.

EVALUATION OF A HUMANIZED SINGLE CHAIN VARIABLE FRAGMENT (SCFV) SPECIFIC TO PROSTATE STEM CELL ANTIGEN (PSCA)

***EMILY KOONS*, NATASCHA DRUDE**

Pancreatic cancer is well known for its aggressive behaviors and high mortality rates. A large contributor to its sinister nature is its difficulty to diagnose. The body's anatomy cleverly disguises the pancreas, making it difficult to visualize progression of the disease. With recent research, promising results for both improved treatment and imaging have arisen. To utilize these new strategies (discussed below), several key aspects of the treatment need to be evaluated. In this study, we successfully created a radiolabeled complex that will specifically bind to only the tumor site. This was completed through the use of a biotinylated single chain variable fragment (scFv) in combination with tetrameric protein NeutrAvidin (NAv) possessing affinity for biotin. Once this construct was completed and deemed pure through high performance liquid chromatography (HPLC), it was then radiolabeled using a radionuclide in combination with a DOTA-Biotin derivative. After a high radiochemical yield (through performance of instant thin layer chromatography (iTLC)) was established, the product was then analyzed in various in vitro experiments to assure it was not internalized by pancreatic cancer cell lines. Once the compound was proven to remain surface-

bound, in vivo experimentation followed. This allowed us to visualize the biodistribution of the injected compound in its entirety through the use of positron emission tomography (PET) and computer tomography (CT) technology. These assays helped us to determine critical time points for injection and imaging of the construct. Acknowledgements: RWTH Aachen Department of Nuclear Medicine, RWTH Uniklinik, and prior grants.

A-SYNUCLEIN EXPRESSION IN YEAST AND APPARENT EFFECTS ON ENDOCYTOSIS

***MAXWELL LAGAS*, ALLISON BUCHANAN, ROSS BUCHAN**

Parkinson's disease is an extremely prevalent neurodegenerative disorder that affects 1 million people in the United States and 10 million people across the world. This disease is incredibly debilitating and leads to a decreased quality of life through death of neurons in the Substantia Nigra of the brain. At the molecular level in these neurons, there is an accumulation of abnormal aggregates known as Lewy bodies. A major constituent of these aggregates is a protein known as a-Synuclein. The focus of the project is using *Saccharomyces cerevisiae* to study how the function of Wild Type a-Synuclein (present in sporadic Parkinson's) and two mutant versions of a-Synuclein (present in genetic Parkinson's A53T and A30P) adversely affect cellular processes in yeast. We could then use this data as a basis for directed testing in human cell systems. Previous data with a-Synuclein yeast models has suggested endocytosis genes impact a-Synuclein toxicity. In this work, an endocytosis rate assays revealed that a-Synuclein WT, A53T, and A30P transfected into yeast causes a decrease in the movement of endosomes to the vacuole in the cell. Continuing in this work growth assays we believe will reveal that a-Synuclein WT, A53T, and A30P have increased toxicity in endocytic yeast mutants but not in autophagy mutants. Studies using the powerful genetic model of yeast may reveal a novel role for endocytosis in Parkinson's pathology that has therapeutic potential for targeting. This project was supported by the National Institute of General Medical Sciences and the Undergraduate Biology Research Program with funds from the BIO5 Institute.

THE ROLE OF NITRIC OXIDE IN CELL QUIESCENCE

***HEBER LARA*, S. CHUNG, W.R. MONTFORT**

The initiation of the cell cycle by a cell is marked by an increase of DNA synthesis along with other metabolic and physical changes. In this state, the cell prepares enough content to split and proliferate. Cell proliferation will only occur if the proper environment is present such as enough energy and a non-stressed microenvironment; when a cell is not under these conditions it can reduce its metabolic activities and halt proliferation, this cell state is called quiescence. Quiescence is a reversible state in a cell and is universal to many cell types including those that have acquired cancerous traits. Based off of genomic data, we believe nitric oxide (NO), a versatile molecular signal, has a role in deepening cell quiescence. Preliminary results in EdU proliferative assays support this role of nitric oxide in MCF7a cells, a mammary epithelium ER+ cancer cell line. Our overarching work focuses on an aggressive and non-specific treatable breast cancer, triple negative breast cancer (TNBC). Under current cancer treatments, cancerous cells that are under quiescence remain unharmed, but if NO is a key player in inducing quiescence, then this work may provide a path for a more robust TNBC treatment. Acknowledgements: NIH MARC Training Grant T34 GM08718, NIH GM117357, and the Montfort Research Group of the Chemistry and Biochemistry Department at the University of Arizona.

SCALE-UP OF PREVIOUS PROTOCOL FOR SYNTHESIS OF POLYSTYRENE NANOPARTICLES FOR ANALYTE TO PROTEIN INTERACTION QUANTIFICATION

***JOO RYUNG LEE*, COLLEEN JANCZAK, CRAIG ASPINWALL**

Protocols for the synthesis of polystyrene nanoparticles for the use of assays in quantification of analyte to protein interaction in free solution and cells have been developed and in working order for decades, however, the protocol has long been inefficient due to the amount of product that could be created per synthesis and the time-consuming process. In order to address the significantly small yield from synthesis of polystyrene nanoparticles, experimentation to scale-up the process while refining the quality of the nanoparticles was conducted during the summer of 2018 that led to increase in yield from mere 100mg of final product to 10g of viable polystyrene nanoparticles that have been proved to be functional and viable for experimentation. Transmission Electron Microscopy imaging showed that the scaled-up protocol produced nanoparticles that were spherical, which allows for most efficient interaction with analytes and proteins, and sufficiently coated with silica to allow for nonspecific binding with proteins, which allows for wide-range use of these nanoparticles. The nanoparticles were also functionalized by binding biotin to the silica coating and experimenting with stripped avidin to calculate the functional efficiency as well as accuracy of quantification of analyte to protein interactions. Finally, the protocol scale-up was concluded by testing with purchased nanoparticles from PerkinElmer which showed competitive results. Research was possible by generous funding from the National Science Foundation, and the \ Undergraduate Biology Research Program with funds from the University of Arizona Office of the Provost.

ATP7A'S ROLE IN COPPER HOMEOSTASIS WITHIN THE FRAMEWORK OF AMYOTROPHIC LATERAL SCLEROSIS

***SAMANTHA MACKLIN-ISQUIERDO*, TAYLOR D. WINGFIELD, BRIGGS S. CARHART, MATTHEW T. CHAUNG, ROBERT KRAFT, DANIELA C. ZARNESCU**

Copper plays an important role in the human body and is crucial for the formation of the brain and nervous system. An imbalance in copper concentrations can lead to life-threatening neurological diseases. We focus on the human copper regulatory protein, ATP7A, due to its strong association with neurodegeneration when mutated. One of these neurodegenerative diseases is amyotrophic lateral sclerosis (ALS), a fatal neurological disease that causes motor neurons to die. Our work seeks to provide further insight into the relationship between ATP7A and ALS. A *Drosophila melanogaster* model of ALS was generated, based on overexpression of wild-type (WT) and mutant (M1311V) human ATP7A. We evaluated locomotor phenotypes using larval turning assays which measure *Drosophila* larvae's capability for movement. Neuromuscular junction (NMJ) dissections of the *Drosophila* larvae were used to determine if there was a morphological phenotype associated with overexpression of the human ATP7A proteins. These experiments showed that both WT and mutant ATP7A cause locomotor dysfunction similar to those found in other *Drosophila* ALS models. Further genetic interactions with TAR DNA Binding Protein (TDP-43) indicate that the mutant ATP7A acts as a loss of function mutation, based on the fact that it exerts a similar effect on TDP-43 as loss of the endogenous *Drosophila* ATP7 gene. Surprisingly, there was no significant effect of human ATP7A on morphological phenotypes at the NMJ. We are currently testing candidate drugs that could mitigate the locomotor phenotype caused by defects in copper homeostasis. Overall, our results indicate there is a correlation between ATP7A and ALS and can help inform how a therapy could be developed. This work was funded by the Undergraduate Biology Research Program (UBRP) with funds from the Office of Research, Discovery & Innovation, the National Institutes of Health (NIH) (R01 NS091299), the Above and Beyond Precision Medicine Initiative, and the Western Alliance to Expand Student Opportunities (WAESO) Louis Stokes Alliance for Minority Participation (LSAMP) National Science Foundation (NSF) Cooperative Agreement No. HRD-1101728.

A CLOSED-LOOP SYSTEM FOR JUXTACELLULAR PIPETTE CONTROL

***MARIANNE MADIAS*, ZHIYUAN CHEN, PAOLA RIOJA, MIHALY VOROSLAKOS, JOHN SEYMOUR, AND EUISIK YOON**

The juxtacellular technique has become a popular method for recording activity in electrophysiology investigations due to the ability to take long-term recordings with single-cell resolution. However, due to the risk of damage to a recording pipette or neuron during certain rapid movements of a freely moving animal, this technique is limited to head-fixed animal recordings. Additionally, the setup for juxtacellular recordings requires expensive stationary equipment that cannot be integrated into a freely-moving system and limits the accessibility of the technique. In response, we propose a closed-loop system that utilizes lightweight, inexpensive components to control a juxtacellular recording pipette and minimize damage to a neuron during freely moving animal recordings. A microcontroller continuously reads 3-axis accelerometer data and will send a command to a linear actuator to retract the pipette if an acceleration threshold is crossed. The parameters considered for components included weight, processing speed, and resolution. The system must be lightweight to be wearable for an animal, it must be fast enough to retract the pipette before damage can occur, and it must have high resolution for reliable and accurate movement within the brain. To determine the latency of the system we compared the time an acceleration threshold is crossed, the time the retraction command is sent, and a waveform of the pipette recording. We demonstrate a minimal delay between the detection of a significant acceleration and retraction of the pipette, as well as accuracy in the motor position. The delay between the time the acceleration threshold is crossed and the time the microcontroller detects the threshold crossing and sends a command is 49 µs. The delay between the time the microcontroller sends the command to the linear actuator and the time the motor reaches the retracted position is between 1.7 to 20 ms. The average error of the linear actuator for 100 µm increments was measured to be 2.4 µm. Future directions include working to reduce system latency and scaling down to a wearable module that integrates multiple pipettes into one system.

INVESTIGATING CONTROL OF NUCLEUS ACCUMBENS DOPAMINE RELEASE BY VENTRAL TEGMENTAL AREA NEURONS AND THE ROSTROMEDIAL TEGMENTAL NUCLEUS

***ERIN MAMARIL*, DANIEL HILL, MITCHELL BARTLETT, STEPHEN COWEN**

Dopaminergic signaling is critical for facilitating movement, reward valuation, and memory. The brain regions involved in the dopamine pathway are well established, but the physiological mechanisms are not yet entirely understood. The rostromedial tegmental nucleus (RMTg) is thought to exert inhibitory control over the ventral tegmental area (VTA) dopaminergic cell activity and thereby inhibiting phasic dopamine release in the nucleus accumbens (NAc). To what degree the RMTg controls the VTA and downstream dopamine release remains poorly understood as these signals have never been measured concurrently. To address this, we used a novel technology developed in our laboratory to record RMTg and VTA electrophysiological activity and NAc dopamine release simultaneously. We hypothesized that non-dopamine RMTg activity would be anticorrelated with VTA dopamine cell firing and NAc dopamine release. Instead we found that both VTA-non-dopamine cell activity and RMTg activity increased preceding dopamine release. To ensure proper electrode placement in the in the targeted regions, we identified the VTA dopamine cells immunohistochemically using a tyrosine hydroxylase antibody and RMTg neurons using a mu-opioid receptor (MOR) antibody. We found that the majority of electrodes targeted to the VTA were surrounded by TH-labeled cells and preliminary data from MOR labeling suggest that those targeted to the RMTg were surrounded by MOR-expressing cells. These findings suggest that electrodes were appropriately targeted and that the above result was not due to poor electrode placement; instead, VTA and RMTg control of dopamine release is likely more complex than previously understood and appears to be highly regulated by non-dopaminergic neurons in these regions. This work was supported in part by the Undergraduate Biology Research Program with funds from the Office of the Provost.

DEVELOPING MORE COST-EFFECTIVE AND MOBILE CAPILLARY ELECTROPHORESIS INSTRUMENTATION THROUGH 3D PRINTING

***JACOB MAPP*, CRAIG ASPINWALL**

Capillary Electrophoresis (CE) is an analytical technique used to separate molecular species based on charge and hydrodynamic radius. CE provides limits of detection with conventional instrumentation in the femtomole to attomole range (10-15 mol to 10-18 mol), making CE applicable for a wide range of uses, such as in hospitals, forensics, food safety, and water purity. To broaden the applicability of CE, we have developed a more mobile and cost-effective CE instrument through the use of additive manufacturing, better known as 3D printing. A 3D printed computer mouse-sized instrument was fabricated that houses the optical components necessary for CE, including an excitation filter, emission filter, dichroic mirror, and microscope objective, as well as a capillary holder. To test the viability of this instrument design for Capillary Zone Electrophoresis (CZE), we analyzed varying concentrations of fluorescein in solution. The overall goal is the optimization of the instrumentation to achieve limits of detection comparable to or better than commercial instrumentation. A small and mobile 3D printed instrument with such limits of detection and cost-effectiveness would greatly increase the applicability and accessibility for CE. Additionally, the 3D printed design is readily transferable, enabling greater potential for replication and relatively quick, in-house modifications to address institution-specific issues and limitations. This research was supported in part by the Undergraduate Biology Research Program with funds from by the Office of Research, Discovery & Innovation.

SPEECH DEFICITS IN APHASIC STROKE PATIENTS

***ALEXIS MORRISON*, LEAH RICE, SARA MOHR, ANETA KIELAR**

Stroke affects almost eight hundred thousand Americans every year and 40% of strokes to left hemisphere perisylvian regions are associated with impairment in language production or comprehension, called aphasia. This study investigated in detail speech characteristics of 10 patients diagnosed with stroke induced aphasia and 18 healthy control participants. All participants underwent a comprehensive battery of cognitive and language assessments. We also collected narrative speech samples using AphasiaBank protocol for the retelling of the Cinderella Story. The Cinderella narratives were transcribed into utterances and then analyzed by coding for various linguistic elements, including morphological and syntactic complexity. Data was gathered on the number of words and utterances produced, the parts of speech present or absent, the level of clausal complexity of the utterances, pauses within and between utterances, and the level of complexity of verb morphology in the speech. Data was also gathered on whether or not the study participants produced the main concepts for the narrative story, and the accuracy and grammaticality of those concepts. This gathered data was then compared to the results of the participants' other cognitive and language tasks to see if there were any correlations. Preliminary results showed that in comparison to the healthy controls, patients with stroke aphasia produced less utterances, and that their utterances were shorter. There was a positive correlation between the words per minute produced and the mean length of the patients' utterances. The results also showed that stroke patients produced fewer main concepts and these correlated positively with the number of verbs spoken; these results might indicate that the parts of the patients' speech affected leads to the breakdown of communicative efficiency. Establishing the connections between the deficits could lead to a better explanation of the condition of aphasia and lead to better assessments and therapeutic techniques to address the underlying disorder. Source of funding: The Undergraduate Biology Research Program with funds from the BIO5 Institute, the University of Arizona Faculty Seed Grant (FSG) to Dr. Aneta Kielar, and the University of Arizona Startup Grant to Dr. Aneta Kielar.

THE MU-DELTA OPIOID RECEPTOR HETERODIMER MAY EVOKE SIMILAR SIGNALING WITHIN THE STRIATUM, PERIAQUEDUCTAL GRAY, AND BRAINSTEM

***PAUL NGUYEN*, ATTILA KERESZTES, SEPH PALOMINO, KEITH OLSON, VICTOR HRUBY, JOHN STREICHER**

Opioid drugs like morphine are the gold standard for treating acute and chronic pain, but they induce detrimental side effects such as tolerance and dependence. It has been suggested that the mu-delta opioid receptor heterodimer (MDOR) transduces some of these side effects and that heterodimer targeted drugs could be a solution to weaken these side effects. We have thus created an MDOR selective antagonist called D24M. We evaluated D24M in vitro and found a ~100-fold selectivity for the MDOR over the monomers. Similarly, we performed hot water tail-flick experiments in mice in the presence of various doses of D24M against CYM51010 and Deltorphin-2 (MDOR selective agonist), and DAMGO (MOR monomer selective agonist), or DSLET (DOR monomer selective agonist), and found that D24M potently (A50=2-7.8 nmol) blocked MDOR activity with no activity against the MOR or DOR monomer up to 10 nmol. We then used D24M to examine MDOR physiology in mice. We found that intracerebroventricular (ICV) injection of 1 nmol D24M strongly increased oxymorphone anti-nociception by ~50-600% in models of tail flick, paw incision, and chemotherapy neuropathy pain. To find the signaling mechanism for this enhancement of opioid analgesia, we injected 1 nmol D24M by the intracerebroventricular route followed by 3.2 nmol CYM51010. Once we acquired the samples, we tested ERK activation via western blot analysis. We found that D24M has similar effects on ERK pathway activation for each part of the three tested brain regions; further confirming that ERK is a possible pathway for the MDOR to promote kinase activation, and that D24M could possibly be a promising drug candidate for opioids at various locations of the brain. These discoveries will further determine the role of the MDOR in vivo and provide a novel tool that could greatly impact opioid heterodimer research. Acknowledgements: Institutional support from the University of Arizona and the National Institutes of Health/National Institute on Drug Abuse R21DA044509.

MODELLING SIMPLIFIED NATURAL LIPID MEMBRANES IN NANODISCS

***JIBRIEL NOUN*, MARIUS KOSTELIC**

Nanodiscs are lipoprotein nanoparticles that self-assemble into a lipid bilayer and have proven useful for studying lipid-protein interactions. By combining nanodiscs with native mass spectrometry (MS), it is possible to keep the nanodisc intact for MS analysis and to characterize embedded membrane proteins. However, most native MS of nanodiscs has focused on homogeneous bilayers or binary mixtures of similar lipids. Creating a heterogeneous lipid environment in nanodiscs that models natural systems would give a more native platform for analyzing membrane proteins. Through assembly of these mixed lipid discs, integral membrane proteins can then be analyzed in a more physiologically relevant state. Building these mixed lipid models can help us better understand natural states of proteins within the lipid membrane environment. This project is supported in part by the Undergraduate Biology Research Program with funds from the BIO% Institute.

APPLICATION OF CHEMICAL AND BIOLOGICAL TECHNIQUES TO CHARACTERIZE THE ORGANIC MATTER WITHIN ENVIRONMENTAL BUFFERS RECEIVING WASTEWATER EFFLUENT

***JULIANA ORDINE*, KEVIN DANIELS, CHRISTIANE HOPPE-JONES, ISRAEL LOPEZ, SHAWN BEITEL, MINKYU PARK, GUILLERMO FLORES, SHANE SNYDER**

As sources of freshwater continue to decline, surface waters influenced by wastewater effluents (WWEs) are becoming increasingly impacted as the volume of waste streams entering surface waters continues to rise. Approximately 15,000 wastewater treatment plants (WWTPs) in the United States produce over 32,000 million gallons of effluent per day, of which, the majority is directly discharged into surface waters (Pabi et al., 2013). Unfortunately, many ecosystems within these surface waters receiving these effluents have experienced irreversible damage. There is a great concern over the diverse organic compounds in WWE that persists through treatment and enters surface waters. This can include bulk organic matter, trace organic contaminants (TOrCs) such as pharmaceuticals, personal care products, natural hormones, industrial/commercial

compounds, and unknown organic compounds. Of the different environmental buffers that these WWEs are discharged into during indirect potable reuse, wetlands and rivers have been shown to be the most promising to decrease these organic compounds. The purpose of this study is to investigate how different types of environmental buffers can alter the composition of organic matter within secondary effluent produced in Tucson, Arizona and the objectives are to investigate how seasonal variance and difference in inlet volume flow rate affect the quality of wastewater in both river and wetlands, and to measure how long it takes for the Sweetwater Wetlands to reach steady-state after an annually controlled fire. Analytical methods include bulk organic parameters (i.e. EEM/TOC) and targeted analysis of trace organics. In addition to the chemical analysis, bioassays are being applied to evaluate the bioactivity of the environmental waters. This project was funded by the Environmental Health Sciences – Transformative Research Undergraduate Experience (EHS-TRUE) through the National Institute of Environmental Health Sciences Grant #1-R25-ES025494, and by the Western Alliance to Expand Student Opportunities (WAESO) Louis Stokes Alliance for Minority Participation (LSAMP) National Science Foundation (NSF) Cooperative Agreement No. HRD-1101728.

COLONY CONTEST IN THE ANT *TEMNOTHORAX RUGATULUS*

***VICTOR PAAT*, KENNY CHAPIN, ANNA DORNHAUS**

As social insects, ants accomplish tasks as a collective of individuals assigned to separate jobs (e.g. brood care, colony defense). Through collective decision-making, the colony can use a behavioral arsenal to address and adapt to environmental stress. Much investigation had been devoted to how ants collectively decide how to interact with their abiotic environments. The rock ant, *Temnothorax rugatulus*, mostly competes for nest sites within their environments. In this study, we aim to expand upon how these ants utilize their behavioral arsenal and unique strategies to address this nest site contest against another colony. Collective decisions across colonies promote multiple avenues of defensive and competitive strategy, but few can be effective at more than one at a time. We specifically analyzed aggressive and defensive interactions at the inter-colony level to test our hypotheses that (i) colonies can employ different strategies when presented with competition and (ii) colonies show preference to certain behavioral patterns. We find that colonies do employ different behaviors and patterns to overrun their opponents. These results highlight the importance of decision and strategy, for if one colony succeeds in their task, the other does not. Special acknowledgements to the Undergraduate Biology Research Program with funds from the Office of the Provost, and Defense Advanced Research Projects Agency (GN D162-005-0227; TN SB162-005) for funding this project.

FACTORS CONTRIBUTING TO EXPLORATION IN FORAGING BUMBLEBEES

***CHLOE PATERSON*, JACK-MORGAN MIZELL, KIARA CASAS, ANNA DORNHAUS**

The exploit-explore tradeoff features prominently in the decision-making strategies implemented by many complex organisms and is well-documented in humans (Wilson et al., 2014). Striking an appropriate balance between exploratory and exploitative behaviors is necessary for survival; for optimum performance, organisms must both draw from resources they know to be reliable and explore options they have less information about. We investigated what is driving exploration in our model, the common eastern bumblebee (*Bombus impatiens*). We tested our animal using a series of Y-mazes in which the bees had to choose between two different artificial flowers supplying different concentrations of nectar. We set up the maze so that four types of choices are possible; a worker bee could choose from either the more or less informative option in the final trial of either the shorter or longer horizon condition. By forcing the bee through a set number of trials, which differed in number by horizon condition, the bee gained more information about the nectar concentration supplied by one type of flower compared to the other. The flower which the bee had less information about was the more informative option. If bumblebees are more likely to select the more informative option in the longer horizon condition compared to the shorter, they are showing directed exploration, or exploration driven by information-seeking. If the probability of this occurring is the same across conditions, then bumblebees show random exploration; that is, their exploration is not driven by information-seeking. Current data shows that bumblebees are slightly more likely to choose the more informative option in the longer horizon condition compared to the shorter, which suggests that bumblebees show directed exploration. However, the sample size is not large enough to form a

conclusion yet; we aim to remedy this in the future by testing more individuals. The results of this experiment may not only answer questions about the strategies that bumblebees use to explore their environments and exploit their resources, but also help us understand how these behaviors are balanced across individuals for the benefit of the colony. We thank the National Science Foundation grant no. DBI 1564521 to Anna Dornhaus, the University of Arizona Graduate and Professional Student Council Reap Grant, and the National Science Foundation Graduate Research Fellowship Program to Jack-Morgan Mizell for funding this project.

TSC2 DEFICIENCY IN OXYTOCIN RECEPTOR NEURONS CAUSES STEREOTYPY AND SEXUALLY DIMORPHIC SOCIAL BEHAVIOR IMPAIRMENT

***NICOLAI PENA*, PRERANA SHRESTHA, ERIC KLANN**

Autism spectrum disorder (ASD) can be challenging to study since a majority of cases have an unidentified, polygenic origin. ASD is a clinically heterogeneous group of disorders and can be categorized into three major areas of cognitive deficit: impaired social behavior, impaired communication ability, and repetitive behavior. Some rare single gene mutations can lead to ASD, including tuberous sclerosis complex (TSC). Roughly 25-60% of tuberous sclerosis patients fulfill the diagnostic requirements for autism and/or intellectual disability. Previous research has shown the value of TSC1/2 mutant animals as models of ASD. In addition to cognitive deficits, there is a skewed male prevalence of ASD in humans (4:1), as well as exclusively female-associated pulmonary tumorous growths in TSC. To further characterize the sexual dimorphism and social impairment related to these conditions, we generated mice with haploinsufficient Tsc2 (Tsc2+/-) oxytocin receptor (OxtR) neurons. Following a battery of social behavior tests and immunohistological analysis, we found these heterozygous mice to have ASD-related cognitive deficits as well as corresponding increases in OxtR neurons. Gq DREADD receptor activation and rapamycin injections were able to normalize some of the observed aberrant behaviors. We were able to delineate both male and female Tsc2:OxtR abnormalities in social behavior, repetitive behaviors, and neuroanatomy. Funding for this research has been provided by the SURP fellowship from NSF, the Simons Foundation (SFARI), and the National Institute of Health, National Institute for Neurological Disorders and Stroke (NS047384) to EK.

HARNESSING THE PAIN RELIEVING PROPERTIES OF NARINGENIN, A CITRUS FLAVONOID

***NANCY PHAM*, ANGIE DORAME, CYNTHIA MADURA, AUBIN MOUTAL, AND RAJESH KHANNA**

Chronic pain affects billions of people worldwide and comes at a high cost to society. The misuse of and addiction to opioids has become a national crisis motivating researchers to develop novel, non-addictive, and effective pain therapies. Using calcium imaging, a technique that images live cells to monitor the changes in intracellular calcium concentration, we investigated the pain-relieving properties of naringenin. Calcium ions play an important role in the generation of a variety of intracellular signals controlling crucial functions in all neuron types such as the transmission of nociceptive signals. Upon applying pharmacological triggers, we observed a decrease in the response of sensory neurons from Sprague Dawley female rats. Naringenin demonstrates much potential to be administered as a pain-relieving therapy due to the inhibited potassium chloride evoked calcium influx. Our findings support the pain-relieving properties of naringenin and offer a potential novel, non-addictive solution to treat chronic pain. This project is supported in part by the Partnership for Native American Cancer Prevention (NACP) through the National Cancer Institute Grant #2U54CA143924.

EVALUATING THE RHIZOSPHERE MICROBIOME ASSOCIATED WITH ALLELOPATHY OF AN ICONIC DESERT SHRUB

***CAROLINE PLECKI*, A. ELIZABETH ARNOLD**

Desert plants have evolved diverse tools for accessing limited water and soil nutrients, including inhibition of seed germination and/or growth of potential competitors. One tool for doing so is allelopathy - the exudation of compounds that inhibit the growth or germination of other plants. The desert shrub *Larrea tridentata* (creosote) is known for allelopathy and thus for forming monodominant stands of evenly spaced plants with few competitors in its extreme natural environments. Increasingly it is appreciated that plant microbiomes, the suite of microbes that live on, in, and in association with plant tissues alter the chemical expression of their host plants. However, the potential roles of rhizosphere microbes in allelopathy are not well known. The aim of this study was to evaluate potential contributions of microbes to allelopathy of creosote. In phase one we surveyed (a) the root microbiome and (b) rhizosphere (soil) microbes associated with creosote in monodominant stands west of Tucson, Arizona, USA. Surveys encompassed aerobic, anaerobic, and oligotrophic microbes and were designed to provide a rich culture library that, after identification with molecular barcoding, was used in phase 2 (inhibition assays, designed to measure the capacity of these microbes, individually and in the context of infecting root tissue of creosote, to inhibit seed germination and growth of representative desert plants). Overall this study advances our understanding of the diversity of microbes associated with an iconic desert shrub and provides a first perspective on the capacity of microbes, or plant-microbe interactions, to influence the powerful allelopathic properties of one of the Southwest's most distinctive plants. This project is supported in part by the Undergraduate Biology Research Program with funds from the College of Agriculture & Life Sciences, the Office of the Provost, and private donors.

SUB-ANESTHETIC KETAMINE INCREASES MICROGLIA RAMIFIED MORPHOLOGY IN A PRE-CLINICAL MODEL OF LEVODOPA-INDUCED DYSKINESIA

***AYUMI POTTENGER*, HELENA W. MORRISON, MITCHELL J. BARTLETT, TORSTEN FALK**

Parkinson's disease (PD) is a neurodegenerative disease caused by the death of dopaminergic neurons in the substantia nigra pars compacta (SNpc) and is characterized by motor dysfunction. PD has no cure, but symptoms can be treated with levodopa (L-DOPA). Continuous L-DOPA use can cause levodopa-induced dyskinesia (LID). Sub-anesthetic ketamine has been shown to reduce LID, as measured by abnormal involuntary movements (AIMs). The literature suggests that ketamine treatment leads to changes in dendritic spines. Microglia may play a role by phagocytosing neuronal spines. We hypothesized that ketamine would prevent AIMs and increase microglia ramified morphology, an indicator of a microglia response. In order to test this hypothesis, we studied the behavioral and histological outcomes in LID rats with and without ketamine treatment. Rats were unilaterally injected with a neurotoxin which targets dopaminergic neurons. Rats were then primed for two weeks with daily injections of L-DOPA. Twice, rats were treated with ketamine or vehicle. AIMs were scored every three to four days to assess changes in LID. On day 14, ketamine-treated rats showed a reduction in AIMs as compared to controls. A sub-analysis of AIMS scores in ketamine-treated animals revealed two subgroups: ketamine responders (K), and ketamine non-responders (KNR), which showed no difference in AIMs, as compared to controls. Coronal slices were processed for immunohistochemical staining using ionized calcium-binding adapter molecule and tyrosine hydroxylase to visualize microglia and dopaminergic neurons, respectively. The SNpc on the ipsilateral and contralateral side were imaged using confocal microscopy to obtain photomicrographs for image analysis. In the K group, a decrease in the number of microglia and an increase in cell ramification was observed. These data indicate that in the vehicle and KNR groups, microglia in the SNpc have a lingering response to the injury, which was increased beyond contralateral conditions after ketamine treatment in the K group. Funding: The Environmental Health Sciences – Transformative Research Undergraduate Experience (EHS-TRUE) through the National Institute of Environmental Health Sciences Grant #1-R25-ES025494, and the Jerry T. and Glenda G. Jackson Fellowship in Parkinson's Research to the University of Arizona.

MODELING EXERCISED INDUCED STRESS WITH ACM ENGINEERED HEART TISSUES

***SHELBY RHEINSCHMIDT*, JARED M. CHURKO, VIC KESCHRUMRUS**

The heart disease arrhythmogenic cardiomyopathy (ACM) can be caused by desmosomal mutations. Overtime, ACM leads to fibrofatty infiltration, arrhythmias, heart palpitations, fatigue, and in the worst case sudden cardiac death. It has been found that the symptoms of ACM are most common in young athletes leading to the hypothesis that exercise induced stress leads to the exacerbation of ACM pathology. In order to test this, we took induced pluripotent stem cells and differentiated them into cardiomyocytes (iPSC-CMs). Using iPSC-CMs, 3D tissue constructs called engineered heart tissues (EHTs) were made to model the tissue in the heart. These tissues are able to beat on their own but can also be paced to mimic the effects of exercise on the heart. To ensure that pacing EHTs is a model for exercise, real time PCR was conducted on paced and unpaced EHTs to assess the levels genes previously demonstrated to increase with exercise (GATA4, MYH6, MYH7, and IGF1). In the future, additional cell lines will be cultured with and without an ACM mutation and further RNA sequencing, RT-PCR, force contraction analysis, and calcium imaging to analyze for arrhythmias. There is variation in the severity of this disease and this research will be able to characterize the different mutations for a better diagnosis of ACM. This project was supported by the Undergraduate Biology Research Program with funds from Dr. Jian Gu, and the Saver Heart Steven M. Gootter Foundation Award awarded to Dr. Jared M Churko.

INDIVIDUAL DIFFERENCES IN VISUAL LEARNING AND BRAIN METABOLIC ACTIVITY IN ANTS

***RACHEL SADLER*, R. KEATING GODFREY, WULFILA GRONENBERG**

Insects use learning and memory capabilities to navigate and interpret the world around them. Color visual learning has been studied extensively in social insects such as bees, but less is known about the abilities of ants to form new color associations, especially on an individual level. By allowing individual ants to explore a bifurcated maze, half illuminated with ultraviolet light and half with green light, we can determine whether ants have innate color preferences. Based on each ant's behavioral results, the specimens are conditioned to reverse their innate preferences via a quinine (punishment) vs. sucrose (reward) paradigm. The ant's behavior prior to and after the conditioning is compared to assess whether or not each ant formed new color associations. Ants are evaluated based on changes to both first choice when entering the bifurcation and distribution of time spent in either half of the maze. Learning assessments are also based upon performance during the training and in an extinction test without reinforcing stimuli. Past projects have demonstrated that most individual ants have innate color preferences. These preferences vary amongst ants selected simultaneously from the same colony. Ant capability of learning new color associations is variable amongst individuals; potential brain differences underlying this variability are investigated via histochemistry. Brains are dissected, and sucrose protected immediately following the final testing phase, and are then cryosectioned and cytochrome oxidase stained. Relative cytochrome oxidase levels are quantified and scaled in Fiji. The combination of behavioral analysis and histochemistry allows for an exploration of possible metabolic differences in the brains of learners vs. non-learners, thus fostering an investigation of potential links between brains and behavior. This project is generously funded by the NSCS Research Award, and the Undergraduate Biology Research Program with funds from the College of Science.

DRUG RESISTANCE MECHANISM MEDIATED BY FUNGAL STEROL TRANSPORT PROTEIN TIR3

***ANDRES SANCHEZ*, MARTINA FRANCIS, VALERY THOMPSON, TARJANI THAKER, THOMAS TOMASIAK**

Fungal diseases are encountered daily in mainly a clinical and agricultural setting. The treatment generally prescribed for such diseases are doses of antifungal agents known as azoles. Azoles work by targeting various enzymes in the biosynthetic pathway of ergosterol, a key component in the structure and maintenance of the fungal cell membrane. However, recently antifungal agents show less lethality to pathogenic fungi due to the rise of resistance to antifungals in pathogenic fungi. Although antifungals generally target the biosynthesis of sterols, fungal cells exhibit the ability to bypass this problem by importing

exogenous sterols from the sterol-rich host, a process known as sterol uptake. Membrane protein AUS1 and cell wall protein Tir3 in the pathogenic fungus *Candida glabrata* are required for sterol uptake and survival in lethal concentrations of antifungals, however, the structure and mechanism of this sterol uptake system is unknown. The results of our future experiments will provide a structure and mechanism of the Tir3-AUS1 system as well as targets for new drugs to inhibit the system. Azole resistance in pathogenic fungi have, as of 2013, been classified as a serious public health threat. These findings may introduce new antifungal drugs that resolve this growing public health hazard. This project was supported by the National Institutes of Health through the Maximizing Access to Research Careers (MARC) Training Grant (T34GM08718) and R00GM11424.

EFFECTS OF ARSENIC ON MOUSE TRACHEAL EPITHELIUM TIGHT JUNCTION INTEGRITY

***ESTEVAN SANDOVAL*, BENJAMIN D. RIVERA, RUBY SIERRA, SARA L. BERTRAM, SCOTT BOITANO**

Arsenic is an odorless, colorless, and naturally occurring metalloid element that, worldwide, presents as the most common natural toxicant. Arsenic is known to contaminate local drinking water supplies and result in both malignant and non-malignant disease. While it is understood that drinking water with arsenic can lead to lung dysfunction and disease, less is known about how inhaled arsenic affects the lung and airways. This project is investigating whether inhalation exposure of arsenic and/or arsenic-linked dusts, that can be found in mine tailings, can affect lung health. I have developed an arsenic exposure model using airway epithelial cells isolated from mice to better model inhalation exposure. Lung epithelial cell function is assessed prior to and following exposure using electrical resistance measurements. Preliminary findings suggest inhaled arsenic can disrupt lung epithelial function by disturbing the epithelial barrier. In future studies I will expand this model to compare dust exposures that mimic mine wastes and tailings (i.e., with arsenic). This project is supported in part by the Undergraduate Biology Research Program with funds from the Office of Research, Discovery & Innovation, and the Western Alliance to Expand Student Opportunities (WAESO) Louis Stokes Alliance for Minority Participation (LSAMP) National Science Foundation (NSF) Cooperative Agreement No. HRD-1101728.

LARGE-SCALE LIFESPAN ANALYSIS OF *CAENORHABDITIS ELEGANS* IDENTIFIES NOVEL AGING GENES

***JOHNNY SCHMIDT*, GEORGE SUTPHIN, HOPE DANG**

Age is the primary risk factor for many prominent diseases in our society, including Alzheimer's disease, diabetes, cancer, and heart disease. As the growing population ages, the problem of age-associated disease becomes increasingly evident. Understanding and favorable manipulation, of the underlying molecular mechanisms of aging has the potential to effectively treat broad categories of age-associated disease simultaneously. This study focuses specifically on uncovering genes which play a major role in the aging process, to provide genetic targets for treating diseases brought on by aging. In earlier work, approximately 1,500 genes which change expression with age were identified in human blood. These genes potentially play a casual role in aging. To determine which of these genes are capable of directly influencing longevity, analogous genes in the roundworm, *Caenorhabditis elegans,* were identified. Short lifespans, and the availability of powerful genetic tools make *C. elegans* an especially convenient choice for large-scale aging studies. To assess its impact on aging, each target gene is knocked down with corresponding RNAi in populations of *C. elegans*, and lifespan is measured. Screening 1,500 genes for lifespan means approximately 150,000 worms must be examined. To accommodate high-throughput lifespan measurement, we constructed automated surveillance robots equipped with cameras to measure worm lifespan. The robots move systematically about an X-Y plane containing an array of plates loaded with *C. elegans*. Live worms are stimulated to move by exposure to a specific wavelength of blue light. Image analysis software from image and video data examines movement from frame-to-frame and allows us to determine when each worm ceases movement. Data for each worm is then plotted on an overall lifespan curve. Once screening of the 1,500 candidate aging genes is complete, promising candidates will be selected for detailed mechanistic studies in worms and mice, with the goal being identification of molecular targets for clinical trials. This study was supported by the State of Arizona Technology and Research Initiative Fund (TRIF) administered by the Arizona Board of Regents, the

Undergraduate Biology Research Program with funds from the BIO5 Institute and conducted in collaboration with the Kaeberlein Lab (University of Washington) and the Fang-Yen Lab (University of Pennsylvania).

SELF-REFERENTIAL PROCESSING IN DOWN SYNDROME

***MARIA CATHERINE SCHOELEN*, STELLA SAKHON, JAMIE O. EDGIN**

The Self Reference Effect (SRE) is when information encoded in relation to oneself is remembered better than information encoded in relation to another person. However, the SRE has not been examined with individuals with Down syndrome. The current study examines the potential learning benefits of self-referential encoding with individuals with Down syndrome and typically developing mental age matched children three to six years old. Participants were exposed to picture cards with images of toys on them to observe SRE in three levels; self, other, and size. The three conditions also allow for a comparison between higher level (self and other) and lower level (size) processing. Participants also wore an Actiwatch for one week in order to obtain sleep measures. We expect that the toys that were assigned to the self-box will be better remembered in the surprise recognition task. We plan to replicate the finding from Cunningham, Vergunst, Macrae, and Turk (2013) in typically developing children and expect to find the SRE with individuals with Down syndrome. This study was supported in part by the Undergraduate Biology Research Program with funds from the Office of Research, Discovery & Innovation and the office of the Provost, and the Western Alliance to Expand Student Opportunities (WAESO) Louis Stokes Alliance for Minority Participation (LSAMP) National Science Foundation (NSF) Cooperative Agreement No. HRD-1101728. References: Cunningham, S. J., Vergunst, F., Macrae, C. N. and Turk, D. J. (2013), Exploring early self-referential memory effects through ownership. Br J Dev Psychol, 31: 289-301. doi:10.1111/bjdp.12005.

CAFFEINE-EMBEDDED TRIAZABUTADIENE AS AN ADENOSINE A2A RECEPTOR INHIBITOR AND PROBE

***YANNICK SCHREIBER*, JOHN C. JEWETT**

Parkinson's disease (PD) is a progressive neurodegenerative disease characterized by the loss of dopaminergic neurons in the brain, leading to a deficiency in dopamine. Recent research has shown that the adenosine A2A receptor, a G-protein coupled receptor found in high concentrations in brain regions principally implicated in PD, is a viable target for treatments ameliorating the motor symptoms associated with this disease. Aryl diazonium ions are attractive chemical biology reagents used to label tyrosine residues on proteins. Triazabutadienes, chemical compounds that liberate aryl diazonium ions in a pH dependent manner, can be used as agents to deliver aryl diazonium ions within a physiologically relevant pH range. A triazabutadiene containing a caffeine scaffold was hypothesized to deliver aryl diazonium ions to tyrosine residues within the pocket of the adenosine A2A receptor to irreversibly modify and inhibit it. The caffeine-embedded triazabutadiene was successfully synthesized and characterized. To further evaluate ligand-receptor interactions between the compounds and the adenosine A2A receptor, structural variants of the caffeine-embedded triazabutadiene were synthesized. A guanidine derivative was synthesized from the caffeine-embedded triazabutadiene using a thermally-induced nitrogen extrusion reaction, and an additional N1-methylated derivative was synthesized to evaluate the nucleophilicity of the triazabutadiene. Future research entails the development of pharmacological assays for characterizing receptor-ligand interactions by our collaborators, as well as the synthesis of a biotinylated triazabutadiene for investigating the off-target effects associated with the caffeine-embedded triazabutadiene compound and its derivatives. Research was supported in part by the Undergraduate Biology Research Program with funds from the Office the Provost, and the Arnold and Mabel Beckman Foundation.

ASSESSMENT OF PULMONARY ARTERIAL STRUCTURE AND ITS ASSOCIATION WITH RIGHT VENTRICULAR FUNCTION IN PULMONARY ARTERIAL HYPERTENSION

***FRANK SERVIN*, JOSE ROSADO, RAJ JANARDHANAN, JASON X.J. YUAN, FRANZ P. RISCHARD, REBECCA R. VANDERPOOL**

Pulmonary arterial hypertension (PAH) is a progressive disease that ultimately results in right ventricular (RV) failure. Symptoms of PAH and RV failure include edema, fatigue, syncope, and dyspnea. PAH is clinically defined by a mean pulmonary arterial pressure (mPAP) ≥ 25 mmHg at rest with a pulmonary arterial wedge pressure (PAWP) ≤ 15mmHg. A decrease in the vascular radius and vascular remodeling contribute to the increased mPAP and pulmonary vascular resistance (PVR). Current clinical assessments of vascular structure from CT imaging are labor intensive and have not been directly associated with RV function. The aim of this preliminary study is to 1) develop methods to quantify pulmonary vascular structure from cardiac magnetic resonance angiograms (MRA) and 2) quantify associations between vascular structure and RV function in patients to distinguish unique PAH phenotypes. This study includes patients who underwent a right heart catheterization (RHC) and a clinical MRA for clinical follow-up or due to a suspicion of having PAH. Results of this study show that it is feasible to detect altered pulmonary vascular structure in patients with PAH from cardiac MRAs. Combining structural vascular assessment with hemodynamic assessment of RV function could be used to identify unique PAH phenotypes based on the correlations between vascular structure and RV function. Funding: National Institutes of Health Maximizing Access to Research Careers Training Grant T34 GM08718 (FS), and the Arizona Biomedical Research Commission New Investigator Award ADHS18-198871.

COMPLEX CONTROL OF EXOSOME RELEASE IN OCULAR TISSUES

***SARA SILLIK*, ANNA G. FIGUEROA, NICOLE R. CONGROVE, RORY COLVIN-MORRISON, BRIAN S. MCKAY**

The two leading causes of irreversible blindness in the world are age-related macular degeneration (AMD) and glaucoma. Both diseases have strong racial biases. Caucasians are at greater risk of AMD while those with Hispanic or African American ethnicity are at greater risk of glaucoma. A key difference among races is pigmentation, and in the eyes, this would suggest the retinal pigment epithelium (RPE) and the ciliary body (CB), two pigmented tissues that participate in AMD and glaucoma, respectively, play a role in the diseases. Exosomes are small secreted extracellular vesicles that function as part of a tissue communication system, changes in the tissue communication may underlie both AMD and glaucoma. To investigate this, we examined control of RPE and CB exosome secretion by dopamine signaling molecules, a pathway related to both AMD and glaucoma. We evaluated the role of the five dopamine receptors (D1-D5) in controlling exosome release from RPE and CB. We isolated fresh RPE and CB tissue from bovine or porcine eyes. For the RPE, eye cups were produced by removing the anterior segment, vitreous, and retina. The eye cup was incubated in culture media with and without various D1-D5 receptor ligands. For the CB, the CB tissue was segmented and distributed among wells of six-well plates containing culture medium as described for RPE. After 30 minutes, medium was collected, and exosomes were isolated by differential ultracentrifugation. Exosome release was quantified by total protein analysis of the isolated exosomes. The release of exosomes in response to dopamine receptor activity was complex in both tissues tested. Individual receptor agonists increased exosome release in some experiments but slowed exosome release in others. In summary, we could not anticipate either RPE or CB tissues response to dopamine receptor agonists. The select agents both upregulated and down regulated exosome release depending on the experiment, suggesting that the dopamine receptor system likely controls exosome release, but we experienced an unidentified confounding variable. Our results suggest that the dopamine receptor signaling may represent novel target avenues for treatments of AMD and glaucoma, but further work is necessary to understand the systems. Support for this research is provided by the National Institutes of Health grant R01 EY026544-01 (McKay), generous support from Friends of Yuma, the Western Alliance to Expand Student Opportunities (WAESO) Louis Stokes Alliance for Minority Participation (LSAMP) National Science Foundation (NSF) Cooperative Agreement No. HRD-1101728, and the Undergraduate Biology Research Program with funds from the Office of Research, Discovery & Innovation.

GENERATION OF REPORTER HUMAN INDUCED PLURIPOTENT STEM CELL LINE USING CRISPR/CAS9 FOR ATRIAL CARDIOMYOCYTE IDENTIFICATION AND EFFICIENT DIFFERENTIATION

***KRISTINA SIN*, JARED M. CHURKO**

Human induced pluripotent stem cells (hiPSCs) offer a promising and inexhaustible source of cells for creating in vitro cardiac models that can faithfully replicate human phenotypes and cellular responses. HiPSCs are reprogrammed cells generated from the patient's somatic cells that can differentiate to every cell type in the body and carry the patient's genetic material. However, current cardiomyocyte (CM) differentiation protocols produce a heterogenous mixture of various cell types, which impedes the creation of reliable cardiac tissue models. To date, the modeling of atrial-specific diseases using hiPSC-derived atrial CMs has been restricted by an incomplete understanding of chamber-specific lineage development and by the lack of reliable atrial markers. To address this, we performed bulk RNA-sequencing on human adult atrial and ventricular tissue, which revealed Wnt ligands, TCF/LEF and Frizzled family members to be highly expressed in the atria compared to ventricles, suggesting canonical Wnt signaling is involved in the atrial lineage. Recent in vivo research of animal embryos also indicates active canonical Wnt signaling as necessary for the specification and proliferation of atrial progenitor cells and restriction of ventricular proliferation. It is hypothesized that canonical Wnt signaling plays a role in increasing atrial cell proliferation, cell size, and/or specification of atrial CMs. To study the involvement Wnt signaling plays in promoting atrial fate, we generated a novel reporter line via CRISPR/Cas9 to enrich for atrial identification and isolation. The reporter line design was driven by our RNA sequencing data that indicated Myosin Binding Protein H Like (MYBPHL) to be highly expressed in the atria, when compared to the ventricles. However, it is unknown if MYBPHL expression can successfully mark hiPSC-derived atrial CMs and if MYBPHL-expressing cells display similar characteristics of functional atrial CMs. To properly assess the promotion of atrial identity and monitor atrial CM differentiation with the activation of canonical Wnt signaling, the reporter line is differentiated with additions of canonical Wnt activator CHIR99021 (4 M; 1 M) and inhibitor IWR1-endo (5 M; 1 M) to undergo CM differentiation. Defining new differentiation protocols for efficient generation of atrial CMs will provide the means necessary for modeling atrial-specific disorders.

VEGF-B OVEREXPRESSION IN PINK1 GENE KNOCK OUT RATS: IS IT NEUROPROTECTIVE OR NEURORESTORATIVE?

***SASKIA SMIDT*, TORSTEN FALK, MITCHELL BARTLETT**

Parkinson's Disease (PD) is caused by the loss of dopaminergic neurons in the substantia nigra pars compacta (SN). No therapies have been found to protect nor slow the progression of PD. Vascular endothelial growth factor B (VEGF-B) has been previously identified as a novel therapeutic candidate that has shown to be upregulated in dopaminergic cells of a rat midbrain culture model upon exposure to rotenone, a suspected PD-inducing toxin, and to be neuroprotective against a rotenone insult (Falk et al. 2009). VEGF-B has also demonstrated neuroprotective effects in the progressive unilateral 6-hydroxydopamine rat PD model, after a single injection of VEGF-B in the striatum (Yue et al. 2014). For this VEGF-B study we injected adeno-associated virus expressing human VEGF-B (AAV2/1-hVEGF-B) unilaterally into SN and striatum of male PTEN-induced putative kinase 1 (PINK1) knockout (KO) rats at five months of age. Mutations in human PINK1 lead to rare familial forms of PD. AAV2/1-hVEGF-B treated PINK1 KO (n=8), untreated PINK1 KO (n=9) and wild type (WT; n=8) rats were then tested under blinded conditions for changes in motor function via foot slip errors during monthly tapered balance beam (TBB) tests. In a prior pilot set of animals (n=4-7) an increased striatal dopamine content in the AAV2/1-hVEGF-B-injected hemisphere of PINK1-KO rats was seen. At 12-months of age the rats (n=6/group) were transcardially perfused. Unbiased stereology of dopaminergic cells in the SN and striatal terminals will be performed after co-staining for tyrosine hydroxylase, a marker for dopaminergic cells, and a neuronal marker, NeuN. The results will allow us to determine if VEGF-B's therapeutic effects on motor function is due to a neuroprotective reduction in the loss of dopaminergic neurons, or a functional improvement in the surviving dopaminergic neurons. Research funded by the Department of Neurology, and in part by the Undergraduate Biology Research Program with funds from the Office of the Provost.

MECHANISMS OF OPIOID-INDUCED TLR4 SIGNALING

***ANGELA SMITH*, AUSTEN THOMPSON, HALEY CICCONE, DIETER MOHTY, TALLY LARGENT-MILNES, TODD VANDERAH**

In the late stages of breast cancer, tumor metastases in the bone is often a source of pain in patients, leading to long term pain management needs, usually met with the use of opioids, specifically morphine. Chronic opioid use has many negative side effects, including tolerance, hyperalgesia, and respiratory depression. In addition, it has been recently suggested that morphine also increases tumor proliferation and loss in bone density, both of which present additional obstacles in and management of the disease. While it is known that morphine acts on the mu opioid receptors (MORs), recent studies have shown that it may also act on the Toll Like Receptor (TLR) family, receptors that activate innate inflammatory pathways following stimulation. Of specific interest to us is TLR4. These innate responses are nonspecific, so they can cause damage to the surrounding healthy tissues, especially when chronically active. We seek to determine the potential relationship between opioid-induced TLR4 signaling and some of the adverse effects of chronic opioid treatment, such as increased tumor proliferation and loss in bone density. In vitro studies of a line of murine mammary adenocarcinoma cells (EO771) are treated with morphine in combination with inhibitors of the receptors of interest for 24 hours (chronic treatment). Now, using Western blot analysis we study the pathways morphine takes in the cancer cells by comparing relative expression of various receptors and transcription factors in the presence and absence of TLR4 and MOR inhibitors. Furthermore, using cell growth assay, we determine how the presence and absence of these inhibitors affects the growth of the cancerous cells. These results can be used in conjunction with whole animal models, whose receptors are also isolated through the use of knockout mice, to determine how morphine induced TLR4 binding contributes to bone density loss and tumor proliferation. Funded in part by an American Society for Pharmacology & Experimental Therapeutics Summer Undergraduate Research Fellows (ASPET/SURF) grant to the University of Arizona and funds from the University of Arizona College of Medicine.

GENETIC AND PHENOTYPIC CHARACTERIZATION OF AN *ARABIDOPSIS* LONG NON-CODING RNA

***JULIAN SOMERS*, KYLE PALOS, MARK BEILSTEIN**

Plant genomes have been studied intensively since the discovery of DNA, and a wealth of information has been established about protein coding regions and the proteins that are synthesized from them. But what about the rest of the genome? Most eukaryotic genomes contain ample non-coding DNA, of which a large portion is transcribed into long non-coding RNA (lncRNA) molecules, and yet we know very little about the impacts these molecules have on the cell. Few lncRNA molecules have been studied. The lncRNA At1NC031460 in *Arabidopsis*, is conserved throughout the plant family Brassicaceae and plants carrying a T-DNA insertion in At1NC031460 are developmentally delayed compared to their wild type counterparts. To confirm the mutation in At1NC031460 is causing the developmental delay, we have been generating additional mutant alleles. These new mutant alleles are being generated using CRISPR genome editing technology. We identified three new mutant alleles from our CRISPR mutagenesis and we are currently determining whether these mutants share the originally described T-DNA insertion phenotype, or additional previously undocumented phenotypes. Our T-DNA and CRISPR mutant plants are developmentally delayed, consistent with previous observations performed by others, suggesting that At1NC031460 may play a role in early plant development. Moving forward, we seek to uncover the molecular mechanisms that this lncRNA molecule plays in Brassicaceae and unveil additional functions of lncRNA molecules. We would like to thank the Undergraduate Biology Research Program with funds from the Office of Research, Discovery & Innovation for financial contributions to our research.

LOST IN SPACE: THE ROLE OF OBJECTS DURING COMPLEX RODENT SPATIAL NAVIGATION

***MADELINE SOUDER*, BRUCE HARLAND, CALVIN HOLST, BLAINE HARPER, JEAN-MARC FELLOUS**

Both humans and rats need to navigate in complex environments, and accordingly need to use dedicated neural systems for complex spatial navigation. Spatial navigation utilizes both path integration and landmark navigation, and it has been shown

that the hippocampus and its place cells are involved in both. Previous studies (de Jong et al., 2011) have used the Traveling Salesperson Problem (TSP) as a model to study spatial navigation optimization in rats. This model is a spatial problem in which the shortest path between a number of cities must be found over multiple trials. Previous versions of this task utilized small environments with cities represented by identical copies of rewarded cups. In the current study, we used a much larger environment and different objects were used as cities. The objects were used in a configuration designed to study optimization and the effect of path manipulation. After the rats optimized, we switched two of the objects with each other and hypothesized that if the rats were using the objects as landmarks for the optimal path, the switch would affect their path of travel. These configurations were compared with the identical reward cups configurations for both male and female rats. Single cell and network activity were recorded from the hippocampus while rats performed the task. Preliminary results show differences in sharp wave activity between cup and object configurations. The results also show that the presence of objects decreases the number of trials to task completion. Future work will focus on the analysis of place cells during the task. Funded by: The Undergraduate Biology Research Program with funds from the Office of the Provost (MPS), the National Science Foundation division of Collaborative Research in Computational Neuroscience #1429937 (MPS and JMF), the National Science Foundation division of Information and Intelligent Systems #1703340 (BRH and JMF), and the Office of Naval Research Multidisciplinary University Research Initiatives Program (BLH and JMF).

DIRECT HYDROGEN PEROXIDE BREAKDOWN BY 3-HYDROXYANTHRANILLIC ACID AS AN OXIDATIVE STRESS RESISTANCE MECHANISM FOR INCREASED LONGEVITY IN *C. ELEGANS*

***ERICA SPENCE*, GEORGE SUTPHIN**

Aging is the primary risk factor of several diseases such as cancer, Alzheimer's Disease, and heart disease. Accumulation of oxidative damage to biomolecules is one proposed mechanism for the deterioration of cells, tissues, and organs with age. This damage is caused by increased production of oxygen free radicals and decreased ability of our cells to combat them. Past work in the Sutphin Lab determined that the build-up of a small molecule 3-hydroxyanthranillic acid (3HAA) in response to inhibition of the enzyme that normally breaks down 3HAA, 3HAA dioxygenase (HAAO), is sufficient to extend life span and increases oxidative stress resistance in *Caenorhabditis elegans*. We hypothesized that 3HAA directly degrades the oxygen free radical, hydrogen peroxide, that is produced as the worms age. To test this hypothesis, we measured the effect of 3HAA on hydrogen peroxide in vivo and in vitro. The results indicated that 3HAA directly breaks down hydrogen peroxide in worms, and the worms with elevated levels of 3HAA release less hydrogen peroxide into the environment in all age groups. In ongoing work, we are looking to see if the reduced hydrogen peroxide is enough to limit age-associated increases oxidative protein and lipid damage in the worms. We are ultimately interested in using these mechanistic results to design targeted treatments to oxidative damage, increasing healthy lifespan, and treat age-associated disease in humans. This work was funded under the state of Arizona Technology and Research Initiative Fund (TRIF) administered by the Arizona Board of Regents. My Undergraduate Biology Research Program position was funded by the Office of the Provost at the University of Arizona.

CRISPR MEDIATED TAGGING OF ENDOGENOUS CELL FATE MARKERS

***SNEHA SRINIVASAN*, COSTANZA LOCASCIO, SHWETAL MEHTA**

Over 20,000 Americans a year suffer from glioblastoma (GBM), a highly aggressive and invasive form of brain cancer. Although GBM is thoroughly characterized and studied, treatment hasn't advanced significantly in the past decades. Standard of care treatment fails to prolong survival, and most tumors return, sending patients back to the hospital. Part of this recurrence could be due to resistance Glioma Stem Cells (GSCs), a subset of cells found in GBM tumors. In response to chemotherapy and radiation, only a fraction of the tumor cells die, while resistant GSCs hide out and form new tumors. While GSCs only make up a small percentage of GBM tumors, they hold characteristics that make them intrinsically more resistant to treatment. For example, GSCs, like may stem cells, have extremely efficient DNA damage repair pathways, as well as drug efflux pumps to negate the effects of targeted drug treatment. Additionally, GSCs proliferate very slowly, making them a difficult target for traditional cytotoxic drugs, which target rapidly dividing cells. While these reasons for resistance are known, studies have

shown that the proliferating GSCs are fairly plastic and may change their phenotype in order to escape treatment. The goal of this project, then, is to explore the changes that resistant GSCs undergo immediately after radiation to further understand this GSC plasticity and how it may relate to their resistance. In order to accurately explore these changes, we decided to tag relevant proteins (SOX2, OLIG2, GFAP) with fluorescent markers, using the CRISPR-Cas9 system. Using PCR, we amplified a region of plasmid that contained a fluorescent marker (mKate2) as well as a selection marker (Neomycin). Currently, we are optimizing the CRISPR transfection to integrate this fluorescent fragment into patient-derived GSCs at the site of the gene of interest (either SOX2, OLIG2, or GFAP). Once this fluorescent tag is successfully integrated, we will select for the cells that have the tag and conduct live cell imaging experiments to visualize protein dynamics in human GSCs after exposure to ionizing radiation. This study will provide an extremely accurate and dynamic view into the mechanisms of GSCs treatment evasion and cellular plasticity. This project is supported in part by the Undergraduate Biology Research Program with funds from the Office of the Provost.

THE VITAL ROLE OF RNA DEPENDENT RNA POLYMERASE (RDR2) IN THE RNA DEPENDENT DNA METHYLATION PATHWAY DURING SEED DEVELOPMENT

***JACK STEARNS*, KELLY DEW-BUDD, REBECCA MOSHER, MARK BEILSTEIN**

RNA-directed DNA Methylation (RdDM) is a gene silencing mechanism responsible for downregulating transcription from specific loci during seed development in plants. In the RdDM pathway, small interfering RNAs (siRNAs), which are abundant during seed development, are produced with the help of RNA Dependent RNA Polymerase 2 (RDR2). After being processed, these siRNAs associate with transcripts synthesized by RNA Polymerase V, and act to target the adjacent DNA for methylation by recruiting the machinery for cytosine methylation. This methylation represses transcription, and thus regulates gene expression during seed development. We hypothesize that RdDM, in part, mediates conflict between parental genomes and/or between competing subgenomes by specifically downregulating transcripts from specific genomes. To distinguish the contribution of RdDM in mediating conflict between parental genomes or among subgenomes in polyploid species, we are altering the RdDM pathway in three different but closely related species of Brassicaceae. We are using a CRISPR-Cas9 complex to generate knockout mutants of RDR2 in species that are obligate outcrossers and in polyploid species with multiple subgenomes. Our initial results suggest that RdDM plays an important role in mediating conflict between parental genomes in outcrossing species. These findings may allow finer control of seed development by moderating the contribution of maternal and paternal genomes. Funding: The National Science Foundation grant # 1546825, and the Undergraduate Biology Research Program with funds from the College of Agriculture & Life Sciences and the Office of the Provost.

CHARACTERIZING AN ALPHA SYNUCLEIN TRANSGENIC MOUSE MODEL IN THE CONTEXT OF PARKINSON'S DISEASE

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Parkinson's disease (PD) is a progressive age-related neurodegenerative disorder which affects over 10 million people worldwide. There is convincing evidence from recent studies that the protein Alpha-Synuclein (α-Synuclein) plays an important role in the pathology of PD. Specifically, it has been shown that the increased expression or aggregation of abnormal forms of α-Synuclein contribute to the oxidative and mitochondrial stress which causes the cellular toxicity and neuronal dysfunction in PD. Hence there is high interest in approaches that can potentially reduce α-Synuclein expression, aggregation, and toxicity. In this context, we are characterizing a transgenic mouse model overexpressing human Alpha Synuclein under the Thy1 promoter (hα-syn +/+), with the ultimate goal of assessing therapeutic strategies to counter Alpha Synuclein aggregation and toxicity. As a first step, we assessed the hα-syn +/+ animals behaviorally by comparing them to wild type control mice (hα -syn -/-). Specifically, we examined mice at 3 months of age, through several PD relevant motor function tests. We find that the hα-syn +/+ mice display significantly decreased grooming, nest building ability, hind limb mobility, and the ability to traverse challenging terrains as well as increased anxiety. Secondly, we determined the expression levels of α-Synuclein in different PD

relevant brain regions (midbrain, cortex, striatum, and hippocampus) using RT-PCR. These data will provide a systematic characterization of how regional α-Synuclein overexpression affects behavior in the context of PD. Future studies will further characterize these mice using other behavioral, protein and immunocytochemical methods, and also pursue the examination of the activation of the Nrf2 pathway as a therapeutic approach to counteract α-Synuclein pathology and associated behavioral changes. This project is supported in part by the Undergraduate Biology Research Program with funds from the BIO5 Institute.

DETERMINING HOW SP-A1 AND SP-A2 MEDIATE THE IMMUNE RESPONSE IN ALLERGIC MOUSE MODELS

***ASHLEY TOLTON*, KEN ADDISON, JULIE LEDFORD**

Human pulmonary surfactant protein A (SP-A) is an oligomeric octadecamer comprised of products encoded by the two functional SP-A genes, SP-A1 and SP-A2. Previous studies have shown that the two main allergens from House Dust Mite (HDM), Der p1 and Der f1, degrade and inactivate SP-A. The purpose of this study is to find how HDM allergens affect the actions of SP-A1 and SP-A2 specifically and how the immune system response during the allergen challenge may be altered by this breakdown. Three groups of mice were challenged with HDM or vehicle (saline) on days 0, 7, and 14. Our model consisted of Wildtype (WT) mice (express SP-A1 only); SP-A deficient mice (SP-A -/-); and humanized SP-A2 transgenic mice (express SP-A2 only). On day 19, bronchoalveolar lavage (BAL), lung tissue, and mediastinal lymph nodes were harvested for analysis. The percentages of white blood cell types present in the BAL were determined using staining and cell morphology. RNA was extracted from the right lung tissue and lymph nodes and used to make cDNA for Real-Time PCR gene expression analysis. We found that after HDM challenge, all groups had significant increases in eosinophils, a type of white blood cell associated with asthma, compared to their saline controls. The SP-A2 expressing mice, compared to the SP-A -/- and WT groups, had the highest percentage and number of eosinophils in the BAL; in contrast, they had the lowest number of eosinophils in the lung tissue and significantly decreased Muc5AC gene expression in the lungs. In the mediastinal lymph nodes, SP-A2 mice had significant reductions in type-2 markers of inflammation (IL-6, IL-13, IL-4: IFN-γ ratio) as compared to SP-A1 (WT mice). In our model, SP-A2 expression appears to be more protective than SP-A1 in attenuating the type-2 immune response, decreasing Muc5AC gene expression and aiding in eosinophil clearance from the lung tissue during an HDM allergen challenge. Grant funding: The National Institutes of Health: HL125602, and the Environmental Health Sciences – Transformative Research Undergraduate Experience (EHS-TRUE) through the National Institute of Environmental Health Sciences Grant #1-R25-ES025494.

EFFECT OF KYNURENINE PATHWAY METABOLITES ON LIFESPAN IN *CAENORHABDITIS ELEGANS*

***EMILY TURNER*, GEORGE SUTPHIN**

The essential amino acid tryptophan is metabolized in the body through various pathways, of which the kynurenine pathway is the primary route. Dysregulation of the kynurenine pathway occurs with age and has been associated with inflammation, neurological disease, cardiovascular disease and other age-related pathologies. Previous work demonstrated that inhibiting certain enzymes or supplementing certain metabolites in the kynurenine pathway is sufficient to increase lifespan of the nematode *Caenorhabditis elegans*. For example, direct supplementation of the metabolite 3-hydroxyanthranilic acid (3HAA) or inhibition of the enzymes HAAO, TDO2, and KYNU extends lifespan of *C. elegans* by as much as 30%. This project was designed to help gain a comprehensive view of the kynurenine pathway and its influence on longevity. In order to investigate the effects of metabolites of the kynurenine pathway on *C. elegans* lifespan, we conducted dose-response experiments for kynurenic acid, kynurenine, anthranilic acid, and quinolinic acid. Direct supplementation of kynurenic acid extends lifespan, while kynurenine and anthranilic acid shorten lifespan. Quinolinic acid did not have a measurable effect on longevity. This work is ongoing, and we will ultimately examine the impact of supplementing every metabolite and knocking down every enzyme in the pathway on lifespan and other aging phenotypes. We are particularly interested in uncovering the molecular mechanisms that mediate

lifespan extension by kynurenic acid supplementation. The long-term goal of this work is to identify molecular targets within the kynurenine pathway for the treatment of age-associated disease. This work was funded under the state of Arizona Technology and Research Initiative Fund (TRIF) administered by the Arizona Board of Regents. My Undergraduate Biology Research Program position was funded by the Office of Provost at University of Arizona.

RESPONSE TO TREATMENT FOR NAMING DIFFICULTY IN INDIVIDUALS WITH APHASIA

***NOELLE VAN LINDEN*, PELAGIE BEESON**

Aphasia is an acquired language impairment associated with damage to regions of the brain that are critical for comprehension and production of language. One of the most common characteristics of aphasia is difficulty coming up with specific words. The word retrieval problem is similar to that experienced by healthy individuals, that is, when a person knows what they want to say, but cannot come up with the word. In some cases, talking about the concept helps to prompt recall of the word, and in other cases an individual has an idea of the first letter or sound that helps to cue the recall. Treatment for word retrieval difficulties can take advantage of the available information in order to help the person cue themselves, or to provide the listener with enough information to identify the intended target. In this study, we examined the response to a treatment that focused on self-cuing, referred to as the Lexical Retrieval Cascade treatment. The pre- and post-treatment performances of 12 individuals with aphasia were examined for the items trained during treatment as well as on the Boston Naming Test (BNT), a standardized measure of naming ability. To capture potential changes in naming as well as the ability to convey the concept, all responses were scored for meaningful information. The group showed significant improvement for the trained items after treatment, whereas scores on the Boston Naming Test were not significantly improved. Of interest, however, was the significant improvement in meaningful information provided that supported communication success. Thank you to the Office of the Provost and the College of Science for helping fund this research through the Undergraduate Biology Research Program.

FORMATIVE QUALITATIVE RESEARCH TO INFORM A COMMUNITY NAVIGATION PROGRAM THAT SUPPORTS CANCER SURVIVORSHIP

***ROXANNE VANN*, JULIE ARMIN, YVONNE BUENO, REBECCA BEDWELL, AND HEIDI HAMANN**

BACKGROUND: A Survivorship Care Plan (SCP) is a resource for oncology patients to manage their care during and after active cancer treatment. The SCP should be shared with primary care providers, as it contains a treatment summary and a guideline for surveillance. SCPs show potential for improving continuity of care for underserved patients, including racial/ethnic minorities. The needs assessment reported here is part of a five-year project funded by the Merck Foundation Alliance to Advance Patient-Centered Cancer Care with the aim to support underserved patients in Southern Arizona by improving provider and patient communication, expand cancer care coordination, and increase psychosocial supportive care. METHODS: In order to supplement a needs assessment developed with data from primary care providers at El Rio Health, a federally qualified health center, the team conducted in-depth interviews (N=14) with English and Spanish-speaking cancer survivors from the University of Arizona Cancer Center [UACC], El Rio Health Center, and the community. Participants engaged in a semi-structured interview about their experience during and after cancer treatment, with particular emphasis on barriers and facilitators to care coordination between primary care and oncology. A priori and emerging themes were identified in the transcripts, which were then coded in Max QDA. FINDINGS: Qualitative findings were mapped onto a social determinants of health framework containing the following domains: individual, interpersonal, organizational, community, and public policy levels. Participants discussed barriers to cancer care, the use of community and clinical support services, experiences with cancer therapy, thoughts about care transitions, and co-morbid conditions that affect their experience with cancer survivorship and might be considered in the creation of an SCP. CONCLUSION: Findings will inform the community cancer navigation program at the UACC, which aims to connect vulnerable patients with support services at diagnosis and at the point of transition from active treatment to primary care. These findings will also be shared with oncology clinical staff who compile SCPs for patients with the goal of informing the planning process. This project is supported in part by the Partnership for Native American Cancer Prevention (NACP) through the National Cancer Institute Grant #2U54CA143924, and the Western Alliance to

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REGULATION OF HTT AGGREGATES IN A HUNTINGTON'S DISEASE YEAST MODEL

***AMANDA WARNER*, ROSS BUCHAN**

Huntington's disease is a devastating neurodegenerative disease which leads to symptoms of involuntary movements, memory loss, and ultimately death. The disease is characterized by a mutation in the huntingtin (Htt) protein which leads to its aggregation inside the cytoplasm of striatum neurons. It is unknown whether these aggregates are directly toxic or if they reflect a cellular protection mechanism. Recently, endocytosis activity has been shown to reduce the toxicity and increase the turnover/degradation of intracellular TDP-43 aggregates present in the neurodegenerative disease amyotrophic lateral sclerosis, or ALS. Conversely, high expression of aggregation-prone TDP-43 can impair endocytosis function. Thus, there is a possibility that Htt aggregates, similar to TDP-43 in ALS, will also inhibit endocytosis and be cleared by the endocytosis pathway. In a Huntington's disease yeast model, wild type and mutant Htt localize to the cytoplasm as well as the vacuole, an acidic organelle where proteins are trafficked by endocytosis and are sent for degradation. The mutant Htt also causes a growth defect when expressed in certain deletion backgrounds, such as vps34Δ and vps15Δ; these PI3K subunit genes are key to normal endocytic function. These results suggest that Htt toxicity, like TDP-43, is regulated by endocytosis. Further research will be conducted to determine if enhancement or suppression of endocytosis leads to clearance or accumulation of Htt in the vacuole respectively. Other cellular degradation pathways such as the proteasome and autophagy will also be tested in a similar fashion. These analyses could suggest a new role of endocytosis in degrading proteins and could be used as a therapeutic target for Huntington's disease. This project was funded by the Undergraduate Biology Research Program with funds from the Arnold and Mabel Beckman Foundation.

INCREASING CRISPR-MEDIATED HOMOLOGOUS DNA REPAIR EFFICIENCY

***BRITTANY WILLIAMS*, DANIELLE ISAKOV, SIDDHARTHA JENA, MAX WILSON, AND JARED TOETTCHER**

CRISPR-Cas9 has emerged as a tool for genome editing capable of inducing modifications in specific genes through either Non-Homologous End Joining (NHEJ) or Homologous DNA Recombination (HDR). NHEJ and HDR provide scientific and clinical applications to further test and treat gene specific diseases. However, CRISPR-mediated HDR is limited by low successful insertion rates. Genetic or chemical manipulation of the NHEJ pathway and the cell cycle has been utilized to increase HDR efficiency, but still results in low success. A recent study using the Cas9-Avidin-Biotin ssDNA (CAB) system showed a tenfold increase in HDR efficiency compared to standard procedures. However, the effects of the various HDR pathway parameters on recombination efficiency are still unknown. Using the CAB system, we sought to understand the relationship between HDR efficiency and two important variable parameters of the donor strand: insert length and homology arm (HA) length. We hypothesize a non-linear relationship between CRISPR-mediated HDR efficiency and insert length or size of HA. We built a Cas9 piggyBac transposon plasmid and transfected NIH 3T3, HeLa and 293T cells to create Cas9 expressing cell lines. Hygromycin B drug selection was used to select for Cas9 integration. Successful HDR was ascertained using inserts of different fluorescent proteins. The number of successful insertions were visualized through microscopy. By plotting the efficiency versus the insert length and HA length we expected to find the optimal settings needed for efficient HDR. Finding the optimal donor strand parameters can then lead to a genomic modification strategy that overcomes the uncertainties of HDR and eliminates the need for genomic PCR. This research was made possible by the generous support of the Genentech Foundation, the Graduate School at Princeton University, and the National Institutes of Health Maximizing Access to Research Careers Training Grant (T34 GM008718).

THE EFFECT OF PUF4 BINDING ON NSR1 MRNA STABILITY

***LAUREN WILSON*, NICHOLE ESHLEMAN, ROSS BUCHAN**

The regulation of messenger RNA (mRNA) is an essential part of eukaryotic gene expression. RNA binding proteins (RBPs) can bind to specific transcripts and influence whether that transcript will be actively translated, stored, or degraded. One region where regulatory protein binding can occur is the 3-untranslated region (3 UTR) of a transcript. This project focused on the role of Puf4, an RBP that binds to the 3UTR of ribosomal biogenesis genes and is generally thought to promote their decay. NSR1 was chosen to serve as a representative ribosomal biogenesis gene. A mutant version of NSR1 lacking the Puf4 binding site in its 3 UTR was created via site-directed mutagenesis and expressed in baker's yeast, *Saccharomyces cerevisiae*. Cells with this mutant copy of NSR1 have a slower growth rate as well as a higher steady-state level of NSR1 mRNA, suggesting that aberrant accumulation of NSR1 mRNA is detrimental to cell viability, possibly due to alterations in ribosome biosynthesis. mRNA Half-life experiments under normal growth conditions showed that NSR1 transcripts with the wild-type Puf4 binding site degraded faster than NSR1 transcripts without the Puf4 binding site, strongly suggesting that the binding of Puf4 is indeed actively destabilizing NSR1 mRNAs. Going forward, more half-life experiments will be done under cellular stress conditions to examine Puf4's role in stress-specific mRNA decay, particularly conditions under which the mTOR signaling pathway is inhibited. The interactions of Puf4 with the mRNA decay machinery will also be explored. In summary, this work adds further evidence that RNA binding proteins, such as Puf4, can contribute to the cells control of gene expression by regulation mRNA decay rates, which may facilitate cellular adaption stress conditions. This work was funded by the Undergraduate Biology Research Program (UBRP) with funds from the Office of Research, Discovery & Innovation (RDI), and the National Institute of General Medical Sciences (NIGMS).

IDENTIFYING TARGETS FOR NECROPTOSIS INHIBITION IN RIPK3-MLKL MEDIATED ACTIVATION

***JULIANA YOUNG*, JONATHAN SANCHEZ, VIJAY GOKHALE, SALVATORE ODDO, MAY KHANNA**

Apoptosis and necroptosis are two classical cell death pathways. Recently, it has been shown that necroptosis is heavily involved in many neurodegeneration diseases such as Alzheimer's disease. Necroptosis is programmed form of necrosis and may be activated by inflammation or other cellular responses. Three key proteins play a role in the necroptosis pathway. RIPK1 and RIPK3 make up the necrosome that phosphorylates MLKL to induce necroptosis. MLKL then causes the breakdown of the plasma membrane of the cell. Using small molecules to target the protein-protein interactions between RIPK3 and MLKL might inhibit the necroptosis activated cell death pathway. In order to evaluate the small molecule inhibitory effects on necroptosis, Transmission Electron Microscopy (TEM) will be used to study the activation of the necroptotic pathway through imaging of morphological characteristics of HT-29 cells. Differentiation between apoptosis and necroptosis is of critical importance due to their intracellular crosstalk. Therefore, morphological characteristics will be assessed by identifying cell swelling and plasma membrane breakdown for necroptosis while apoptosis would produce cell shrinkage, nuclear fragmentation, and membrane blebbing. Small molecules that inhibit necroptosis will be followed up by a Western blot analysis of activated RIPK3 and MLKL to determine the site of inhibition. The identification of any small molecules that inhibit the necroptosis-signaling pathway will hopefully lead to a potential therapeutic for Alzheimer's disease. This research was funded by the Undergraduate Biology Research Program with funds from the Office of Research, Discovery & Innovation, the Center for Innovation of Brain Science, and the Western Alliance to Expand Student Opportunities (WAESO) Louis Stokes Alliance for Minority Participation (LSAMP) National Science Foundation (NSF) Cooperative Agreement No. HRD-1101728.