52nd Annual

TEXAS GENETICS SOCIETY 2025

Barbara Bowman Distinguished Geneticist Award Keynote Speaker

Loren Skow
Texas A&M University

Invited Speakers

Sarah Williams-Blangero
University of Texas Rio Grande Valley

Alicia Rogers
University of Texas Arlington

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Do you want to join the Board?
Questions?
Please talk to or email a board member!
We welcome self-nominations!

Speaker Biographies

2025 TGS Barbara Bowman Distinguished Geneticist

Reflections on the Golden Age of Genomics

Dr. Loren Skow is Senior Professor Emeritus in the Department of Veterinary Integrated BioSciences at Texas A&M University. His research has been devoted to the comparative analysis of mammalian genomes with emphasis on animal models of human genetic disorders. He served on the organizing committees for both the bovine and the equine genome sequencing initiatives and is particularly interested in how variation in the architecture and evolution of the major histocompatibility complex (MHC) influences the function of the immune system.

Keynote Speaker

Sarah Williams-Blangero, University of Texas Rio Grande Valley

Human Genetics in South Texas

Dr. Sarah Williams-Blangero is a genetic epidemiologist who received her Ph.D. in Biological Anthropology from Case Western Reserve University in 1987. She completed a postdoctoral fellowship in genetics at the Texas Biomedical Research Institute and was then appointed to the faculty of Texas Biomed in 1990. Dr. Williams-Blangero became Chair of the Department of Genetics at Texas Biomed in 1999 and additionally Deputy Director of the Southwest National Primate Research Center in 2012. In 2014, she moved to the University of Texas Rio Grande Valley (UTRGV) to become the Founding Director of the South Texas Diabetes and Obesity Institute, and in 2017 was appointed Chair of the Department of Human Genetics in the UTRGV School of Medicine. Dr. Williams-Blangero's research has focused on the genetic determinants of risk for complex diseases in minority populations, including the Jirel ethnic group of Nepal and Mexican Americans.

Keynote Speaker

Alicia Rogers, University of Texas Arlington

RNAi pathways coordinate to protect fertility

Dr. Rogers investigates the mechanisms that maintain RNA interference (RNAi) pathway homeostasis to ensure robust gene regulation and execution of cellular and physiological processes, such as fertility and development, during normal and stress conditions. Dr. Rogers completed her undergraduate degree in Computer Science at Baylor University before pursuing her Ph.D. in Molecular Biology and Biochemistry in the laboratories of Dr. Kata Fejes Toth and Dr. Alexei Aravin at the California Institute of Technology (Caltech). She was awarded a National Science Foundation Graduate Research Fellowship to investigate the molecular mechanisms of RNAi-mediated transcriptional silencing in *D. melanogaster*. Then, as an American Cancer Society Postdoctoral Fellow, she joined the laboratory of Dr. Carolyn Phillips at the University of Southern California (USC) where she studied the mechanisms by which RNAi pathways maintain fertility during stressful environmental conditions in *C. elegans*. In January 2022, she opened her independent laboratory at the University of Texas at Arlington.

R Workshop director

Heath Blackmon, Texas A&M University

Dr. Heath Blackmon is an Associate Professor who joined the Biology Department at Texas A&M University in 2017. He earned his BS in Environmental Science at Oregon State University and his Ph.D. in Quantitative Biology at the University of Texas at Arlington. His research is in genome evolution, specifically sex chromosomes and structural evolution. His group develops methods and databases that accelerate the analysis of data within theoretical, quantitative genetic and phylogenetic frameworks. His recent work has shed light on the evolutionary forces that shape chromosome number evolution across the tree of life. He is a member of the Genetics Society of America, Society for the Study of Evolution, American Genetics Association.

2025 Meeting Sponsors

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Human Genetics Doctoral Program

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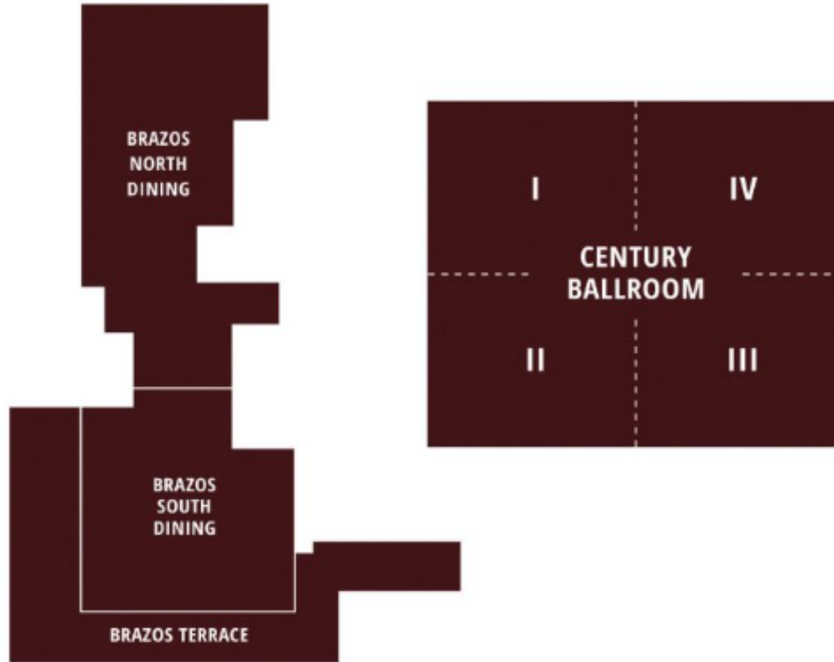
Thank you to all our sponsors for their commitment to the TGS meeting and for making this annual meeting possible!

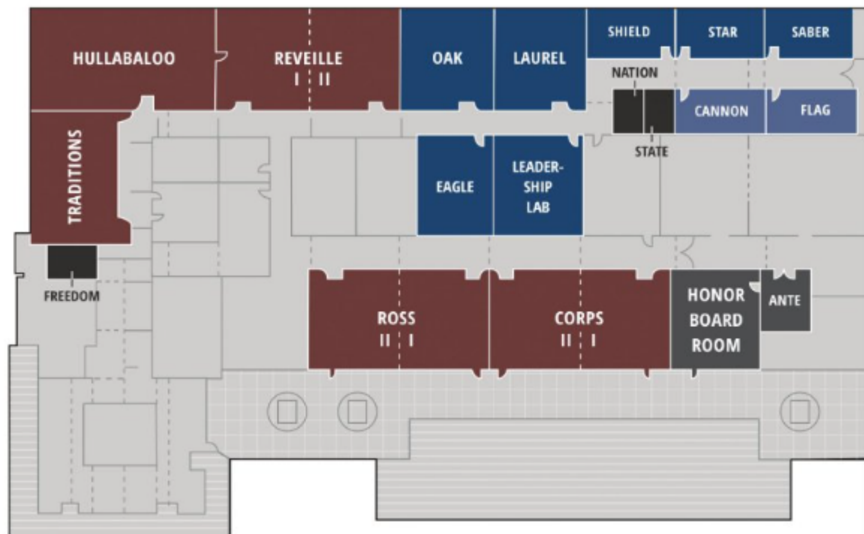
-TGS Board of Directors

Meeting Room Information

1ST FLOOR



2ND FLOOR



Previous Texas Genetics Society Meetings, 1974–2024

No.	Year	Location	Organizer
1	1974	Galveston	Barbara Bowman
2	1975	Houston	Margery Shaw, Tom Caskey
3	1976	Austin	Eldon Sutton
4	1977	San Antonio	John Prince
5	1978	Dallas	Raymond Lewandowski
6	1979	Galveston	Lillian Lockhart

No.	Year	Location	President	TGS Distinguished Geneticist Award	TGS Service Award
7	1980	Houston	Eldon Sutton	--	--
8	1981	College Station	Barbara Bowman	--	--
9	1982	San Antonio	Robert Ferrell	C.P. Oliver	--
10	1983	Austin	Bob Sanders	Meta S. Brown	--
11	1984	Dallas	Lillian Lockhart	Bob Wagner	--
12	1985	Galveston	Arthur Beaudet	Rose Schneider	--
13	1986	Houston	Margery Shaw	T.C. Hsu	--
14	1987	College Station	Don Barnett	Margery Shaw	--
15	1988	Denton	Satish Srivastava	Eldon Sutton	--
16	1989	San Antonio	Frank Greenberg	Lillian Lockhart	--
17	1990	Austin	James Womack	Barbara Bowman	--
18	1991	Dallas	Charleen Moore	Dorothea Bennett	--
19	1992	College Station	Stephen Daiger	Bill Stone	--
20	1993	Galveston	Olivia White	Mike J. Siciliano	--
21	1994	Houston	John VandeBerg	Jack Schull	--
22	1995	San Antonio	Mary Jo Harrod	Frank Greenberg	--
23	1996	Austin	Fred Elder	James Womack	--
24	1997	Dallas	Bill Stone	Louise Strong	Don Barnett
25	1998	Austin	Sue Naylor	Tom Caskey	Eldon Sutton
26	1999	Austin	Ann Killary	Arthur Beaudet	Olivia White
27	2000	Houston	Mike Siciliano	Robert Ferrell	Fred Elder
28	2001	San Antonio	Paul Samollow	Sue Naylor	Charleen Moore
29	2002	South Padre	Ronald Walter	Alfred Knudson, Jr.	Andrew Dewees
30	2003	Austin	Jim Derr	Masatoshi Nei	Sue Ann Berend
31	2004	South Padre	Robert Baker	James Lupski	Sue Naylor
32	2005	Dallas	Christi Walter	Robert Baker	Paul Samollow
33	2006	Galveston	Rodney Nairn	Bert O'Malley	James Womack
34	2007	San Antonio	Sue Ann Berend	Jacqueline Hecht	Robert Baker
35	2008	College Station	Carol Wise	Larry Thompson	Christi Walters
36	2009	Austin	Laura Cox	Richard Gibbs	Michael J. Sicilliano
37	2010	Houston	Loren Skow	David Nelson	Rodney Nairn
38	2011	Dallas	Bhanu Chowdhary	David Russell	Carol Wise
39	2012	San Antonio	Ralf Krahe	Sen Pathak	Ann M. Killary
40	2013	College Station	Heather Conrad-Webb	Stephen Daiger	Joe Angel
41	2014	Waco	Penny Riggs	Gigi Lozano	Loren Skow
42	2015	Dallas	John (Trey) Fondon	Jonathan Cohen	Heather Conrad-Webb
43	2016	Houston	Clare Gill	Ralf Krahe	Stephen Daiger
44	2017	College Station	Erika Abel	Ann Killary	Penny Riggs
45	2018	College Station	Sarah Canterberry	David Threadgill	Erika Abel
46	2019	College Station	Jonathan Rios	Brendan Lee	David Nelson
47	2020	canceled	Caleb Phillips	--	--
48	2021	virtual	David Aiello	Mark Kirkpatrick	Tina L. Gumienny
49	2022	Bryan	Deborah Threadgill	--	Kelli Kochan
50	2023	Austin	Tina L. Gumienny	Nancy Moran	Heath Blackmon
51	2024	College Station	Heath Blackmon	Deborah Bell-Pedersen	David Aiello

Texas Genetics Society 52nd Annual Meeting
March 20–March 22, 2025
Texas A&M Hotel and Conference Center
177 Joe Routt Blvd
College Station, TX 77840

Thursday, March 20th

1:00–5:00 PM	Registration Name tags, drink tickets, talk file submission	**first floor (Pre-Function space)**
2:00–5:00 PM	R workshop Heath Blackmon	**Hullabaloo (second floor)**
5:30–6:00 PM	TGS Board Meeting	**Honor Boardroom**
6:00–9:00 PM	Hullabaloo and Reveille (second floor) will be open to hang posters. All posters should be hung so that attendees can view throughout the conference.	
6:30–7:00 PM	Welcome and announcements Megan Keniry, TGS President 2024–2025	**Century I and II**
7:00–8:00 PM	Vendor Exhibition/ Happy Hour Opening Reception; drink tickets can be used for beer or wine at the reception (cash bar for liquor, craft beer, and mixed drinks)	**Pre-Function I and II**

Century I and II
Platform Talks: Moderator Alex Tice (Texas Tech University)

8:00 PM	*Defining mitochondrial protein functions using deep neural networks* Abhinav B. Swaminathan, Sofia Calabrese, Mohammad Zulkifli, Rachel Guerra, Amy Spelbring, Harman Kaur, Dimitris Kalafatis, David Barondeau, David J. Pagliarini, Vishal M. Gohil, Texas A&M University, Graduate Student
8:15 PM	*Heritable Tissue-Specific Gene Expression Associates With Chronic Wound Microbial Species* Khalid Omeir, Jacob Ancira, Rebecca Gabrilska, Craig Tipton, Clint Miller, Ashley Noe, Kumudu Subasinghe, Megan Rowe, Nicole Phillips, Joseph Wolcott, Caleb D. Philips, Texas Tech University, Graduate Student
8:30 PM	*First genetic evidence of a hybrid Virginia's x Colima warblers in West Texas, featuring patterns of admixture and SNP-phenotype associations.* Ari Rice, Joseph Manthey, Texas Tech University, Graduate Student

8:45 PM *Modulating Karyopherin Alpha and Beta Levels Ameliorates Mutant Ataxin-1-Induced Neurodegeneration in Drosophila*
Khondker Salim, Elena Ruff, Dylan Timperman, Adulfo Amador, Isabella Aguirre Lamus, Maria de Haro, Ismael Al-Ramahi, Baylor College of Medicine, Research Technician

9:00 PM *Genetics and Cellular Transcriptomics Regulating Pigmentation Patterns in Chicken Feathers*
Pei-Jung (Cindy) Hsin, Zheng Li, Leif Andersson, Brian W. Davis, Department of Veterinary Pathobiology, Texas A&M University, College Station, TX, Graduate Student

9:15 PM TGS members are free to converge at the Texas A&M Hotel and Conference Center bar or local venues.

Friday, March 21st

Breakfast (7:00–8:00 am) **Pre-Function I and II**

Century I and II
Platform Talks: Moderator Megan Keniry (University of Texas Rio Grande Valley)

8:00 AM *Phosphatidylethanolamine exposure is recognized by transthyretin-like protein TTR-53 for phagocytosis*
Dylan Suriadinata, Bianca Guerra, Riley Harrison, Julia Frondoni, Gabriela S. Paredes-Devalillo, Charlotte Kommini, Ann M. Wehman, Texas A&M University, Post-Doc

8:15 AM *The Evolution of SNHG14: Understanding the Development of a Disease-Relevant Polycistronic Transcription Unit in Placental Mammals*
Alasdair Taylor, Scott V. Dindot, Texas A&M University, Graduate Student

8:30 AM *Phylogeography of a forest generalist bird reflects glacial expansion and sex-biased dispersal*
Swapnil S. Boyane, Javier E. Colmenares-Pinzón, Ethan F. Gyllenhaal, Ari A. Rice, María C. Tocora, Ben D. Marks, Joseph D. Manthey, Texas Tech University, Post-Doc

8:45 AM *Fusions of autosomes with sex chromosomes are disfavored in mammals*
Kenzie G. Laird, Maximos Chin, Matthew Marano, Michelle M. Jonika, Heath Blackmon, Texas A&M University, Undergraduate Student

9:00 AM *Endangered and Endemic Beetle Genomic Study*
Sean Chien, Jen-Pan Huang, Heath Blackmon, Texas A&M University, Graduate Student

9:15 AM — *Population expression ceilings predict gene duplication sensitivity*
Iyer, S.K. *, Sanchez, S.M. *, Frohock, B.A., Groh, J.C., Agnihotri, A., Beckett, E.L., Bigham, C., Dermott, E., Fiorito, A.E., Jones, R.C., Mourao, N., Perks, K.M., Smith, S.R., Syed, B., Pierce, J.T. (* Authors contributed equally), University of Texas at Austin, Graduate Student

Hullabaloo and Reveille (second floor)

9:30–11:00 AM — Poster Session #1, odd poster presentations
(see end of program for abstracts)

Century I and II

11:00–12:00 PM — Keynote: *Human Genetics in South Texas*
Sarah Williams-Blangero, University of Texas Rio Grande Valley

12:00 PM — Vendor workshops and lunch sponsored by Texas A&M Institute for Genome Sciences and Society (TIGSS) and 10X Genomics

Platform Talks: Moderator David Aiello (Austin College)

1:30 PM — *A Genomic and Morphological Assessment of the Pinyon Deermouse, Peromyscus truei (Cricetidae: Neotominae)*
Javier E. Colmenares-Pinzón, Caleb D. Phillips, Robert D. Bradley, Joseph D. Manthey, Texas Tech University, Graduate Student

1:45 PM — *Disentangling the roles of selection and drift in the origins of microproteins: a case study using the chromosomal distribution of human genes encoding microproteins*
Matthew Marano, Claudio Casola, Interdisciplinary Doctoral Program in Ecology and Evolutionary Biology, Texas A&M University, Graduate Student

2:00 PM — *A comprehensive multi-omics analysis to assess the strain-dependent effects of dietary vitamin A and fat intake on the liver of female mice*
Marianny Alvarado-Gonzalez, Yuta Matsuno, Younkyung Kim, Jeniffer Aguilan, Samuel Rosean, Simone Sidoli, Loredana Quadro, Masako Suzuki, Texas A&M University, Graduate Student

2:15 PM — *Somatostatin is reduced in the frontal cortex of an Angelman syndrome pig model*
Ashley Coffell, Sarah Christian, Scott V. Dindot, Texas A&M University, Graduate Student

2:30 PM — *Mutations in the androgen receptor gene and other sex development key genes are associated with equine disorders of sex development*
Hailey Anderson, Sam Stroupe, Rytis Juras, Brian Davis, Terje Raudsepp, Texas A&M University, Graduate Student

2:45 PM — *Examining the Role of TOR Signaling in the* Saccharomyces cerevisiae pgm2Δ *mutant*
Micaiah M. Wetzold, David P. Aiello, Austin College, Undergraduate Student

3:00 PM — Coffee break

Hullabaloo and Reveille (second floor)

3:00–4:30 PM — Poster Session #2, even poster presentations
(see end of program for abstracts)

Century I and II
Platform Talks: Moderator Tina Gumienny (Texas Woman's University)

4:30 PM — *Neo-sex chromosome evolution in treehoppers despite long-term X chromosome conservation*
Daniela Palmer Droguett, Micah Fletcher, Ben Alston, Sarah Kocher, Diogo Cabral-de-Mello, Alison Wright, The University of Texas at Arlington, Faculty

5:00 PM — *Sequencing For Everyone: Single Molecule Sequencing In The Classroom*
Brian Teague, Danielle Palow, Trinity University, Faculty

5:30 PM — *A bacterial expression cloning screen reveals single-stranded DNA-binding proteins as potent desicco-protectants*
Jonathan D. Hibshman, Courtney M. Clark-Hachtel, Kerry S. Bloom, Bob Goldstein, Southern Methodist University, Faculty

6:00–6:30 PM — Visit vendor displays, network

6:30–8:00 PM — Barbara Bowman Award: *Reflections on the Golden Age of Genomics*
Loren Skow, Texas A&M University

Banquet and service award presentation, acknowledgement of sponsors, first time attendees, first time presenters

8:00 PM — TGS members are free to converge at the Texas A&M Hotel and Conference Center bar or local venues.

Saturday, March 22nd

Breakfast (7:00–8:00 am) **Pre-Function I and II**

Century I and II
Platform Talks: Moderator Megan Keniry (University of Texas Rio Grande Valley)

8:00 AM	*The Equine Pangenome: Improvements in Structural Variant Detection and Genotyping for Horses* Sam Stroupe, Jonah N. Cullen, Sian A Durward-Akhurst, Jessica Petersen, Ted Kalbfleisch, Molly McCue, Brian W. Davis, Texas A&M University, Post-Doc
8:15 AM	*High Quality Alpaca Genome VicPac4 and Oligo-FISH Reveal a Satellite Sequence Specific to South American Camelids* Mayra N. Mendoza, Brian W. Davis, Terje Raudsepp, Texas A&M University, Graduate Student
8:30 AM	*Telomere-to-Telomere References and Pangenomes for Domestic Dog* Sarah Fross, Sam Stroupe, Anna Kukekova, Hannes Lohi, Jeffrey Schoenebeck, Brian W. Davis, Texas A&M University, Graduate Student
8:45 AM	*Transgene removal using DNA repair* Joseph S. Romanowski, Keun Chae, Kevin M. Myles, Zach N. Adelman Texas A&M University, Graduate Student
9:00 AM	*Transcriptomic analysis of the stable fly brain and genetic control approaches* Tyler Chan, Zachary Adelman, Texas A&M, Graduate Student
9:15 AM	*DirectRepeateR: An R package for annotating direct repeats in genome assemblies* Megan Copeland, Andres Barboza, Joseph Romanowski, Zach Adelman, Heath Blackmon, Texas A&M University, Graduate Student

Pre-Function I and II

9:30 AM	Coffee break, vendor breakdown, poster breakdown

Century I and II

10:00 AM	Keynote: *RNAi pathways coordinate to protect fertility* Alicia Rogers, University of Texas Arlington
11:00–12:00 PM	TGS business meeting and awards presentations
12:00 PM	Meeting adjourned

Poster Abstracts

P1 ***Molecular and genetic interactions between the DBL-1/BMP signaling pathway and BLMP-1/BLIMP1 regulate organismal traits in* Caenorhabditis elegans**

M. Farhan Lakdawala, Matt Crook, Tina L. Gumienny
Texas Woman's University

Bone morphogenetic protein (BMP) signaling helps orchestrate multiple organismal traits in animals by regulating target gene expression. Regulation of this signaling pathway is critical for normal development and homeostasis. However, understanding how this pathway's transcriptional regulators, called Smads, control target gene expression to generate different traits is not well understood. Using the *C. elegans* system, we identified the chromatin remodeler B-lymphocyte maturation protein-1 (BLMP-1) as a partner in Smad-mediated gene expression regulation. BLMP-1 controls organismal traits that the DBL-1/BMP pathway also affects. While body size blmp-1 mutants were epistatic to *DBL-1* pathway mutants for male tail development, hermaphrodite gonad development, brood size, movement, and survival traits. DBL-1 signaling and BLMP-1 transcriptionally regulate each other. DBL-1 pathway Smads and BLMP-1 physically interact and regulate expression of common downstream target genes. This work identifies novel interactions between the DBL-1 signaling pathway and BLMP-1, two conserved major transcriptional regulators, that ultimately influence a spectrum of organismal traits. We propose that BLMP-1 regulates BMP signaling by acting as a gatekeeper, remodeling the chromatin architecture to permit the Smad complex access to target genes.

P2 ***Regulating Breast Cancer EMT Capacity with Molybdenum Disulfide (MoS_2) Nanoparticles***

Samantha M. Foster, Kanwar Abhay Singh, John Soukar, Olajumoke Ogunlusi, Christian Nguyen, Subiksha Sankar, Anna Keller, Irtisha Singh, Tapasree Roy Sarkar, Akhilesh Gaharwar
Texas A&M University

The differentiation of epithelial cells into mesenchymal cells, epithelial-to-mesenchymal transition (EMT), plays a significant role in the risk and development of metastatic cancers. Epithelial cells exhibit high cell-cell adhesion properties which form tight junctions, highly important for mechanical-based signaling, and diminished motility properties, while mesenchymal-like cells exhibit decreased cell-cell adhesion and increased migratory and metastatic capacity. While EMT plays a role in physiological functions such as wound healing, the development of a mesenchymal phenotype within the tumor microenvironment is detrimental, promoting cancer cell extravasation and development of the metastatic niche. EMT poses a potential therapeutic intervention for preventing development of metastases. Here, we introduce molybdenum disulfide (MoS_2) nanoparticles as a potential drug-free inhibitor of EMT, which is advantageous over traditional chemotherapy-type drugs. This study investigates the impact of MoS_2 nanoparticles on epithelial-to-mesenchymal transition in highly metastatic breast cancer both in vitro and in vivo. Treatment of 25 µg/mL MoS_2 nanoparticles decreased migratory capacity of hMSC and MDA-MB-231 cells in a wound healing assay, comparable to a commercial focal adhesion kinase (FAK) inhibitor, demonstrating the anti-metastatic motility property of MoS_2. We observed decreased expression of key proteins of focal adhesion site formation such as integrin, vinculin, FAK and smooth muscle actin. Furthermore, the expression of EMT-related genes such as *TWIST*, *SMAD4*, and *TGFβR1* are decreased in MoS_2 treated MDA-MB-231 cells after 72h of exposure. Combined, these results

indicate that MoS_2 nanoparticles may inhibit EMT progression in a manner comparable to TGFβ1 inhibitors such as RepSox. Additionally, mammosphere assays indicated reduced clonogenicity in cells following MoS_2 exposure. In vivo, primary tumor MoS_2 injection resulted in decreased tumor burden and lung metastases. Thus, our work demonstrates that MoS_2 nanoparticles inhibit integrin activity as well as the TGFβ signaling cascade pathway, blocking the transition to a mesenchymal-like phenotype. These findings suggest that MoS_2 nanoparticles hold promise for drug-free anti-metastatic therapeutics.

P3 ***Determining lifespan, fertility, and fecundity changes in*** **Aedes aegypti** ***SGS1/SGS1b double knockout mosquitos***

Emily Korger, Joseph Romanowski, Evan Patel, Bianca Kojin, Daniel Whitefield, Zach N. Adelman
Texas A&M University

Determining lifespan, fertility, and fecundity changes in *Aedes aegypti* SGS1/SGS1b double knockout mosquitos Malaria is one of the most prevalent and deadly vector-borne diseases in the world, responsible for over 600,000 deaths annually. The disease is caused by the parasitic Plasmodium, which is transmitted through the bite of infected mosquitoes. A critical step in the transmission process is the invasion of the mosquito's salivary glands by Plasmodium sporozoites. Understanding the molecular mechanisms involved in this invasion could provide valuable avenues for controlling vector-borne diseases. Previous research has shown that knocking out the *SGS1* salivary gene in *Aedes aegypti* disrupts sporozoite invasion of the salivary glands. This project's objective is to observe the effects of a double knockout of both *SGS1* and *SGS1b* genes on *Aedes aegypti* mosquito's fertility, fecundity, and life span, and eventually the effects on transmission of the malaria parasite. By exploring these effects, this research could contribute to novel approaches in malaria vector control.

P4 ***Exploring the enzymatic function of BRCA1 through nucleosome ubiquitylation in*** **C. elegans**

Meagan McMann, Lucy McCollum, Nathalie Carlon, Mikaela Stewart
Texas Christian University

BRCA1 protects genomic stability by signaling for the homologous recombination pathway, DNA repair, and transcriptional regulation. A pathogenic mutation in the *BRCA1* region causes a higher predisposition to the development of breast and ovarian cancer. Our lab is exploring the different enzymatic functions of BRCA1 by looking at its role in histone ubiquitylation, leading to transcriptional regulation of certain parts of the genome. Join us to see our plan for connecting molecular mechanisms of a large, multi-functional gene to the phenotype of an organism. A homolog of *BRCA1* is conserved in *C. elegans* as BRC-1. We propose that mononucleosome ubiquitylation is a key mechanism contributing to the cellular functions of BRC-1. Understanding the significance of mononucleosome ubiquitylation in BRC-1 with *C. elegans* gives insight into the mechanisms of genetic variations in *BRCA1* and further expands *C. elegans*' function as a model organism. We have generated a *C. elegans* mutant with two point mutations that alter the ability of BRC-1 protein to interact with the nucleosome and ubiquitinate histone H2A while retaining all other functions. We hypothesize this mutation increases DNA damage accumulation and disrupts transcriptional regulation to establish nucleosome ubiquitylation as a necessary precursor for these, but likely not all, BRC-1 functions. We compare three strains of *C. elegans* (wildtype, *brc-1* knockout, and our mononucleosome ubiquitylation-deficient mutant) in different

conditions designed to induce cellular stress or DNA damage accumulation. We find that BRC-1 nucleosome ubiquitylation contributes to embryonic survival under standard conditions as well as DNA damage-inducing conditions. We also share preliminary results regarding the role of nucleosome ubiquitylation in transcription regulation and reactive oxygen species generation. Our findings further the understanding of the many enzymatic functions of the large *BRCA1* gene.

P5 ***Learning genetics by "making a baby" with a deck of cards for majors or non-majors courses***

Tina L. Gumienny, Lionel Faure
Texas Woman's University

Genetics can be a difficult topic to master. For some students, the random yet precise segregation of chromosomes during meiosis and different inheritance patterns are especially hard to grasp. To help students understand these basic genetic concepts, we developed, implemented, and refined a "card baby" active learning activity over eight years. This activity can be done in class or online, and in a non-majors or majors course. After instruction on meiosis, the animal life cycle, and basic inheritance patterns, students get to apply what they learned by "making a baby". In-class students pair and are given a deck of cards. Each card represents a chromosome. The two black suits are the dad's two chromosome sets. The two red suits are the mom's two chromosome sets. Students are instructed to perform meiosis: after laying out cards in order by suit, one student in the group makes the haploid "sperm" chromosome set by randomly selecting one of each card number from clubs and spades. In a similar way, another student makes the "oocyte" chromosome set from heart and diamond cards. The group performs "fertilization" by matching up the two sets of cards. They confirm no aneuploidies. After students have successfully "made a baby", they get a table with the genotypes associated with each chromosome and the inheritance pattern. Real human traits that generally follow autosomal recessive or dominant, sex-linked, incomplete, and polygenic inheritance patterns are provided for the students to interpret. The majors course includes an example of epistasis. The students' goal is to interpret the genotype and phenotypes of their "baby" based on the randomly selected card chromosomes their "baby" has. They fill in a paragraph describing their baby's traits based on the genotype and the given inheritance patterns. At the end of the class (or in a discussion board, if online), groups read their paragraph to the class so students can see the variety in the "siblings" the class made. Students provided overwhelmingly positive responses when asked if this activity helped them understand the patterns of inheritance and if this activity was enjoyable. This activity is adaptable to one's favorite inheritance patterns, traits, and diploid, sexually reproducing, multi-chromosomal organism. Practically, it is inexpensive, doable in a 50- or 80-minute class, and scalable to large classes (especially with help from teaching assistant(s).

P6 ***Imbedded Reporters: Loading Introns with Reporter Gene Cargo as a Genetic Tool***

Daniel B. Whitefield, Zach N. Adelman
Texas A&M Agrilife Research

The goal of this pioneering work is to establish a new genetic tool that will expand the investigation capabilities of researchers across a wide array of biological disciplines. Our new technique was validated in the *Aedes aegypti* model – a mosquito species relevant to public health commonly known as the Yellow Fever mosquito.

Introns, or intervening sequences, are non-coding RNA sequences in a pre-mRNA molecule found between Exons, the coding sequences. Most introns are spliced out of pre-mRNA by the Spliceosomal Complex during mRNA maturation. The presence of introns enables Alternative Splicing to produce multiple versions of proteins from the same gene. Many genes of *Ae. aegypti*, the Yellow Fever mosquito, contain introns that can be quite large – in excess of 100kb.

For decades genetic engineers have used fluorescent proteins as reporters to verify the presence of their transgene in the genome of the organism or cell line that they are studying. However, this process is not always so straight forward. In the case of fluorescently tagged proteins coded for by the transgene, the presence of extra amino acids may interfere with protein folding. Alternatively, steric hindrance from the fluorescent protein may render the tagged protein of interest non-functional. Other strategies involve experimental transgenes and separate reporter transgenes included in the same cassette but whose products are not physically linked (as in the case of fluorescently tagged transgenes). In these experiments the possibility arises that the two genes become decoupled, which renders the reporter useless.

Here, we attempt to address the challenges to reporter effectiveness by loading introns within the parent gene with a reporter gene. This has the advantage over fluorescent tagging by removing the potential to disrupt the activity of the protein of interest. Similarly, loading introns with reporters intrinsically links the genes – an advantage over strategies in which linkage is only accomplished by proximity.

First, we show that constitutively spliced introns from riboprotein genes will properly splice in the context of a novel parent gene with the parent gene maintaining functionality. We then show that introns loaded with a cargo gene are also able to be spliced while the parent gene maintains expression. In order to obtain a measure of splicing efficiency, total RNA was extracted from transfected cells expressing our construct so that cDNA could be synthesized and sequenced. The number of reads showing intron splicing were compared to the number of reads still containing the intron. Finally, we show that, when injected into mosquito embryos, somatic expression of both parent and cargo genes is visible in G0 larvae.

P8 ***Retrospective Analysis of Acute Diarrhea in Dogs Reveals Patterns that can be Modeled by Machine Learning***

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Background –Acute diarrhea (AD) is a common self-limiting GI condition in dogs in which the direct cause is usually unknown. AD signs have been associated with increases entomopathogens like C. perfringens and E. coli. Machine learning models like the dysbiosis index have provided a foundation for better understanding of other GI diseases in dogs with chronic enteropathy.

Objective – Evaluate fecal microbiota in dogs with AD and train a machine learning model to integrate patterns across AD dogs that distinguish them from HC's.

Animals – 79 dogs with uncomplicated AD lasting < 5 days and 79 healthy dogs (HC).

Methods – Retrospective pooled analysis evaluating key intestinal microbiota in fecal samples via qPCR. Universal bacterial markers and taxa such as *Faecalibacterium*, *Turicibacter*, *Streptococcus*, *E. coli, Blautia*, *Fusobacterium*, *P. hiranonis*, *Bifidobacterium*, *Bacteroides*, and *C. perfringens* were measured. Day 0 AD (n=74) and HC samples (n=79) were selected to train and test a machine learning model that predicts likely phenotype based on similarity scores. Follow-up AD samples (D 4, 7, 35, and 42) were evaluated with this model.

Results – The trained model was able to accurately determine the phenotype of HC or AD 91% of the time. In the 46-sample testing set the model achieved a sensitivity of 93% (25/27) and specificity of 89% (17/29). This is based on a combination of consistent differences observed across AD samples compared to HC, including an increase in universal, *E. coli*, and *C. perfringens* ($p < 0.01$) as well as increases in Streptococcus and Fusobacterium ($p = 0.03$). While *Faecalibacterium*, *Bifidobacterium*, and *Bacteroides* were decreased ($p < 0.01$). Interestingly while *C. hiranonis* was increased in AD ($p < 0.01$) similar rates of functional loss of *hiranonis* was observed in similar proportions of the AD and HC were observed, 6.3% and 9.25 respectively. At AD day 7, 1/18 samples were classified by the model as healthy and at AD day 42, 9/19 samples were classified as healthy.

Conclusions and clinical importance – These results indicate that are consistent patterns in AD that can be captured by machine learning. Development of this model has the potential to observe minor changes across key bacteria and track normalization of minor disease.

P9 ***Association of genetic background dependent gene expression variations of Glutathione (GSH)-system related genes and metabolomic profiles in mice liver***

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Obesity is a growing public health concern, with CDC data showing that 1 in 7 children aged 2 to 5 are obese. At the molecular level, obesity is linked to oxidative stress—an imbalance between reactive oxygen species and antioxidants—leading to inflammation and cellular damage. Glutathione (GSH), a genetically regulated antioxidant, plays a critical role in maintaining redox balance, yet the influence of genetic background on GSH-related gene expression and liver metabolism remains unclear. This study investigates the relationship between genetic background, GSH-related gene expression, and liver metabolism in response to an obesogenic diet. Liver samples from 20 inbred mouse strains were analyzed for expression variations in five key GSH-related genes (*Gstm1*, *Gstm4*, *Gstm6*, *Gstm7*, and *Gsto1*) using qRT-PCR. Metabolomic profiling will further identify metabolites linked to these genetic differences. Preliminary analyses of 9 strains revealed significant variation in GSH-related gene expression ($p<0.0001$ for Gstm1, Gstm4, Gstm6, Gstm7; $p<0.0004$ for Gsto1), with the obesity-prone strain NZO/HILtJ and recombinant inbred strains, such as CC009/UncJ and CC040/TauUnc, showing distinct expression patterns compared to the reference strain C57BL/6J. These findings emphasize the role of genetic background in shaping oxidative stress responses and metabolic outcomes in obesity. Identifying strain-specific expression patterns may contribute to precision nutrition approaches, where individualized genetic profiles guide targeted nutritional and therapeutic strategies to mitigate obesity-related complications.

P10 *Translational Control by 5′ UTRs During Viral Infection*

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RNA (mRNA) contains multiple regulatory regions throughout its sequence, such as the 5' cap and poly(A) tail. In addition to these key elements, untranslated regions (UTRs) are important mediators of post-transcriptional regulation, especially the 5' UTR, which recruits ribosomes to the mRNA and initiates the translation process. During stress, global translation is repressed, while the translation of specific transcripts is selectively upregulated. This sparked a question about the role of the 5′ UTR in modulating translational activity during stressful conditions. Although considerable research has focused on how viral 5′ UTRs influence the host translation machinery, the effects of variation of host cell 5′ UTRs and their interactions with RNA-binding proteins during viral infection are not well understood. We hypothesize that specific sequences within the 5′ UTRs of both host and viral transcripts enable them to bypass global translational repression. To test this hypothesis, we will design a massively parallel reporter assay to measure the translation of mRNAs with different 5' UTRs during viral infection. This approach will allow us to identify specific sequences that drive translation regulation in response to infection.

P11 *Variation in C. elegans social clumping behavior reveals polygenicity of ASD risk genes*

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Autism spectrum disorder (ASD) is a neurodevelopmental condition characterized by atypical social behavior. Although more than 100 *ASD* risk genes have been identified, how mutations in these genes contribute to ASD-related phenotypes remains poorly understood. While rodent models have facilitated some progress, generating transgenic rodent models to test individual genes takes months, making it challenging to study multiple genes at a time. Thus, to accelerate discoveries in this field, a genetically tractable animal with orthologs for *ASD* risk genes, associated quantifiable phenotypes and capability to faster high-throughput functional analyses, is needed.

Interestingly, the small nematode *Caenorhabditis elegans*, has orthologs for more than 70% of human *ASD* risk genes and due to its short development cycle and large brood size, it is a powerful model for high-throughput functional screens. Although less explored, C. elegans also displays a robustly quantifiable kind of social behavior called social clumping. Our lab found that most wild C. elegans strains, isolated from different habitats around the world exhibit high levels of social clumping (50-70%) while strains carrying deleterious variants in *ASD* risk orthologs (*nlg-1/NLGN1*, *gap-2/SYNGAP1*, *mbk-1/DYRK1A*) show reduced clumping (0–50%). Transforming these low clumping wild strains with functional copies of *ASD* risk orthologs significantly boosted their clumping levels. Conversely, mutating genes (*athp-2*/BAZ1B and *mrck-1*/DMPK) related to a type of ASD with hypersociality, known as Williams syndrome (*WS*), boosted clumping in a low clumping strain. Collectively these findings suggest that *ASD* and *WS* related genes play a role in modulating social clumping behavior.

We hypothesize that social clumping behavior represents a phenolog of human social behavior as they are both affected by *ASD* risk gene mutations and potentially involve functional interactions of *ASD* risk genes. To test our hypothesis, we conducted a genome wide association (GWA)

analysis for clumping behavior in genetically diverse wild strains of *C. elegans*, an approach previously unexplored. We identified two significant quantitative trait loci (QTL) associated with clumping variation. Notably, we identified that some of the most significant variants within one QTL are predicted to damage *jmjd-3.2*, an ortholog of high-confidence ASD risk gene KDM6B. Consistent with our hypothesis, this result suggests that clumping behavior could be a potential phenolog of social behavior as more *ASD* risk genes are associated with clumping behavior. Efforts to fine map this top QTL and identify causal roles of candidate genes are currently underway. Further epistasis analysis of these causal genes with canonical *ASD* risk orthologs, could potentially uncover previously unidentified functional interactions of *ASD* risk orthologs and expand our understanding of polygenicity of *ASD* risk genes.

P12 *Genetic biocontrol tools for the suppression of invasive rodents*

Ana Velasquez, David Threadgill
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Invasive rodents on islands are one of the main drivers of global biodiversity loss. Specifically, they are predominantly responsible for the risk of extinction of terrestrial mammals and island invertebrates. Although arguably successful, current population control tools, such as anticoagulant bait or trapping, are likely to cause harm to off-target species and have potential for long-lasting detrimental effects in the environment. An increased risk of harm to endemic island species and anticoagulant contamination to agricultural plots and livestock raise a need for species-specific population control tools.

Current research explores the potential use of genetic engineering and selfish genetic elements, or gene drives, to create self-driven, endogenous, species-specific population suppression and eradication tools. This project aims to use the naturally existing murine gene drive, the t-haplotype, to create a mouse that can only have male progeny, i.e., a daughterless mouse.

We have created a gene construct designed to express *Sry*, the mammalian sex determination gene, in the mouse embryo, to drive male development of XX and XY embryos. This construct was successfully inserted into chromosome 17 of t-carrying mice and has the potential to be used to generate a daughterless mouse population.

If effective, a heterozygous male mouse with t-haplotype/*Sry* (*t-SryT*) will produce more than 95% male offspring upon reproduction and serve as a genetic biocontrol tool. Targeted release of these mice in areas where invasive mice reside would be an equally effective and more humane alternative for species-specific eradication with fewer off-target implications than anticoagulant toxicants.

P13 *HoloFold: A new machine-learning tool to accurately predict metal-protein interaction*

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With the advent of novel protein folding prediction software like AlphaFold3, it is becoming increasingly easier to guide experiments based on predicted protein domains, interacting partners, or ligands. However, predicted ligand binding has high false positive rates, which is especially true when the ligand is a metal ion. To solve this problem, we developed HoloFold, a machine-learning model that incorporates evolutionary, structural, and metal-specific

information to accurately and quickly predict protein-metal interactions. We show that HoloFold is a highly accurate model with low false discovery rate. For example, HoloFold is able to recall ~20% of true copper binding proteins with 100% precision in a curated dataset composed of 5% copper, 81% zinc and 14% non-metal binding proteins. Using the same dataset, we demonstrate that HoloFold far outperforms AlphaFold 3, which cannot distinguish between different metals. By applying HoloFold to the human and yeast proteomes, we are generating a high confidence metalloproteome inventory with important implications for disease and new biology.

P14 ***Chromosomal Architecture in Flux: Unraveling the Mechanisms Behind Gene Density Variation in Vertebrates***

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The democratization of sequencing has led to a wealth of high-quality genome assemblies from across the Tree of Life. One pattern that has emerged is that chromosomes within a genome can vary dramatically in their gene density (e.g., human chromosomes 18 and 19 with gene densities of 4.1 and 26.7 genes/Mb, respectively). To our knowledge, the cause of this variation in gene density has not been explored. In this study, we leveraged genome assemblies of 262 vertebrate species to explore the range of within-genome variation in gene density. We combined gene density data with repeat landscape analyses in each species and examined within-genome variation in gene density using probabilistic phylogenetic models across species and least-squares models within species. Preliminary data suggested that recent repeat expansions increase within-genome gene density variation by preferentially targeting specific genomic regions, while chromosomal rearrangements such as fusions, fissions, insertions, deletions, and inversions homogenize gene density in the absence of repeat expansion. Our analysis finds a significant but varied effect of repeat expansions, and additional processes likely also contribute to gene density variation.

P15 ***Analyzing Endogenous Cas9 Expression in Tribolium castaneum***

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Tribolium castaneum is model organism for other Coleoptera species due to their entire genome being available to analyze, their ability to be reared in a laboratory setting, as well as their relatively short generation time and high fecundity. Cas 9-based editing is invaluable in the field of genetic engineering and with editing anticipated to be significantly more efficient when expressed directly in the insect instead germlineCas9 protein under the control of the Vasa promoter; transgenic strains were identified by a GFP marker in the eyes with Cas9 expression documented by Western blot analysis of both the somatic and germline tissue. To verify the gene editing ability of each strain, we performed microinjections of Cas9+ *T. casteneum* embryos with synthetic guide RNA targeting the ebony gene, where knockout results in a dark coloration of the adult cuticle. In addition to screening for somatic mutagenesis, we also outcrossed injected G0 offspring with a previously established ebony strain to identify germline mutations. Inverse polymerase chain reaction (PCR) was also used to demonstrate the integration of the transgene within the genome. Through this research, we have found at least two Cas9-expressing strains of *T. castaneum* that can trigger gene editing. Future directions include analyzing the location of the genomic insertion of the transgene within each line to determine the effect the Cas9 transgene has on the organism.

P16 *Development of Recombinant* Saccharomyces Cerevisiae *Strains for Lactose Fermentation*

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Cheese whey is a byproduct of cheese curd production. Currently, 115 million tons of whey are produced annually and 47% of this is discharged into the environment without prior treatment. With the demand for cheese only increasing, the need for a remedy to this pollutant is apparent. Because up to 70% of dissolved material in whey is lactose, we propose using fermentation to ethanol as a means to remediate cheese whey. This would enable the whey to be converted to an industrially useful product. However, industrial strains of yeast fail to ferment lactose effectively and efficiently due to the absence of two proteins, *Lac4* (a beta-galactosidase) and *Lac12* (a lactose permease).

Our approach to solve this problem is to engineer a strain of *Saccharomyces cerevisiae* that expresses the Lac4 and Lac12 genes. To do this, we will use recombinant DNA methods to test which combination of enzyme expression level (strong, medium, or weak) is optimal for whey fermentation. To vary levels of expression we are creating plasmids of different promoter strengths to assist in lactose fermentation. The genes were taken from two nonindustrial strains of yeast to make two 3x3 matrices using combinations of strong, medium, and weak promoters making 18 strains. Varying the strength of the promoters and performing fermentation will allow us to determine the optimal promoter strengths for the maximum efficiency of ethanol production. We currently have built 12 of the 18 final plasmids and are at present constructing the rest of the plasmids required to complete the set of 18. Using this approach, we hope to build a yeast strain which is viable for the fermentation of lactose for industrial ethanol production.

P17 *Identification of lineage-specific genes and de novo genes with the Lineage-specific gene universal annotator (Lingua)*

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Understanding the genetic basis of phenotypic diversity, adaptation, and innovation is crucially informed by our knowledge of proteome evolution. Mechanisms such as gene duplication and horizontal gene transfer have been identified as major sources of new genes. However, they rely on preexisting genes and thus required prolonged evolutionary timescales to produce proteins with novel functionality. Furthermore, the study of these processes does not address the evolution of the very first genes or proteins. Over the past two decades, it has been shown that entirely novel protein-coding genes can evolve from ancestrally noncoding DNA in a process known as de novo gene birth. De novo genes (DNGs) have been identified across eukaryotes and bacteria and represent a major source of novel proteins. Despite these advances, the prevalence of DNGs remains unclear beyond a few well-characterized model species due to limits in the availability of comparative genomic resources, particularly synteny conservation data, that have been traditionally required to detect DNGs. In this study, we present the Lineage-specific gene universal annotator (Lingua) tool, a computational pipeline integrating comparative genomics and phylogenetics to identify lineage-specific genes and identify candidate de novo genes. Lingua relies on orthology relationships and extensive homology-based searches to extract lineage-specific genes, of which de novo genes are a subset, from a given group of species genomes.

Synteny data can be further integrated into the pipeline to validate candidate DNGs by identifying substitutions that enable the transition from noncoding to coding DNA. Although this tool can be applied to any taxon with sufficient genome coverage, we have first tested it on 20 *Brassicaceae* genomes. This work not only advances our understanding of proteome evolution but also highlights the potential for discovering novel proteins that contribute to phenotypic diversity and adaptation.

P18 *A Biosensor for Measuring Mitochondrial Outer Membrane Permeabilization in Humanized Yeast Strain*

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Apoptosis dysregulation plays a pivotal role in tumor malignancy and degenerative diseases. The initiation step of apoptosis is mitochondrial outer membrane permeabilization (MOMP), which is regulated by Bcl-2 family proteins. Bcl-2 Homology (BH) domains are shared between all members of the family, which include proapoptotic, antiapoptotic, and sensitizers. Upon activation, proapoptotic proteins insert into the mitochondrial outer membrane, form oligomers, and create a proteinaceous pore that further progresses cell death.

Despite extensive research, the precise network of interactions governing MOMP remains incompletely understood, largely due to the complexity of the Bcl-2 protein family interrelationship. In mammalian cells, all components of this system coexist, making it challenging to isolate how individual protein-protein interactions lead to the initiation of apoptosis.
To simplify this system, we developed a Bcl-2 proteins-free environment in a *Saccharomyces cerevisiae* strain with a YBH3 knockout. Yeast was chosen because it has only one BH protein, YBH3, allowing for a more controlled study of Bcl-2 protein interactions.

To detect mitochondrial membrane rupture, we designed a fluorescence-based biosensor using split fluorescent protein (sFP). During MOMP, intramitochondrial proteins that were tagged with B11 sFP subunits, exit the mitochondria and fuse with B1-10 subunits, producing a detectable fluorescence signal.

The results showed that upon acetic acid-induced apoptosis, MOMP occurred, leading to the fusion of sFP-tagged intramitochondrial proteins and a 0.5-fold increase in fluorescence. Such an increase demonstrates the functionality of the biosensor and proves its ability to sense MOMP.

P19 *Characterizing the fungal and bacterial community of South Central Texas oak samples using genomic analysis*

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Wine is made by fermenting grape juice with yeast and is enjoyed by about 75% of adults. Many winemakers introduce predictable fermentation behavior by using a commercial yeast, often *Saccharomyces cerevisiae.* Although *S. cerevisiae* is widely used for commercial brewing, not much is known about its ecology.

Previous research has noted a relationship between *S. cerevisiae* and *S. paradoxus*, a closely related undomesticated species, and oak trees. Studies have independently enriched and studied yeast

samples from oak bark, leaves, and leaf litter to understand global yeast distribution and local yeast genomics, yet no study has comprehensively compared the microbial community composition between different regions of the tree. Trees are known to have distinct microenvironments in their crown, trunk, and roots, which may change yeast growth behavior.

Our lab previously collected three oak bark samples from South Central Texas, used a genomic analysis to characterize the fungal and bacterial species present in the samples, and found S. cerevisiae and organisms of the class *Malasseziomycetes* within all samples. We plan to expand upon this work by sampling oak bark, leaves, and leaf litter to genomically characterize the fungal and bacterial communities in these distinct microenvironments, and to determine the relative yeast concentration across samples. Through the characterization of fungi and bacteria across samples, we hope to develop a better understanding of the competition of yeast with other microorganisms. Comparing the prevalence of different yeasts across sampling locations may suggest S. cerevisiae and S. paradoxus metabolic needs based on the location(s) that they are most abundant.

P20 *Dietary methyl donor intervention reverses memory of prior American diet exposure in C57BL/6J males*

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Metabolic disorders such as obesity and diabetes continue to increase in prevalence in the United States showing a need for more effective interventions. The American diet, which generally promotes obesity and metabolic disorders, is high in carbohydrates and fats. There has been interest in the low carbohydrate ketogenic diet as an intervention for obesity.

While ketogenic diets are highly effective for some individuals, not all respond to this intervention. We have previously investigated the efficacy of ketogenic dietary interventions in genetically distinct mice. Our group has demonstrated that when C57BL/6J (B6) males are exposed to the American diet their fat percentage is 1.77-fold higher than B6 males consuming a ketogenic diet, suggesting these mice are responsive to carbohydrate restriction in the form of a ketogenic diet.

To test a ketogenic intervention, B6 mice were first exposed to an American diet before being given a ketogenic diet intervention to which they failed to respond. To test whether B6 mice exposed to the American diet have an epigenetic memory preventing their response to the ketogenic intervention, we provided a diet that has either an excess or deficient of methyl donors to those previously receiving an American diet for one month before testing a ketogenic intervention. Body composition measurements were collected at each stage of the dietary treatment and up to 6 months of the ketogenic intervention.

After the methyl intervention diet, mice on the methyl donor deficient diet had a significant loss of total fat mass with little impact on lean mass. One month post intervention, we observed that exposure to the methyl donor deficient diet resulted in mice that gained 3.9 +/- 2.2 gm of fat mass while those that had been on the methyl donor supplemented diet showed a fat gain of 11.5 +/- 3.7 gm. After 6 months on the ketogenic intervention, mice from the methyl donor deficient treatment gained 12.48 +/- 4.68 gm of fat mass while those on the methyl donor supplemented treatment had gained 22.60 +/- 3.22 gm of fat. Based on these responses, we speculate that the exposure to the

methyl donor deficient diet can reverse memory of the prior American diet exposure. Effects of the interventions on the epigenome are currently being tested.

P21 *Developing Flight Assays to Test the Flight Performance of Genetically Modified Mosquitoes*

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Aedes aegypti are vectors of yellow fever, Zika fever, dengue fever, and chikungunya. Previous literature targets flight in female *Aedes aegypti* as a potential vector control strategy. While some flight gene knockouts result in flightless mosquitoes, others result in mosquitoes with seemingly reduced flight performance. A flight assay is needed to quantify and compare the flight performance of these genetically modified mosquitoes to that of wild-type mosquitoes. A wind tunnel was developed to measure flight performance of blood-seeking mosquitoes. Additionally, a flight assay originally developed for testing *Drosophila melanogaster* was adapted to test *Aedes aegypti*. This two-tiered approach will allow us to compare and categorize the flight performance of various gene knockouts and potentially develop a vector control strategy.

P22 *Investigating the Correlation Between Stress Granule Formation in Mammalian Cells and the Stages of Chikungunya Virus Infection*

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Stress Granules (SGs) are biomolecular condensates that are formed through phase separation in the eukaryotic cytoplasm. These granules are induced by cellular stressors such as oxidative stress, heat shock, or viral infections. The membrane-less cytoplasmic assemblies contain mRNAs and proteins of the host cell. One such protein, G3BP1/2 acts as a core component of the SGs in mammalian cells. With limited knowledge of the composition of SGs, their function during stress in cells is not well understood.

Chikungunya virus (CHIKV) is an alphavirus known to cause severe joint pain and myalgia and has been responsible for many major disease outbreaks. The genome of CHIKV contains 4 non-structural proteins that are translated first, followed by 5 structural proteins. Working on the hypothesis that SGs play a role in the antiviral response, it has been noted that many viruses have evolved to regulate their formation, while others like CHIKV form proteins that interact with SGs to remodel them. It has also been observed that CHIKV is unable to replicate in humans in the absence of G3BP1. By uncovering the connection between CHIKV translation, SG formation, and the stages of viral replication, we would better understand which of these stages is most strongly impacted by SGs.

To better understand CHIKV's complex interaction with SGs, this study focuses on correlating the stages of stress granule formation and dispersion with the various stages of CHIKV infection. To further focus on the cell-to-cell variation of this interaction, single-cell readouts will allow us to map this connection more precisely. This will be studied using reporters at different stages of CHIKV replication.

Methods: Plasmid design using the Gibson cloning technique was utilized to make fluorescent reporter-linked G3BP proteins and to design viral strains of CHIKV with reporters for different

stages of replication. The cDNA of different CHIKV strains will be amplified, transcribed, and transfected into BHK-21 cells sourced from ATCC for viral propagation. HEK293T cells will be used to perform viral infections. Fluorescent microscopy equipment at the Imaging Core will be used for live imaging and tracking the formation of SGs with the viral replication.

P23 *Loss of Erbb2 triggers compensatory EGFR activation in a mouse model of colorectal cancer*

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ERBB2 belongs to the ERBB family (EGFR, ERBB3, ERBB4) of receptor tyrosine kinases and exhibits unique structural morphology with no known ligand binding domain of its own. Its constitutively open conformation supports increased ligand binding efficiency upon heterodimerization with an ERBB family member, resulting in amplified cellular signals regulating cell proliferation, survival, differentiation, angiogenesis, and apoptosis. While Erbb2 modulation has been identified in breast, gastric, and ovarian cancers, its contributions to colorectal cancer (CRC), where it is upregulated in 7% of all CRC cases, remain largely unknown. To elucidate the mechanistic effects of Erbb2 during CRC progression, an *Erbb2*f/f, *ApcMin*/+, *Tg*(*Vil1*-Cre) transgenic mouse model and matched controls were utilized. A comprehensive molecular predictive analysis encompassing ingenuity pathway analysis (IPA) and gene set enrichment analysis (GSEA) was validated with RT-qPCR and protein detection assays. In Erbb2 knockout tumor samples, phosphorylated EGFR is shown to be upregulated compared to control tumors, indicating a compensatory mechanism of EGFR in the absence of Erbb2 with other ERBB family members. Differential gene expression showed amplification of *Mapk* and *Ctnnb1* in *Erbb2* knockout tumors suggesting increased activation of the Ras-MAPK pathway, linked to cellular proliferation and regulation of cell behavior through gene expression. Colonic epithelial crypts displayed no signs of developmental differences due to *Erbb2* loss, which suggests a specific role of *ERBB2* in tumorigenesis compared to normal tissue homeostasis. Overall, loss of *ERBB2* promotes compensatory activation of EGFR to further promote tumorigenesis in the *ApcMin*/+ mouse model. These results will be utilized to inform the characterization of loss of *Erbb2* in both inducible and transgenic colorectal cancer mouse models. Further investigation of the EGFR compensatory mechanisms will gain insight into how Erbb2 modulation impacts the ERBB family. This all-encompassing approach will allow us to inform better preclinical approaches to precision cancer drug development.

P24 *Artificial cellular communication in yeast* Saccharomyces cerevisiae *using human Epidermal Growth Factor (hEGF) and Signal Transducer and Activator of Transcription (STAT)*

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Cellular communication is essential for coordinating behaviors in multicellular organisms and synthetic biological systems. Inspired by Alan Turing's reaction-diffusion model, where a morphogen changes the gene expression of cells, our research concerns developing artificial intercellular communication in *Saccharomyces cerevisiae* using the human Epidermal Growth Factor (hEGF) and Signal Transducer and Activator of Transcription (STAT) signaling pathways. The purpose of this research is to integrate the human EGF hormone signaling pathway into yeast cells to control their patterning behavior.

We designed and assembled plasmids via Golden Gate assembly to introduce components of the hEGF-STAT signaling pathway into yeast. These plasmids contain an *Epidermal Growth Factor Receptor* (*EGFR*), either the *STAT3β* or *STAT5a* transcription factor, and a fluorescent reporter gene (Venus). Each STAT was coupled with a transactivation domain (*Msn2*, *rTA*, or *VP16*) to activate reporter gene expression.

Further work will focus on transforming the plasmids into yeast. We wish to see the signaling cascade process by following the expression of the Venus tag. This entails the yeast cells being exposed to hEGF, leading to receptor phosphorylation, STAT activation and translocation to the nucleus, where the transactivating domain (TAD) will induce Venus expression. We will use flow cytometry and fluorescence microscopy to measure fluorescence in response to hormone application, demonstrating that human signaling molecules can function in yeast. Additionally, we will establish which STAT-TAD combination provides the greatest difference in fluorescence between basal and maximum transcription. Ultimately, we want to build a system wherein cells can autonomously send and receive signals, eliminating the need for external involvement. This research has broader implications for programmable biological programming and synthetic tissue engineering.

P25 *Heterogenous response to ERBB3 inhibition in colorectal cancer*

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Colorectal cancer (CRC) is the second leading cause of cancer-related deaths in the United States. Significant progress has been made in early detection, diagnosis, and treatment through the developments in precision medicine in efforts to reduce this significant health burden. Increased understanding of molecular mechanisms which govern CRC progression have aided in this progress, as mortality rates have trended downward over the last five decades. However, the mortality trend for those under fifty is on the rise and there is a need for improved targeted therapeutic approaches.

This preclinical study aims to understand how host genetic variation impacts tumor molecular signatures and response to therapy to address the variable responses of heterogenous patient populations in clinical trials. The ERBB receptor tyrosine kinase (RTK) family govern various complex biological function that are associated with dysregulated cell proliferation and survival that have been investigated as therapeutic targets in promising preclinical studies. The related ERBB3, a pseudo-kinase that lacks intrinsic kinase activity, relies on transactivation of other ERBB receptors. In homogenous preclinical mouse models, intestinal- specific deletion of ERBB3 leads to a significant reduction in colon and intestinal tumor multiplicity. In clinical trials, inhibitors against ERBB3 had little to no efficacy and even trended to poorer outcomes.

With this knowledge, we investigated if patient heterogeneity contributed to the translational failure. Using heterogenous preclinical mouse models, we found that the impact on tumor growth by inhibition of ERBB3 is genetic context dependent. Inhibition of ERBB3 on the 129S1/SvlmJ (129) background reduces tumor growth, while on a C57BL/6J (B6) background, ERBB3 inhibition leads to enhanced tumor growth, which explains the translational failure. This study

aims to use mouse models to identify genetic modifiers and molecular signatures in response to *ERBB3* loss so that failed clinical trials can be rescued.

We generated an F2 population from the 129 and B6 backgrounds to identify regions associated with polyp count distribution through quantitative trait loci analysis. The distribution of the F2 population encapsulates polyp quantities from both genetic backgrounds, with 27% of the distribution mimicking the B6 population of enhanced tumor growth, and 31% of the distribution being 129-like with reduced tumor growth. The F2 animals are being genotyped to identify genetic markers for ERBB3 response that will be presented.

P26 *Lipid Metabolism and Mitochondrial Surveillance are Linked to Host Defense against* **Pseudomonas aeruginosa** *Infection*

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The development and spread of antimicrobial resistance have dramatically increased in recent decades. Simply relying on existing (or even new) antimicrobials will not solve this crisis. Among innovative solutions proposed is the idea that we can modulate host and bacterial pathways in order to favor the host. However, this requires extensive understanding of the pathways involved in innate immunity and host defense.

Previous research in *Caenorhabditis elegans* suggests that lipid metabolism could be involved in host response to infection. It was shown that the monounsaturated fatty acid, oleate, is required for innate immune effector activation. Additionally, it was demonstrated that the evolutionarily conserved mediator subunit: MDT-15/MED15, which regulates lipid metabolism, is also involved in host defense against Gram-negative pathogens such as *Pseudomonas aeruginosa*.

We set out to characterize the host lipid metabolism pathways promoting survival against infection with P. aeruginosa, using a well-established, liquid-based pathogenesis model called Liquid Killing (LK-Pa). Previous research in our lab demonstrated that pyoverdine, a siderophore from P. aeruginosa is produced in liquid and damages *C. elegans* mitochondria, resulting in an iron-dependent hypoxic crisis and eventual host death. To alleviate this mitochondrial damage, *C. elegans* activates the Ethanol Stress Response Element (ESRE), a conserved mitochondrial surveillance pathway.

We looked at *C. elegans*' transcriptional profile during infection with *P. aeruginosa* and saw significant enrichment of lipid metabolism genes in LK-Pa condition. Screening under LK-Pa conditions revealed 22 lipid genes are indispensable for host defense. Additionally, five of these genes are required for full ESRE activation, indicating a relationship between lipid metabolism and mitochondrial surveillance in host defense. This work establishes the involvement of lipid metabolism in defense response against Gram-negative bacterial pathogens and it sets the groundwork for the discovery of candidate genes that can be enhanced for the host's benefit in host-pathogen interactions.

P27 ***Connecting mechanosensation and social behavior in relation to ASD risk genes***

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Autism spectrum disorder (ASD) is a condition marked by social difficulties and accompanying sensory symptoms. Although ASD has been found to disrupt function of the central nervous system, recent studies have revealed a correlation between disruption of the peripheral sensory system and social dysfunction. This raises the intriguing hypothesis that core ASD symptoms may be relieved in part by improving peripheral sensory signaling. In particular, mechanosensory circuits are suspected, as about 95% of the socially impaired autistic individuals exhibit abnormal sensitivity to tactile stimulus. Tactile deprivation studies further support this hypothesis by revealing correlations between tactile experiences, neuronal development, and atypical social behaviors. However, it is unclear whether there is a causal relationship between abnormal mechanoreception and social functions in people with ASD.

Study of this topic is challenging because ASD is a complex polygenic disorder, caused by genetic alterations of at least 100 ASD risk genes. Yet it remains unclear how these genes individually or combinatorially affect mechanosensation and sociality.

To gain insight into which of the many ASD risk genes may disrupt mechanosensory functions and potentially contribute to ASD-related social dysfunction when mutated, we turned to *C. elegans*. The worm serves as a convenient model to study this topic because 70% of the ASD risk genes and most mechanosensory pathways, such as MEC/DEG, TRP, Piezo, and TMC, are conserved. In addition, worms exhibit a social behavior termed clumping, in which they are guided by pheromones and other sensory cues to form aggregates. We recently discovered that mutations in many ASD risk orthologs causally contribute to the varying degrees of clumping in wild strains and the lab strain N2. We also are beginning to understand how distinct mechanosensory pathways, which express specific ASD risk orthologs, promote or decrease clumping. Uncovering connections between mechanosensation, sociality, and ASD risk genes may reveal insight on ASD in humans. In a best case scenario, novel ASD treatment targets in the peripheral nervous system may be identified, which unlike most other ASD drug strategies, may safely avoid crossing blood brain barrier.

P28 ***Fusions of autosomes with sex chromosomes are disfavored in mammals***

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Fusing autosomes with sex chromosomes is hypothesized to be advantageous because it can resolve sexual antagonism at autosomal loci. Here, we evaluate the patterns and frequency of autosome sex chromosome fusions across mammals. We test whether fusions involving sex chromosomes are overrepresented in mammals using a comprehensive dataset including 950 mammalian species and novel extensions to stochastic mapping. Our research combines empirical data analysis with simulation studies to estimate the proportion of fusions involving sex chromosomes. Contrary to initial expectations, we find a paucity of fusions that join autosomes and sex chromosomes. We consider alternative evolutionary pressures that might influence the prevalence of fusions involving sex chromosomes, such as dosage compensation, meiotic sex chromosome inactivation, and structural characteristics of mammalian sex chromosomes. Our findings suggest that while sexual antagonism may contribute to the fixation of fusions with sex

chromosomes, the fusion process is intricately linked with broader evolutionary dynamics, demonstrating the complex and likely countervailing selection pressures acting on structural mutations like fusions joining an autosome and a sex chromosome. Our study underscores the need for targeted genomic studies that could distinguish among the possible forces that disfavor fusions of autosomes with sex chromosomes.

P29 *Endangered and Endemic Beetle Genomic Study*

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Habitat fragmentation, driven by natural events, human activities, and environmental changes, disrupts gene flow among populations, leading to genetic isolation. Isolation can result in reduced genetic diversity due to bottlenecks and genetic drift, diminishing populations' adaptive capacities and increasing extinction risks. High-quality reference genomes are essential for genomic studies addressing demography, adaptation, and population structure, thereby informing conservation strategies. This study presents a de novo genome assembly and population genomics analysis of *Cheirotonus formosanus*, an endangered and endemic beetle species from the mountain forests of Taiwan and *Dynastes grantii,* one of the largest and most charismatic beetles in North America. These genomic resources will offer insights into the evolutionary history of these beetles and accelerate future population genetics work that can provide a basis for scientifically informed conservation efforts.

P30 *The* Arabidopsis *telomerase RNP: echoes of mammalian and ciliate enzyme complexes*

Chinmay Phadke, Saundarya Mishra, Jiarui Song, Claudia Castillo Gonzales, Edward Marcotte, Ophelia Papoulas, Dorothy E. Shippen
Texas A&M University

Telomeres are repetitive DNA sequences that cap the ends of chromosomes. Telomeric DNA is synthesized by the telomerase reverse transcriptase, a large ribonucleoprotein (RNP) complex containing a catalytic subunit TERT and an intrinsic RNA template TR. Despite its highly conserved function, the protein composition and biogenesis of telomerase varies widely across different eukaryotic lineages. Previously, we characterized TERT and TR from the flowering plant *Arabidopsis thaliana* as well as two other associated proteins: dyskerin, a core component of human telomerase, and Protection of telomeres 1a (POT1a), a highly conserved telomere end-binding protein. Here we seek to identify and characterize additional telomerase accessory proteins that might be important for RNP maturation or enzyme activity.

Quantitative mass spectrometry (qMS) carried out with plants expressing tagged AtTERT revealed AtLa1, a genuine La protein, and a member of a class of RNP maturation factors known to interact with the 3'UUU tail of pol III transcripts. Notably, the La-domain protein p65 is a core component of the Tetrahymena telomerase enzyme. Unexpectedly, however, our qMS experiment failed to uncover dyskerin or AtPOT1a. To examine the in vivo role of AtLa1 in telomere biology, we obtained plants that overexpress AtLa1 (expression driven from a strong 35S CaMV promoter) or are deficient in AtLa1. Overexpression of AtLa1 did not significantly stimulate telomerase activity, indicating that AtLa1 is not limiting for telomerase enzyme activity. Because AtLa1 is essential for embryogenesis, we created inducible knockdown mutants using an estradiol-inducible

RNAi system. Experiments are underway to determine if AtLa1 is required for enzyme activity or AtTR stability.

In parallel, we conducted biochemical experiments to study AtLa1 interactions with telomerase. Electrophoretic Mobility Shift Assays (EMSA) revealed AtLa1, like the ciliate La protein, binds AtTR. Binding does not require the evolutionarily conserved pseudoknot (PK) and template region, but it does require the terminal 3' UUU and the 3-way junction. Intriguingly, dyskerin engages this same region of AtTR, suggesting that dyskerin and AtLa1 may compete for binding AtTR in vivo. We are now testing this hypothesis. Taken together, these experiments may yield new insight into the evolution and biogenesis of the plant telomerase enzyme.

P31 *Optimization of an in vitro Model to Study HIV Production in Human Pulmonary Artery Smooth Muscle Cells*

Karsyn Clouse, Amanda Garcia, Sharilyn Almodovar
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Pulmonary arterial hypertension (PAH) is a potentially fatal condition characterized by changes in pulmonary vasculature, increased vascular resistance in the pulmonary artery, and eventual right heart failure. Human pulmonary vasculature contains human pulmonary arterial endothelial cells (HPAEC) and pulmonary arterial smooth muscle cells (PASMC), which regulate vascular tone. People living with Human Immunodeficiency Virus (PLWH) are more likely to develop PAH relative to the population without HIV. PASMCs are known to have two different phenotypes — contractile or synthetic — but little is understood about which phenotype exhibits greater HIV production. Additionally, not much is known about the effects of angiotensin II, a vasoconstrictor, on the vasoconstriction of pulmonary arterial cells. The purpose of this study is to measure the effect of drug treatment duration on biomarkers of vasoconstriction in human pulmonary arterial cells. This study is part of a broader effort to optimize an in vitro model of the constrictive PASMC phenotype for the purpose of determining which PASMC phenotype is associated with higher HIV production.

To quantify the role of angiotensin II pulmonary vasculature, PASMC and HPAEC were co-cultured and treated with 100 nM angiotensin II with dimethyl sulfoxide (DMSO). Cells were lysed for RNA at different timepoints; the cDNA was used in qPCRs for ITPR1 and MKI67, markers of vasoconstriction and proliferation respectively. Angiotensin II had a significant effect on inducing vasoconstriction at 0 and 30 minutes and on inducing proliferation at 4, 24, and 48 hours of drug exposure. These results suggest that angiotensin II is effective at inducing vasoconstriction in PASMCs and that PASMCs respond to vasoconstriction with a proliferative response.

P32 *Deciphering the Roles of Petunia SMAX1 Isoforms in the KAI2-Mediated Signaling Pathway*

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Plants release volatile organic compounds (VOCs) to communicate with microbes, insects, and other plants as well as between different tissues within a plant. Terpenoids, one class of VOCs, act like hormones to influence reproductive organ development. Specifically, the sesquiterpene (-)-germacrene D is emitted from developing tubes of petunia flowers and accumulates in the stigma

where it is perceived by a member of the intermediate clade of karrikin-insensitive alpha/beta hydrolase receptors, PhKAI2ia. The signaling cascade that follows is distinct, with some similarities to the canonical karrikin signaling pathway that acts through the Skp1-Cullin-F-box (SCF) E3 ubiquitin ligase complex, including the F-box protein MORE AXILLARY GROWTH 2 (MAX2), as well as the ubiquitination and degradation of the transcriptional corepressor, SUPPRESSOR OF MAX2 1 (SMAX1). Interestingly, petunia has two MAX2s that both interact with PhKAI2ia; however, while it also contains two SMAX1s, only SMAX1a degradation is induced by the volatile signal. This raises the question of the differential physiological roles of the two SMAX1s in planta. In silico protein analyses predicted several noteworthy differences in primary sequence and protein structure between SMAX1a and SMAX1b, primarily in the domains essential for KAI2-mediated degradation. We hypothesize that these structural differences between the two proteins are key determinants in their role and determine specificity of downstream KAI2-mediated signaling response(s). This study aims to identify the biological impact of these structural differences and elucidate the SMAX1-dependent signal transduction steps in the PhKAI2-mediated signaling pathway(s).

P33 *Investigating the Role of a Specific CAF Population in Mammary Tumorigenesis*

Chris Teichmann, Tapasree Roy Sarkar
Texas A&M University

Breast cancer is a leading cause of cancer deaths worldwide, with about 670,000 deaths reported in 2022. The tumor microenvironment is a culmination of cell types including immune cells, the extracellular matrix, blood vessels and stromal cells such as cancer-associated fibroblasts (CAFs), which help in stabilization of the tumor and the development of cancer. CAFs play a crucial role in cancer cell survival, proliferation, and evasion through their release of cytokines and chemokines. By using single-cell RNA-sequencing, our preliminary study showed that a specific CAF population (S100a4+) is increased with the progression of tumor. This study aims to functionally characterize S100a4 CAF population and to investigate the molecular mechanism underlying S100a4+ mediated tumor progression.

P34 *Investigating DNA methylation patterns in the* **pgm2Δ** *mutant using Oxford Nanopore technology*

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Austin College

In *Saccharomyces cerevisiae*, the enzyme phosphoglucomutase (PGM) is responsible for the interconversion of glucose-1-phosphate (G1P) and glucose-6-phosphate (G6P). The gene *PGM2* encodes for the major isoform of this enzyme. Previous research has shown that yeast lacking *PGM2* exhibit several defective phenotypes when grown on galactose-containing media including slow growth and increased Ca2+ uptake and accumulation. Epigenetic modifications, such as DNA methylation, play an important role in regulating gene expression by altering chromatin accessibility. Although ubiquitous in most mammals, DNA methylation was considered to be absent in many lower order eukaryotes including *S. cerevisiae*; however, recent publications that utilized gas chromatographic methods or Oxford Nanopore sequencing suggest that *S. cerevisiae* is capable of epigenetic DNA methylation at very low occurrence. Using Oxford Nanopore sequencing, Dorado basecaller, and computational tools such as Modkit and Nanopolish, the occurrence and location of DNA methylation were compared between *pgm2*Δ and wild type strains on both glucose and galactose containing media. Preliminary results indicate very low rates of

cytosine methylation with minimal differential methylation between strains and media conditions. Between 4 and 10 methylation sites were found on the mitochondrial genome between strains and media types suggesting that *S. cerevisiae* has some capacity to methylate mitochondrial genetic material despite having no known methyltransferase.

P36 *Investigating the Ability of Foxo1 to Maintain Stem Cells*

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The University of Texas Rio Grande Valley

Background: Our group discovered that FOXO transcription factors drive stem gene expression in cancer to promote aggressiveness. Work by our group and others demonstrated that FOXO factors universally maintain stem cells including in cancer, embryonic, hematogenic and neuronal contents. Our current efforts are delineating the molecular underpinnings by which FOXO factors halt differentiation to maintain stem cells. In this project, we are employing myoblasts as a valuable model to examine how Foxo1 maintains stem cells. Foxo1-regulated genes in myoblasts closely parallel its targets in glioblastoma and basal breast cancer stem cells, including *Leukemia Inhibitory Factor, Lif*, encoding a cytokine that prevents differentiation. Understanding how Foxo1 maintains stem cells is crucial, as it holds the potential to uncover new therapeutic options that could target the fundamental biological processes involved in cancer progression and chemotherapeutic resistance.

Methods: RNAi was performed on C2C12 myoblasts cells to create *Foxo1* knockdown and control lines, followed by assessment of target genes involved in differentiation, proliferation, and muscle fiber types using qRT-PCR. Fluorescent microscopy was utilized to investigate the structural differences in actin filaments and nuclei between Foxo1 RNAi cells and the control group. Our initial work, including investigating candidate genes using qRT-PCR. We are currently taking genomics approaches to investigate the role of Foxo1 in myoblast/stem cell differentiation.

Results: In Foxo1 RNAi cells, there was a notable decrease in *Lif* expression, suggesting differentiation. Downregulation of genes like *Igfbp1, Socs1*, and *Socs2* indicates possible direct or indirect activation by Foxo1, with implications for cell growth and cytokine signaling. Additionally, downregulation of *Pepck* and the modulation of energy metabolism pathways suggest altered metabolic states. The downregulation of *Stat1* and *Wnt3* implies disruptions in pathways that promote proliferation to favor differentiation. This aligns with observations of increased nuclei and actin filament abundance in Foxo1 RNAi cells, reflecting enhanced muscle differentiation and myotube formation.

Conclusion: Foxo1's involvement in regulating cellular dynamics through gene expression is complex and dynamic, impacting differentiation and proliferation, with notable changes in the cytoskeleton facilitating myoblast fusion and differentiation. Gaining insights into the relationship between Foxo1 and target genes will clarify potentially conserved roles that determine the differentiation status of stem and progenitor cells. We anticipate that this model system will allow us to glean fundamental mechanisms that maintain stems cells to ultimately target cancer stem cells, which are known to trigger recurrence and chemotherapeutic resistance.

P38 ***From Micro to Macro: Avian Chromosome Evolution is Dominated by Natural Selection***

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Texas A&M

Birds display striking variation in chromosome number, defying the traditional view of highly conserved avian karyotypes. However, the evolutionary drivers of this variability remain unclear. To address this, we fit probabilistic models of chromosome number evolution across birds, enabling us to estimate rates of evolution for total chromosome number and the number of microchromosomes and macrochromosomes while simultaneously accounting for the impact of other evolving traits. Our analyses revealed higher rates of chromosome fusion than fission across all bird lineages. Notably, much of this signal was driven by Passeriformes, where migratory species showed a particularly strong bias towards fusions compared to sedentary counterparts. Furthermore, a robust correlation between the rearrangement rates of microchromosomes and macrochromosomes suggests that genome-wide processes drive rates of structural evolution. Additionally, we found that lineages with larger population sizes exhibited higher rates of both fusion and fission, indicating that positive selection plays a dominant role in driving divergence in chromosome number. Our findings illuminate the evolutionary dynamics of avian karyotypes and highlight that, while the fitness effects of random structural mutations are often deleterious, beneficial mutations may dominate karyotype divergence in some clades.

P39 ***Uncovering RNAi and chromatin modifying pathway co-regulation that protects germ cell identity during heat stress***

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Robust gene regulation is important for cellular homeostasis, particularly during stressful environmental conditions such as elevated temperatures that adversely affect germ cell identity and fertility. RNA interference (RNAi) pathways and chromatin modification pathways are both important for gene regulation, resulting in proper cellular and developmental programs. We seek to understand how RNAi pathway and chromatin modification pathways collaborate in maintaining germ cell identity and fertility under stressful conditions in *C. elegans*. Work from our lab and others found that nuclear RNAi mutants experience a mortal germline (Mrt) phenotype and exhibit sterility after several generations of being exposed to heat stress (25˚C). However, why each mutant reaches sterility at a different generation remains unclear. Multi-omic analyses (mRNA-seq, small RNA-seq, and Assay for Transposase-Accessible Chromatin (ATAC)-seq) from two RNAi mutants (*mut-16(pk710)* and *hrde-1(tm1200)*) mutants showed the onset of the Mrt phenotype corresponds with aberrant expression of somatic and spermatogenesis-related genes within the germline that correlated with genome-wide increase in chromatin accessibility, resulting in loss of germ cell identity. Previous studies carried out in *D. melanogaster* have shown similar aberrant gene expression and loss of germ cell identity in mutants for a factor that links the small RNA and chromatin modifying pathways. This suggests the mechanisms by which RNAi and chromatin modifying pathways co-regulate gene expression to maintain germ cell identity may be evolutionarily conserved. Here, we aim to first establish if the onset of heat stress-induced sterility in each of six RNAi and chromatin modifying pathway mutants is triggered by defects in oocytes and/or sperm. Then we will determine the same subset of somatic and spermatogenesis genes are dysregulated specifically during the generation at which heat stress-induced sterility manifests in each mutant. With future experiments that assess changes in the chromatin landscape,

we will advance our understanding of how RNAi mechanisms and chromatin-modifying pathways co-regulate gene expression, preserving germ cell identity and overall fertility during stress.

P40 *Perinuclear Germ Granules as Regulators of RNAi Pathway Fate*

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RNA interference (RNAi) pathways are crucial for maintaining gene regulation by silencing transposable elements and ensuring proper endogenous gene expression in the germline. Perinuclear germ granules serve as hubs for RNA-induced silencing complex (RISC)-mediated mRNA processing, including the amplification of small RNAs required for robust target silencing. In *C. elegans*, distinct branches of the RNAi pathway either repress or promote gene expression, and proper sorting of RNAs between these pathways is essential for fertility. However, the molecular mechanisms governing RNA sorting and pathway selection remain poorly understood. In *D. melanogaster*, it has been shown that a transcript's proximity to the piRNA machinery in nuage is sufficient to trigger piRNA production, suggesting that transcript processing may be influenced by subcellular localization within germ granules. This raises the possibility that RNAi-mediated transcript fate is not solely dictated by small RNAs but also by the spatial organization of RNAi factors. We hypothesize that the sorting of transcripts into distinct RNAi branches is mediated by their shuttling along specific pathways between perinuclear germ granules. To test this hypothesis, we have adapted an in vivo heterologous RNA-to-protein tethering assay for germline-specific expression in *C. elegans*. This system allows us to tether a reporter transcript to the core components of the germ granules, enabling targeted recruitment of transcripts to germ granules and systematic assessment of the impact on transcript processing. Our preliminary results reveal that recruitment of a reporter transcript to distinct germ granules elicits different regulatory outcomes, suggesting that perinuclear granules are not passive sites of RNA processing but actively contribute to transcript fate determination. To further characterize these effects, we are performing quantitative RT-PCR to measure reporter transcript levels and small RNA sequencing to assess the initiation of small RNA production. If recruitment triggers reporter transcript silencing, we will use chromatin profiling to assess changes in the epigenetic landscape at the reporter's genomic locus. These experiments provide a framework for understanding how spatial compartmentalization within germ granules influences RNAi-mediated gene regulation. Ultimately, understanding these mechanisms will shed light on the broader principles of RNA-based gene regulation and may provide insights into fertility regulation and RNA dysregulation in disease contexts.

P41 *Uncovering Key Regulators for the Mitochondrial Ethanol and Stress Response Element Pathway*

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Mitochondria have long been oversimplified as "the powerhouse of the cell" when in reality these organelles play key roles in regulating a variety of important biochemical processes that determine cellular health. Mitochondrial dysfunction is at the core of a series of metabolic, neurodegenerative, and cardiovascular diseases, including cancer, and also plays a deterministic role in healthy aging. To maintain mitochondrial homeostasis, multicellular organisms have developed multiple surveillance mechanisms and pathways. A variety of processes, including

mitochondrial bioenergetics and proteostasis are constantly surveyed by feedback signaling pathways that coordinate gene expression between the mitochondrial and nuclear genomes. The most studied of these is the mitochondrial unfolded protein response (*UPR*mt), which responds to proteotoxic stress. Previous research using Caenorhabditis elegans has shown that another key pathway for mitochondrial surveillance, the evolutionarily-conserved Ethanol and Stress Response Element, is activated in response to reactive oxygen species (ROS), liquid-based infection with *Pseudomonas aeruginosa* (LK-Pa), and mitochondrial damage. The ESRE pathway acts through a DNA element comprised of a conserved, 11-nucleotide motif (TCTGCGTCTCT) found in the promoter region of various genes. Despite efforts, regulation of the ESRE network remains largely uncharacterized.

C. elegans is a model nematode with several attractive features for conducting genetic studies. Its small size and short generation time facilitate high-throughput experimentation as well as substantial automation. Additionally, its transparent body allows for in vivo fluorescence microscopy. Finally, *C. elegans* shows strong genetic conservation with mammals, improving research translation to humans.

We found 22 potential key regulators involved in mitochondrial ESRE pathway activation by conducting a primary screen on a library of transcription factors and kinases using the transgenic worm line *3XESRE*::GFP, which carries three tandem repeats of the 11-nucleotide *ESRE* motif fused to a green fluorescent protein, giving us a convenient readout for *ESRE* activation. To assess the specificity of these 22 hits to the ESRE pathway, we conducted a secondary screen in which we induced two other mitochondrial mitochondria surveillance pathways through double knockdown of metalloprotease spg-7 (activates *MAPK*mt and *UPR*mt) and our 22 hits. Worm reporter strains *Phsp-6*::*GFP* (SJ4100) and *Ptbb-6*::*GFP* (SLR115) were used to check for activation of the *UPR*mt pathway and *MAPK*mt cascade, respectively. Similar to the primary screen, activation of the latter pathways was visualized using GFP. This work aims to identify a regulatory cascade for *ESRE* in order to better understand mitochondrial surveillance and prevent or treat mitochondrial dysfunction.

P43 ***Phylogeography of* Camponotus modoc *and its Blochmannia endosymbiont in Western North America and characterization of a tri-lineage hybrid zone.***

Swapnil Boyane, Joseph Manthey
Texas Tech University

Hybridization is a common evolutionary phenomenon that allows two or more diverging or related species to interbreed and produce fertile hybrids. While hybridization between two species is well documented, tri-lineage hybridization is relatively uncommon and often results in increased genetic diversity. These hybrid zones are considered natural laboratories for understanding evolutionary processes like natural selection and gene flow. The Carpenter ants (*Camponotus spp.*) represent one of the most speciose genera of ants, with 11 species found in North America. In this study, we used 151 whole-genome sequences to investigate phylogeographic patterns in *Camponotus modoc* and its endosymbionts and to explore tri-lineage hybridization between *C. modoc* (East), *C. modoc* (West), and *C. herculeanus*, looking for evidence of the presence of F1 or advanced generations.

Using principal components analysis (PCA) and ADMIXTURE to estimate genetic structure, we identified three distinct genomic clusters, with admixed individuals positioned centrally. To estimate patterns of gene flow, we used Estimation of Effective Migration Surfaces (EEMS), which indicated a corridor for gene flow in the *C. modoc* (West) population. Next, observed heterozygosity (Ho) was calculated as a measure of genetic diversity; the highest genetic diversity was observed in admixed individuals, while the lowest Ho was recorded in *C. modoc* (East). Finally, we assessed whether hybrids belonged to F1, F2, or advanced generations. Our results revealed the presence of F1 hybrids and a few backcrossed colonies. Overall, our analysis suggests phylogeographic codiversification in *C. modoc* and confirms tri-lineage hybridization among *Camponotus* ants.

P44 *MDT-15/MED15 regulates innate immunity and mitochondrial surveillance via fatty acids*

Alicia Chan, Lois Armendariz, Elissa Tjahjono, Meggie Wang, Natalia Kirienko
Rice University

Multicellular organisms are constantly interacting with biotic and abiotic stressors that threaten their homeostasis. To maintain cellular homeostasis, they have evolved a series of conserved defense networks, which provide constant cellular surveillance. We focus on mitochondrial surveillance pathways in response to disease and infection, which are very notable given the mitochondria's roles in energy production, lipid metabolism, ROS production, and innate immunity. Mitochondrial dysfunction is at the core of a series of metabolic, neurodegenerative, and cardiovascular diseases, including cancer, therefore understanding these mitochondrial surveillance pathways is crucial.

Previous research in *Caenorhabditis elegans* suggests that lipid metabolism is involved in host response to infection. Anderson et al. showed that the monounsaturated oleic acid is required to activate innate immunity. Previously, the Kirienko lab identified a set of small molecule immune stimulants that increased *C. elegans* survival during the exposure to *Pseudomonas aeruginosa* in liquid (LK-Pa). Preliminary data of *C. elegans* treated with LK56, one of these molecules, showed significant enrichment of lipid metabolism genes, reinforcing a connection between lipid metabolism and innate immunity. Previous studies have shown that the evolutionarily conserved mediator subunit MDT-15/MED15 plays a role in initiating an immune response against Gram-negative pathogens, and it is required for the LK56-mediated rescue. Furthermore, MDT-15/MED15 is also an important regulator for lipid metabolism, as it regulates *fat-6* and *fat-7*: two fatty acid desaturases that convert stearic acid to oleic acid in *C. elegans'* polyunsaturated fatty acid synthesis (PUFA) pathway. However, the mechanism by which lipid metabolism modulates host immunity remains unknown.

We set out to characterize host lipid metabolism pathways involved in the defense against infection with *P. aeruginosa*. Previous research in our lab established that the siderophore pyoverdine is produced in LK-Pa and damages *C. elegans* mitochondria, resulting in a hypoxic crisis and eventual host death. To mitigate mitochondrial damage, *C. elegans* activates the *Ethanol Stress and Response Element* (*ESRE*), a mitochondrial surveillance pathway. We saw that MDT-15 and its downstream effectors, as well as Box C/D snoRNPs (small nucleolar ribonucleoproteins) were required for *ESRE* activation. Interestingly, supplementation of downstream fatty acids of *C. elegans'* PUFA pathway rescued ESRE activation in their knockdowns. Additionally, we saw that

mdt-15, *fat-6*, and *fat-7* RNAis led to decreased worm survival during LK-Pa, indicating their role in *C. elegans'* host defense. This work will allow us to find ways to modulate *ESRE* during infection and disease in order to benefit the host.

P46 *RNA-Seq Analysis to Identify Differentially Expressed Genes in* Saccharomyces cerevisiae pmr1Δ *Mutants*

Shambhavvi Anand, David P. Aiello
Austin College

In *Saccharomyces cerevisiae*, the interconversion between glucose-1-phosphate (G1P) and glucose-6-phosphate (G6P) is catalyzed by phosphoglucomutase 2 (Pgm2p). The deletion of *PGM2* (*pgm2*Δ) results in a slow growth phenotype and has been associated with changes in the G1P to G6P ratio, as well as increased calcium uptake and accumulation when grown on galactose-containing media. Calcium homeostasis defects in *S. cerevisiae* activate the calmodulin-calcineurin pathway, regulated by several proteins, including the Ca2+-ATPase Pmr1p essential for calcium and manganese ion transport into the Golgi apparatus. Previous research has indicated that the deletion of *PMR1* (*pmr1*Δ) results in increased Ca2+ accumulation and the upregulation of genes by the *Tcn1p/Crz1p* transcription factor. RNA sequencing (RNA-seq) was performed to identify differentially expressed genes in *pmr1*Δ strains relative to wild-type cells grown in glucose-containing media. Analysis will focus on genes associated with calcium signaling, cellular stress responses, and potential targets of *Tcn1p/Crz1p*. Furthermore, the study will examine whether gene expression changes in *pmr1*Δ strains overlap with those observed in *pgm2*Δ mutants, potentially revealing the mechanisms behind the observed growth defects.

P47 *Cellular Stress Caused by the Removal of HSP26, SLT2, and YAP1 is Not Remedied by the Loss of SPT4 in the* S. cerevisiae pgm2Δ *Mutant*

Marcia Pinto*, Maryam Zeeshan*, David P. Aiello
Austin College

In *S. cerevisiae*, the enzyme phosphoglucomutase (PGM) facilitates the conversion between glucose-1-phosphate (Glc-1-P) and glucose-6-phosphate (Glc-6-P). Studies have shown that strains lacking the major isoform of this enzyme (*pgm2Δ*) develop a variety of defects when grown on galactose-containing media. These defects include an increased unfolded protein response (UPR), sensitivity to heat, cell wall instability, and heightened susceptibility to oxidative stress. To identify mutant alleles that could suppress these defects, EMS mutagenesis was performed and identified mutations in *SPT4* which suppressed *pgm2*Δ defects and completely rescued the UPR induction observed in these strains. To examine whether the rescuing phenotype associated with spt4Δ extends to other stress-related pathways, knockouts of *HSP26*, *YAP1*, *HYR1*, and *SLT2* were constructed in the context of *pgm2Δ* and *spt4*Δ strains. These genes play key roles in several stress response pathways which include heat-shock response, oxidative stress response, and the cell wall integrity (CWI) MAPK pathway, respectively. The data shows the *pgm2Δhsp26Δ* strain displayed no additional sensitivity on galactose or galactose supplemented with cyclosporin A (CsA) upon heat shock. Furthermore, the previously reported lethal phenotype of *pgm2Δslt2Δ* on galactose, in the presence of cell wall stressors ($MnCl_2$ and NaCl), and CsA was confirmed. Triple knockouts with *hsp26Δ*, *slt2Δ*, *yap1*Δ, along with *pgm2*Δ and *spt4*Δ were constructed. Loss of *spt4* in *pgm2Δhsp26Δ* increased the heat shock sensitivity of the double mutant. Additionally, the *spt4*Δ allele did not suppress the lethal phenotype of *pgm2Δslt2Δ*. Regarding *YAP1*, *pgm2*Δ*yap1*Δ, *spt4*Δ*yap1*Δ, and *pgm2*Δ*spt4*Δ*yap1*Δ strains demonstrated lethal phenotypes when grown under

oxidative stress. To examine the role of *SPT4* in the oxidative stress response pathway, total gene knockouts of *HYR1*, an activator of *YAP1*, were constructed. The *spt4Δhyr1Δ* and *spt4Δyap1Δhyr1Δ* strains displayed a normal growth phenotype, including under oxidative stress. These findings suggest that the rescuing phenotype associated with the removal of *SPT4* may not extend to other stress-related phenotypes associated with the *pgm2Δ* mutant.

P48 *Utilizing Third-Generation Sequencing to Identify pgm2Δ Suppressor Mutations*

Pavithra N. Upadhya, David P. Aiello
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Advances in sequencing technology have greatly improved the efficiency of sequencing samples. A relatively newer technology, the Oxford Nanopore Technologies MINion portable sequencing device, has been shown to be versatile in sequencing a variety of samples relatively quickly and inexpensively, but a drawback of the device is its high error rate.

Calcium homeostasis is a highly regulated process responsible for a variety of cellular functions, and defects in calcium homeostasis lead to cellular stress responses related to growth and protein processing, among others. Phosphoglucomutase (Pgm2p) is an enzyme that interconverts glucose-1-phosphate to glucose-6-phosphate in the central metabolism. In *Saccharomyces cerevisiae* strains lacking *PGM2* gene, it was found that the mutant exhibited a high accumulation of glucose-1-phosphate and, concomitantly, a high accumulation and uptake of calcium. While the mechanism for calcium accumulation in the *pgm2Δ* mutant is unknown, it was also previously found that high uptake and accumulation of calcium is most likely due to the change in relative amounts of glucose-1-phosphate and glucose-6-phosphate.

Previous work in the lab has identified 16 candidate strains with mutations that suppress *pgm2Δ* growth defects. One particular gene, *SPT4*, was identified as a suppressor using a plasmid genomic library screen. Another strain containing a suppressor mutation of *pgm2Δ* was sequenced using the Oxford Nanopore Technologies MINion portable sequencing device to determine if the device would significantly expedite the process of successfully identifying similar suppressors of *pgm2Δ* defects. Using sequencing data from the suppressor strain, isogenic parental strains *pgm2Δ* and wild-type strains, and four strains from a tetrad expressing the suppressor phenotype in a 2:2 segregation pattern, data analysis was performed to identify the suppressor mutation in question.

P49 *Analyzing whether altered activity of Pmc1p is responsible for* **S. cerevisiae pgm2Δ** *mutant phenotypes*

Niki M. Hamraei, David P. Aiello
Austin College

Phosphoglucomutase (PGM) is responsible for interconverting glucose-1-phosphate (G1P) and glucose-6-phosphate (G6P) in the yeast *Saccharomyces cerevisiae*. Yeast strains lacking *PGM2*, the major isoform of PGM, exhibit defects in calcium homeostasis, particularly increased calcium uptake into the vacuole, when grown on media utilizing galactose as the carbon source. Previous research has demonstrated that knocking out the gene encoding for the vacuolar calcium ATPase, *PMC1*, partially rescues the calcium defects observed in the *pgm2Δ* mutant, demonstrating a link between Pmc1p function and increased calcium sequestration in this strain. RNA sequencing and qPCR data indicate no altered gene expression of *PMC1* in the *pgm2Δ* mutant. These data suggest hyperactivity of Pmc1p in the *pgm2Δ* mutant may play a role in increased vacuolar calcium uptake.

One known method of Pmc1p regulation is by the v-SNARE Nyv1p through protein-protein interactions. The mechanisms behind Pmc1p regulation are further examined in this study. We found that *NYV1* is alternatively spliced in the *pgm2Δ* mutant grown in galactose media, suggesting the intron-removed variant of *NYV1* is responsible for interactions with Pmc1p. Prior studies predict possible Pmc1p ubiquitinated lysine residues, suggesting ubiquitination and degradation as a possible method of protein regulation. Additionally, the protein is predicted to have phosphorylated serine and threonine residues, suggesting protein activity may be regulated by phosphorylation. However, neither degradation nor phosphorylation of Pmc1p has yet been studied directly. This study seeks to determine if altered protein degradation, mediated by ubiquitination, or protein activity, mediated by phosphorylation, leads to hyperactivity of Pmc1p resulting in the altered calcium homeostasis phenotypes in yeast *pgm2*Δ mutants.

P50 ***Identifying Spt4-regulated genes contributing to spt4Δ-mediated rescue in*** **S. cerevisiae**

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Calcium homeostasis is an integral part of cellular survival and imbalances in calcium levels can lead to the activation of cellular stress responses. Protein folding is also vital for the function of cells and misfolded proteins can cause loss of protein function. The unfolded protein response helps to refold proteins in the ER and is mediated by Hac1, a transcriptional activator. In *Saccharomyces cerevisiae*, the PGM enzyme (phosphoglucomutase) mediates the interconversion of glucose-1-phosphate and glucose-6-phosphate. This interconversion is important for carbohydrate metabolism in eukaryotic organisms to use galactose as a carbon source. *PGM2* is responsible for 90% of PGM activity and *pgm2*Δ mutants are seen to have Ca2+ homeostasis defects and increased unfolded protein response (UPR). *HAC1* when knocked out in conjunction with *pgm2*Δ strains, exhibits a lethal phenotype in galactose containing media suggesting a requirement for UPR in the *pgm2*Δ mutant. Previous work in the Aiello lab on the *pgm2*Δ strain revealed spt4Δ mutants to be a suppressor for *pgm2*Δ-related growth defects. When SPT4 was knocked out of the genome in the *pgm2*Δ*hac1*Δ strain, a similar rescue phenotype was observed. In addition, the *hac1*Δ mutant is lethal with tunicamycin (Tm), an ER stressor, added to the media, and in conjunction with *spt4*Δ, this lethal phenotype was suppressed. This study uses RNA-sequencing analysis to investigate how the loss of SPT4 is able to rescue these growth defects.

P51 ***Genetic Susceptibility Of Elevated Serum Alanine Transaminase And Liver Dysfunction In A/J Mice Fed A Japanese Diet***

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The Japanese diet is associated with populations that have healthy, long lifespans. Although at the population level this is a healthy diet, little is known on whether all individuals will benefit from it. To determine whether the Japanese diet is a universally healthy diet, four strains of mice were provided a Japanese diet for six months. At the end of the exposure, mice were clinically analyzed for metabolic and other health effects. We found that all strains had improved health based on clinical measures compared to an American diet except A/Js. A/J mice fed a Japanese diet showed elevated serum alanine transaminase (ALT) levels that suggest liver damage, which was then confirmed through histological analysis.

To further investigate the mechanism driving this increase in serum ALT levels in A/J mice fed a Japanese diet (high carbohydrate, low fat contents), additional cohorts of A/J and C57BL/6J mice (with the latter being used as a control group) were set up and exposed to either a Japanese diet, an American diet or a control diet. These mice were then assigned to dietary interventions planned to last either 3, 6 or 9 months in length. This design will allow to investigate how different lengths of dietary interventions may influence serum ALT levels and health outcomes. The 6- and 9-month dietary intervention cohorts are in progress, while the 3-month dietary intervention cohorts will follow. Body composition, metabolic rate, and serum hepatic enzymes will be assessed during and at the conclusion of the dietary intervention, followed by histological analysis to confirm any potential liver damage.

We hypothesize that variations in genetic background among different inbred strains of mice impact diet-induced liver dysfunctions. These findings could advance the field of precision nutrition and reinforce the notion that dietary interventions may not be a one-size-fits-all approach.

P52 *Studies on structural and molecular mechanisms of transcription factor NKX2-2 and its pathogenic mutations in gene regulation*

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Diabetes and obesity are the two significant health problems in South Texas. Many efforts are being made to understand the underlying pathogenesis including genetic and non-genetic factors to develop potential therapies and prevention strategies. This study aims to elucidate the structural and molecular mechanisms of transcription factor NKX2-2 and its disease-inducing mutations in regulating target genes implicated in diabetes and obesity. NKX2-2 is a member of the mammalian Nk2 homeobox transcription factor family. It is expressed in the ventral CNS and the pancreas and plays crucial roles in the specification and differentiation of pancreatic endocrine cells in the growing embryo. Several mutations of *NKX2-2* have been identified and found causing congenital diabetes, infantile obesity, and developmental delays. However, the underlying pathogenesis is still unclear. To get structural insight into gene regulatory functions, the full-length structures of wild-type and mutations of NKX2-2 were computationally generated by protein structure prediction programs for structural analysis. Moreover, the homeodomain gene of NKX2-2 was subcloned to make a recombinant DNA plasmid and expressed in E. coli. Recombinant NKX2-2 homeodomain proteins were purified by affinity and size exclusion chromatography columns and used for NMR structural determination. In addition, the interaction studies between NKX2-2 homeodomain and sequence-specific DNA duplex were conducted by NMR titration and the results were used for generating a complex by computational docking program. As a result, this study provides structural elucidation for functional understanding of NKX2-2 gene regulation and its mutations included pathogenic developmental pathways for identification of therapeutic targets.

P53 *Elucidating the mechanisms of α-Synuclein-lipid interactions using site-directed mutagenesis*

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α-Synuclein (α-syn) is a small protein that is involved in cell vesicle trafficking in neuronal synapses. A progressive aggregation of this protein is the expected molecular cause of Parkinson's disease, a disease that affects millions of people around the world. A growing body of evidence

indicates that phospholipids can strongly accelerate α-syn aggregation and alter the toxicity of α-syn oligomers and fibrils formed in the presence of lipid vesicles. This effect is attributed to the presence of high copies of lysines in the N-terminus of the protein. In this study, we performed site-directed mutagenesis and replaced one out of two lysines at each of the five sites located in the α-syn N-terminus. Using several biophysical and cellular approaches, we investigated the extent to which six negatively charged fatty acids (FAs) could alter the aggregation properties of K10A, K23A, K32A, K43A, and K58A α-syn. We found that FAs uniquely modified the aggregation properties of K43A, K58A, and WT α-syn, as well as changed morphology of amyloid fibrils formed by these mutants. At the same time, FAs failed to cause substantial changes in the aggregation rates of K10A, K23A, and K32A α-syn, as well as alter the morphology and toxicity of the corresponding amyloid fibrils. Based on these results, we can conclude that K10, K23, and K32 amino acid residues play a critical role in protein-lipid interactions since their replacement on non- polar alanines strongly suppressed α-syn-lipid interactions.

P54 ***Chaos in the Genome: An Educational Genome Evolution Video Game Development Project for Middle and High School Students***

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This project aims to develop a fun and engaging supplementary tool for teachers to utilize in helping middle and high school students understand and apply genome evolution concepts in and outside the classroom. Understanding and applying concepts of genome evolution can be challenging for both instructors and middle and high school students. This project aims to develop a fun and motivating educational tool to make genome evolution tangible for students. Using the style of a deck-building strategy card game, players can interact with an organism's genome as it evolves. This is relevant because it combines a unique blend of genetics, genomics, computer science, education, and game design. The game's intended audience is middle and high school students, teachers/mentors, and parents/guardians. However, the game aims to be accessible to students of all ages and learning abilities. It is meant to be a supplementary tool that can be accessed in and outside of the classroom. The anticipated timeline for the project begins with outlining the logic of the game and storyboarding before transitioning into building a playable paper prototype to test the logic and mechanics of the game. Currently, the game is in the storyboard phase. The focus is on the theme of the game, the mechanics, and the basic objects/attributes of the game. The next steps will be to build simple prototypes to test the specific mechanics of the game before developing an in-depth paper prototype for initial playtesting.

P55 ***Phylogenomic analyses and meta "omic" search tools help clarify the evolution and ecology of a divergent lineage of free-living and fecal-associated protists (Sainouroidea, Rhizaria)***

Aaron De Souza, Gabriel A. Schuler, Monika Wiśniewska, Martin Kolísko, Jeffery D. Silberman, Matthew W. Brown Alexander K. Tice
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Sainouroidea, is a clade of protists that belongs to the eukaryotic assemblage Rhizaria. Sainouroidids exhibit remarkable genetic and phenotypic heterogeneity. Members can be flagellates or amoeboid organisms; some are strictly unicellular, while others can be facultatively multicellular, and one member even has an alternative nuclear genetic code. Sainouroidids can be found in marine, freshwater, and terrestrial environments, as well as the gut contents and feces of

various animals. A well-resolved phylogeny and data from non-primer biased eDNA studies are crucial first steps in developing hypotheses regarding the evolutionary history of diverse traits and lifestyles exhibited by sainouroidids. The small subunit ribosomal RNA (SSU RNA) gene is the most used single gene marker for molecular phylogenetic and amplicon-based eDNA studies in protists. However, the exact phylogenetic placement of Sainouroidea within Rhizaria as well as their presence in diverse environments is obscured by the highly divergent nature of this marker in members of this clade. To date, multigene phylogenies have done little to resolve this issue due to limited genomic data from sainouroidids and close relatives. To help resolve the position of sainouroidea within Rhizaria as well as the internal relationships between members of the group, we generated novel transcriptomic data from five sainouroidid taxa. We use these data to perform multigene phylogenomic analyses of Rhizaria, including Sainouroidea. Additionally, to better understand the ecological niche range and genetic diversity of sainouroidids we query publicly available meta "omic" datasets using the recently developed tool NCBI tool "PebbleScout" for the presence of diverse sainouroidids.

P56 *Investigating the Role of the Conserved Notch Pathway in Glioblastoma Cells*

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Glioblastoma accounts for half of all malignant brain tumors today, yet the survival rate remains only about 6.9%, with an average survival length of 12 months. These characteristics of poor prognosis categorize glioblastoma as a Grade IV cancer—fast-growing and highly aggressive. Evidence gathered in our lab suggests FOXO transcription factors drive the NOTCH signaling pathway in glioblastoma cells.

Evolutionarily conserved FOXO transcription factors—FOXO1, FOXO3, and FOXO4—play crucial roles in cell metabolism and stress response. Notably, these factors sustain stem cells such as embryonic, hematopoietic, cancer, and neural. FOXO4 localizes to the nucleus in a series of glioblastoma cell lines, including U87MG. Deletion of FOXO4 downregulates Notch pathway genes in U87MG cells, including *NOTCH1*, *NOTCH3*, *HEY1*, and *HES1*.

In this project, we are examining which NOTCH protein (NOTCH1 or NOTCH3) drives *HES1* and *HEY1* (and other NOTCH target genes) downstream of FOXO4 in glioblastoma cells. NOTCH1 supports neural stem cell maintenance and T-cell lineage, whereas NOTCH3 regulates vascular homeostasis in smooth muscle function. Our goal is to ascribe which facets of FOXO4 function in glioblastoma require NOTCH1 and/or NOTCH3. Delineating the molecular mechanisms employed by FOXO4 in glioblastoma to promote gene expression and cancer stem cell maintenance will enable researchers to rationally design novel targeted therapies for this aggressive cancer.

P57 *Mosaic Trisomy 10 Caused by Pericentric Inversion of Chromosome 10: A Novel Case of Prolonged Life Span*

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INTRODUCTION: Trisomy 10 is an incredibly rare genetic abnormality that is usually incompatible with life. There are less than 40 published cases and specifically less than 10 published cases of mosaicism Trisomy 10. Clinical features can include dysmorphisms such as

hypertelorism, micrognathia, and unilateral talipes, growth and mental delays, cryptorchidism, furrows in the plantar and palmar regions, bilateral ectrodactyly, renal anomalies, and congenital heart defects. Currently, case reports disclose life spans from 37 days to 5 years and 4 months, as well as one case report of a patient with Trisomy 10 who was alive at 16 years. Here we report a novel case of pericentric inversion of chromosome 10 who lived to 20 years of age. CASE DETAILS: The patient presented with spastic tetraplegic cerebral palsy, microcephaly, hypertonia, calculus of kidney and ureter, glomerular kidney disease, neurogenic bladder, osteoporosis, scoliosis, muscle contractures, hypomotor seizures, malnutrition, and dysmorphic features. Genetic testing revealed a pericentric inversion of chromosome 10. The patient survived to age 20, and cause of death was fatal cardiac arrhythmia. CONCLUSIONS: Here we report a novel germline mutation leading to a trisomy pericentric inversion of chromosome 10, which is potentially of germline origin as the paternal aunt presented with the same trisomy. These findings are novel and will better help the understanding of future cases of the rare disease and its presentation.

P59 *Sema6a Haploinsufficiency Causes A Novel Autosomal Dominant Neurodevelopmental Disorder With Incomplete Penetrance*

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SEMA6A is a transmembrane protein that is expressed in the developing central nervous system and has been shown to play a role in axon guidance and cell migration. Consistent with this role, Sema6A null mice have abnormal forebrain and retinal inner plexiform morphology. In humans, SEMA6A haploinsufficiency is predicted to be deleterious, but the phenotypes associated with loss of SEMA6A function have not been documented. We predicted SEMA6A haploinsufficiency to be deleterious. The purpose of this study was to document the phenotypes associated with loss of SEMA6A function in humans. Here we describe 7 individuals who underwent genetic testing that revealed putatively damaging variants affecting *SEMA6A*. Four had microdeletions that included *SEMA6A* and three carried single nucleotide variants (SNVs)—one splice site variant and two coding for single amino acid changes. All of these individuals (100%) had neurodevelopmental phenotypes that included developmental delay (71%), intellectual disability (57%), autism spectrum disorder (29%), behavioral problems (57%), and/or ADHD (29%). Behavioral problems documented in this cohort included oppositional defiant disorder, mood swings, tantrums, anger, acting out, and aggressiveness. The only other recurrent phenotypes seen in this cohort were prominent brow/forehead (28%) and megacephaly (28%). Two of the *SEMA6A* deletions were inherited from asymptomatic mothers. We conclude that *SEMA6A* haploinsufficiency causes a novel autosomal dominant neurodevelopmental disorder with incomplete penetrance.

P60 *Epistatic Capacitance: The Adaptive Reservoir of Populations*

Andres Barboza Pereira, Zoya Wani, Heath Blackmon
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Traits under strong selection often show minimal additive variation but retain significant epistatic variation. This epistatic variation acts as an “adaptive capacitor,” converting to additive variation when selection shifts or bottlenecks fix alleles, revealing new genetic potential. Factors such as

selection strength, the type of epistasis, and the number of genes underlying a trait influence equilibrium epistatic variation. In this project, we will explore these dynamics through a forward-time population genetics approach. Our goal is to determine which traits can quickly adapt to new selection pressures and which are less responsive to sudden environmental changes.

P62 *Integrating Patient Genomics and Wound Microbiomes into a Structural Equation Model for Healing Time*

Jacob S. Ancira, Khalid Omeir, Rebecca Gabrilska, Craig Tipton, Clint Miller, Joseph Wolcott, Todd D Little, Caleb D. Phillips
Texas Tech University

Background: Chronic non-healing wounds are a national epidemic. Variation among patients in healing outcomes is multifaceted, yet there has been little progress integrating the many potentially important variables into a predictive model. This is unfortunate as being able to identify more difficult to treat wounds early on might indicate the need for personalized intervention. Here, with the goal of providing such a predictive framework, a structural equation model (SEM) integrating patient data from electronic medical records, wound microbiomes, and patients' genomic information was developed to model the chronic wound environment in relation to healing.

Methods: The study was based on 127 chronic wound patients whose wound microbiomes were characterized at initial visit using 16S sequencing, and their genome was characterized at 6.2 million single nucleotide polymorphisms (SNPs) using genotyping arrays and imputation. Developing on work recently reported by our team for the integration of microbiomes into SEM, candidate human genomic regions influential to healing differences were identified through a novel sliding window approach, and identified regions were modeled as latent variables. These genomic latent variables, a wound microbiome latent variable, and various patient and wound data were evaluated for model fit in the SEM.

Results: The final SEM model included four genomic regions, a microbiome latent construct associated with faster healing, *Psuedomonas aerogenosa*, smoking, wound volume, slough, exudate, edema, percent granulation, and wound type. The model explained 71% of variation in healing time with the microbiome contributing the largest proportion of variance explained. None of the genomic latent variables on their own significantly accounted for variation among wound healing time, but through their covariance with microbiome and wound variables increased explanatory power by 15%. The importance of this covariance indicates the genomic regions influence wound bed morphology and physiology.

Conclusions: The modeling strategy presented here provides a framework to integrate genomics into a predictive model. The addition of patient genomics into a model of healing, which is presented for the first time in this work, expands upon our other recent work demonstrating that patient genetic differences influence wound microbiomes and that wound microbiomes influence healing. This model is also flexible to integration of other data types, such as gene expression and blood biomarker data. Future work will benchmark our genomic latent variable approach against other GWAS-related methods. Important for clinical adoption, the predictive utility of the SEM will also be evaluated through independent cohorts.

P63 *Establishing a machine learning-based hepatic retinoid-level prediction model for a precision nutrition foundation*

Brighton Garrett, Ayyappa Sista, Alexandra Naron , Yoshinori Seki, Marianny Alvarado, David Threadgill & Masako Suzuki
Texas A&M

Hidden hunger—adequate caloric intake but insufficient micronutrient levels—affects many Americans, particularly those living in poverty. This is especially detrimental for pregnant women. During pregnancy, deficiencies in essential nutrients like vitamin A (vitA) can lead to adverse maternal and fetal outcomes. However, excessive vitA intake can also be teratogenic, making precise monitoring and treatment critical. VitA levels are most reliably measured in liver tissues which can be obtained through biopsy, but this method is invasive. To improve precision nutrition strategies, we aim to develop a machine-learning model using simplified diversity outbred (SDO) mice to accurately predict hepatic retinoid levels from plasma metabolomic profiles, a noninvasive sample.

The SDO mice reflect the genetic diversity seen in human populations. We have observed significant variation in serum and hepatic retinoid levels among the three wild-type founder strains (CAST/EiJ, PWK/PhJ, and WSB/EiJ), highlighting the impact of genetic diversity on vitA metabolism. Previously, we successfully built a model using liver transcriptome data to predict serum retinoid levels on inbred mice, and we will extend this approach to genetically heterogeneous mice. Additionally, high-fat diets have been correlated with elevated hepatic retinoid levels. To further investigate dietary influences, we will subject SDO mice to either an American (high-fat, high-cholesterol) or Japanese (low-fat, low-cholesterol) diet, encompassing a broad range of vitA levels.

Currently we are in the early stages of the project, establishing the necessary mouse models and optimizing experimental conditions. Tissue and serum collection is set to begin shortly and these findings will inform the development of the model. This noninvasive approach could provide a valuable tool for assessing vitA status in the liver and guiding dietary recommendations in at-risk human populations in the future.

P64 *Investigating the Role of a Specific CAF Population in Mammary Tumorigenesis*

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Breast cancer is a leading cause of cancer deaths worldwide, with about 670,000 deaths reported in 2022. The tumor microenvironment is a culmination of cell types including immune cells, the extracellular matrix, blood vessels and stromal cells such as cancer-associated fibroblasts (CAFs), which help in stabilization of the tumor and the development of cancer. CAFs play a crucial role in cancer cell survival, proliferation, and evasion through their release of cytokines and chemokines. By using single-cell RNA-sequencing, our preliminary study showed that a specific CAF population (S100a4+) is increased with the progression of tumor. This study aims to functionally characterize S100a4 CAF population and to investigate the molecular mechanism underlying S100a4+ mediated tumor progression.

P65 ***Phylogenetic Insights into Conserved and Divergent Recombination Landscapes in Felidae***

Elise Baugh, Nicole Foley, William Murphy,
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Meiotic recombination shapes genome evolution, yet its rates vary widely among species, reflecting diverse ecological, evolutionary, and anthropogenic influences. Felidae, encompassing domesticated and endangered species, provides an ideal system to investigate how these factors drive recombination rate evolution. We hypothesized that domestication and demographic constraints explain differential recombination patterns within this lineage. We generated high-resolution recombination landscapes with recurrent neural networks using whole-genome sequencing and SNP genotyping. Our findings show elevated recombination rates in domesticated felids, contrasted by reduced rates in endangered taxa like Panthera pardus, likely linked to historical bottlenecks. Phylogenetic comparisons highlight conserved and divergent recombination signatures across felid clades, reflecting the interplay of population history and selection. These genomic analyses further clarify the history of recombination's evolution under various selection pressures. By revealing the genetic underpinnings of recombination, our study paves the way for more informed conservation strategies aimed at maintaining genetic diversity. Finally, these insights offer support for predictive models and potential manipulation of recombination landscapes in future mammalian genomics research.

P66 ***Nanomaterial-Induced Mitochondrial Biogenesis Enhances Intercellular Mitochondrial Transfer Efficiency in Human Mesenchymal Stem Cells***

John Soukar, Kanwar Abhay Singh, Ari Aviles, Sarah Hargett, Harman Kaur, Samantha Foster, Shounak Roy, Feng Zhao, Vishal M. Gohil, Irtisha Singh, Akhilesh K. Gaharwar
Teas A&M University

Intercellular mitochondrial transfer—the spontaneous exchange of mitochondria between cells—is a recently described phenomenon crucial for cellular repair, regeneration, and disease management. Enhancing this natural process holds promise for novel therapies targeting diseases associated with mitochondrial dysfunction. Here, we introduce a nanomaterial-based approach employing molybdenum disulfide (MoS_2) nanoflowers with atomic-scale vacancies to stimulate mitochondrial biogenesis in cells to make them mitochondrial biofactories. Upon internalization, these nanoflowers activate the PGC-1α pathway within donor cells, resulting in a twofold increase in mitochondrial mass and enhancing mitochondrial transfer to recipient cells by several-fold. This enhanced efficiency of transfer significantly improves mitochondrial respiratory capacity and adenosine triphosphate (ATP) production under physiological conditions. In cellular models of mitochondrial and cellular damage, MoS_2 enhanced mitochondrial transfer achieved remarkable restoration of cell function. This proof-of-concept study demonstrates that nanomaterial-boosted intercellular mitochondrial transfer can enhance cell survivability and function under diseased conditions, offering a promising new strategy for treating mitochondrial dysfunction-related diseases.

P68 *FOXO FACTORS' ABILITY IN BINDING TO AND INDUCING TCF7 IN GLIOBLASTOMA CELLS*

Stephanie Oyervides, Megan Keniry
University of Texas Rio Grande Valley

Glioblastoma Multiforme (GBM) is an aggressive astrocytoma tumor type with poor prognosis and limited immunotherapeutic options for those inflicted. Gene expression of this cancer indicates a direct relationship with the transcription factors, Forkhead box subfamily O (FOXO -1, -3, and - 4). These transcription factors are evolutionarily conserved and partially redundant. They perform diverse and fundamental biological processes such as longevity, stem cell homeostasis, cell fate determination, cell cycle maintenance, metabolism, and apoptosis. Increasing evidence suggests interconnectivity between the WNT Pathway and FOXO transcription factors; however, the mechanism and the full extent to which these interactions play a role in determining FOXO output is yet to be delineated. Under oxidative stress seen in color cancer, myoblasts, and osteoblasts, FOXO factors hinder canonical WNT pathway output by disrupting the interaction between beta-catenin and TCF4. Through a genomics and CRISPR Cas9 genome editing approach, we are the first group to report that FOXO factors promote canonical WNT Pathway gene expression in glioblastoma cells. Additionally, ChIP Seq analysis with FOXO1, FOXO3, and FOXO4 antibodies revealed *TFC7* as an integral target. Therefore, it is hypothesized that FOXO factors promote WNT Pathway output through the induction of *TCF7* to impact proliferation, colony formation, and cancer stem cell maintenance.

P70 *Exploring ATG17 and GRE3 as Potential Suppressor Mutants of* pgm2Δ

Karsyn Clouse, Lily Ordoñez, David P. Aiello
Austin College

In *Saccharomyces cerevisiae*, phosphoglucomutase (PGM) catalyzes the interconversion of glucose-1-phosphate (G-1-P) and glucose-6-phosphate; *PGM2* is responsible for 90% of PGM activity in *S. cerevisiae*. The pgm2Δ mutant exhibits hyperaccumulation of G-1-P and calcium homeostasis deficiencies on galactose, but the exact mechanism of these calcium homeostasis deficiencies is unknown. The *pgm2Δ* also exhibits sensitivity to oxidative stressors. Further, *pgm2Δ* calcium homeostasis deficiencies are rescued in *pgm2Δspt4Δ*. RNA sequencing data of the *pgm2Δ* and p*gm2Δspt4Δ* strains revealed *ATG17* and *GRE3* are highly upregulated in *pgm2Δspt4Δ* relative to *pgm2Δ,* suggesting *ATG17* and *GRE3* function may be important for *pgm2Δ* viability. *ATG17* encodes a protein involved in the formation of the phagophore assembly site during autophagy and in regulating the magnitude of the autophagic response. The secretion of glutathione, an antioxidant, is increased in *atg17Δ*. To characterize the role of ATG17 in the *pgm2Δ* mutant, *atg17Δ* and *pgm2Δatg17Δ* strains were constructed and spot-plated on various media types, including oxidative stressors. *GRE3* encodes the protein aldose reductase, which converts galactose to galactitol using NADPH. In *pgm2Δ* mutants, galactose-1-phosphate (Gal-1-P) accumulates in the cell. Previous studies suggest that elevated levels of both Gal-1-P and galactitol may contribute to galactose toxicity, which is hypothesized to disrupt calcium homeostasis. Accumulation of galactitol additionally causes oxidative stress by depleting NADPH and decreasing glutathione reductase activity. To characterize the role of *GRE3* in *pgm2Δ, gre3Δ* and *pgm2Δgre3Δ* strains were constructed and spot-plated on various media types, including multiple galactose concentrations and oxidative stressors. This study characterizes the growth phenotypes of *atg17Δ*, *pgm2Δatg17Δ*, *gre3Δ,* and *pgm2Δgre3Δ* across various media types.

Talk Abstracts

Talk_1G. *Defining mitochondrial protein functions using deep neural networks*

Abhinav B. Swaminathan, Sofia Calabrese, Mohammad Zulkifli, Rachel Guerra, Amy Spelbring, Harman Kaur, Dimitris Kalafatis, David Barondeau, David J. Pagliarini, Vishal M. Gohil
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Despite the importance of mitochondria in cellular metabolism, we still do not know the molecular function of many mitochondrial proteins. To link uncharacterized mitochondrial proteins to known mitochondrial metabolic pathways, we repurpose the protein structure prediction algorithm – AlphaFold Multimer – into a classification model to predict protein-protein interactions. We show that AlphaFold Multimer can successfully identify 85% dimeric interacting pairs and 50% oligomeric interacting pairs at a false discovery rate of 15%. After establishing this benchmark, we applied this algorithm to the mitochondrial proteome of ~1100 proteins and screened 630,000 possible binary combinations for protein-protein interactions to identify 2895 known and novel interactions involving 1004 proteins. We predicted at least one interacting partner for 85 of the 101 uncharacterized mitochondrial proteins, linking them to a known biochemical pathway. We experimentally validate our prediction by showing that Coa4 and Cmc2, two poorly characterized cytochrome c oxidase (CcO) assembly factors, are involved in specific steps in the assembly of CcO. Combining our data set with mass spectrometry data, we were able to build a structural model of the nine-subunit coenzyme Q synthome complex, which has not been amenable to structural studies. Finally, we predicted an interaction between the human uncharacterized protein ARM1 and mitochondrial aconitase. Follow-up experimental work on ARM1 shows that it is a 2Fe-2S cluster-containing protein that functions as a reductase in the repair of oxidatively damaged aconitase. Our work expands the utility of AlphaFold beyond the structural realm and provides a foundation for the complete understanding of mitochondrial proteome.

Talk_2G. *Heritable Tissue-Specific Gene Expression Associates With Chronic Wound Microbial Species*

Khalid Omeir, Jacob Ancira, Rebecca Gabrilska, Craig Tipton, Clint Miller, Ashley Noe, Kumudu Subasinghe, Megan Rowe, Nicole Phillips, Joseph Wolcott, Caleb D. Philips
Texas Tech University

The reasons for interpatient variability in chronic wound microbiome composition are thought to be complex but are poorly known. To investigate how patients' genetically regulated tissue expression may influence chronic wound bacterial composition, we performed a microbiome-transcriptome-wide association study. This approach involved estimating for 509 patients their tissue-specific gene expression from DNA genotypes, followed by associating gene expression to the relative abundances of species detected in their wounds as provided on clinical reports to the physician. Comparisons to artery, blood, fibroblast, skeletal muscle, skin, subcutaneous fat, and nerve tissue resulted in 251 transcriptional differences at 109 genes significantly explaining abundances of 39 different species. Overall, these species were detected in ~63% of wounds. A similar number of associations per tissue was observed (range 31-39), and many genes were associated at multiple tissues in distinct ways. The cumulative variance across loci for species relative abundance explained ranged from ~3-36%, depending on species. Although the same gene was almost never associated with more than one species, ~14% of enriched pathways were independently enriched for multiple species, which may reflect the diversity of ways microbes interact with partially overlapping attributes of the wound bed. Commonly enriched pathways

pertained to collagen formation and modification, cell signaling, cytoskeletal dynamics, interactions with extracellular matrix, transmembrane proteins, among others. This work expands the new perspective that individual genetics may partially determine microbial colonization and infection.

Talk_3G. *First genetic evidence of a hybrid Virginia's x Colima warblers in West Texas, featuring patterns of admixture and SNP-phenotype associations.*

Ari Rice, Joseph Manthey
Texas Tech University

Despite being the focus of many investigations on phylogenetics and hybridization, *Parulidae* (wood-warblers) contains several genera that are poorly studied in this regard. *Leiothlypis* represents one such genus, in which none of its members were known to regularly hybridize until the 2002 discovery of suspected Virginia's (*L. virginiae*) x Colima warbler (*L. crissalis*) population in the Davis Mountains of west Texas. Since then, the composition, history, and trajectory of this seemingly isolated population has remained unknown. Here, we present the first genetic evidence of *L. virginiae* x *L. crissalis* hybridization based on blood samples from wild-caught birds. We also discuss the ecological and evolutionary implications of our findings, the possibilities of admixed birds existing elsewhere, and the extent to which admixture is reflected in birds' physical appearances. Finally, we lay the groundwork for an upcoming study addressing whether hybridization between these species is locally adaptive or simply a matter of small population size and limited mate choice in the Davis Mountains.

Talk_1P. *Modulating Karyopherin Alpha and Beta Levels Ameliorates Mutant Ataxin-1-Induced Neurodegeneration in Drosophila*

Khondker Salim, Elena Ruff, Dylan Timperman, Adulfo Amador, Isabella Aguirre-Lamus, Maria de Haro, Ismael Al-Ramahi
Baylor College of Medicine

Spinocerebellar Ataxia Type 1 (*SCA1*) is an inherited neurodegenerative disease caused by translated CAG repeat expansion in the *Ataxin-1* (*ATXN1*) gene. The resulting *ATXN1* protein, which contains an expanded polyglutamine (PolyQ) tract, misfolds and accumulates in several neuronal cell types, disrupting cellular processes and leading to neuronal cell loss. The toxic gain-of-function mechanisms underlying neuronal cell death caused by polyQ-expanded *ATXN1* remain incompletely understood, and effective therapies have yet to be developed. Recent research highlights the critical role of nucleocytoplasmic transport (NCT) in neurodegenerative diseases. Mutant *ATXN1* accumulation in the nucleus is essential for *SCA1* pathogenesis. Moreover, the *ATXN1* interactome includes several NCT proteins, and mutant *ATXN1* can disrupt normal NCT by sequestering these proteins in aggregates. However, the functional significance of ATXN1's interactions with NCT proteins remains unexplored. Karyopherins, a family of proteins that facilitate NCT, have also been shown to chaperone the disaggregation of mutant RNA-binding proteins implicated in neurodegenerative diseases. In this study, we investigated the effects of modulating karyopherin alpha (KPNA) and karyopherin beta (KPNB) levels on mutant *ATXN1*-induced neurodegeneration in a *Drosophila* model of *SCA1* utilizing overexpression of mutant *ATXN1* (*82Q*). We show that increased levels of KPNAs ameliorate mutant *ATXN1*-induced retinal degeneration and motor impairment in *Drosophila*. Surprisingly, overexpression of KPNAs did not result in increased nuclear translocation of mutant *ATXN1*. Instead, immunohistochemical analysis revealed that increased KPNA levels sequestered mutant *ATXN1* in the cytoplasm and

lowered nuclear mutant ATXN1 levels. We also show that KPNAs interact with mutant ATXN1 and reduce mutant ATXN1 oligomerization in Drosophila central nervous system. These findings suggest that KPNAs function as molecular chaperones in SCA1 pathology. KPNAs may promote the disaggregation of mutant ATXN1 oligomers and sequester them in the cytoplasm, thereby preventing their nuclear translocation and subsequent pathogenic (or cytotoxic) effects. Since KPNA may be translocated to the nucleus in a KPNB-dependent manner, we examined how KPNB knockdown affects cytoplasmic KPNA levels and mutant ATXN1-induced neurodegeneration. We found that pharmacological inhibition of KPNB1 increases cytoplasmic KPNA and reduces nuclear mutant ATXN1 levels in DAOY cells. Additionally, the knockdown of KPNB1 also ameliorated mutant ATXN1-induced retinal and motor impairment phenotype in Drosophila and lowered nuclear mutant ATXN1 levels in Drosophila neurons. We propose that the neuroprotective effects of KPNB1 knockdown may result from both increased cytoplasmic KPNA levels and the prevention of mutant ATXN1 nuclear translocation. These findings indicate that cytoplasmic sequestration of mutant ATXN1 could be a viable therapeutic strategy for *SCA1*. As karyopherins are dysregulated in multiple neurodegenerative diseases and have an emerging role as chaperones, our results may have broader relevance beyond SCA1, potentially extending to disorders such as Alzheimer's and Parkinson's disease.

Talk_4G. ***Genetics and Cellular Transcriptomics Regulating Pigmentation Patterns in Chicken Feathers***

Pei-Jung (Cindy) Hsin, Zheng Li, Leif Andersson, Brian W Davis
Department of Veterinary Pathobiology, Texas A&M University, College Station, TX, USA

Pigmentation plays an important role in biology, and color variation is crucial for adaptation in the wild, and is being selected in domestic populations. Bird feathers exhibit highly diverse pigmentation patterns and morphologies, which vary both within a single feather and across different body regions. However, genes that regulate these complex feather phenotypes remain unclear.

This study uses chicken as a model to explore the genetic basis of feather pigmentation patterns. Intercrossing F1 hybrids of wild-type Red Junglefowl (RJF) and derived Silver Sebright (SS) produced at least 10 pattern categories across 200+ F2s. Whole-genome sequencing was performed on a Mendelian hybrid cross involving parental RJF and SS, F1, and F2 intercross progeny. Preliminary genome-wide association (GWAS) results highlight three known pigmentation related genes and several other previously undocumented genes are involved. The wild-type RJF haplotype surrounding *SOX10* gene is related to nearly-black feathers compared to nearly-white. For the associated gap-junction gene GJA5, in F2s, the homozygous RJF haplotype causes nearly-white feathers, partial single-lacing (where the feather has dark pigment around the edge) are heterozygous, and most of the single-lacing and nearly-black F2 are homozygous SS. The MC1R RJF haplotype is associated with nearly-white and partial single-lacing patterns compared with single-lacing and almost all-black patterns which have the SS haplotype. Other signals with unknown candidate genes will be further analyzed.

To investigate the molecular addresses that dictate the morphology of feather follicles in different body regions, single-cell RNA sequencing was performed on feather follicles actively producing feathers from four body regions (breast, leg, dorsal, and hackle) in an adult male RJF. Twelve major cell types were identified. *HOX* genes were highly expressed in follicular stem cells and

differentially expressed in the four body regions. By comparing expression within each cell type between body regions, genes responsible for feather identity are identified.

This study combines classical genetics and modern *omics to generate data to reveal variants and expression patterns influencing diverse pigmentation patterns and morphologies in the feather.

Talk_2P. *Phosphatidylethanolamine exposure is recognized by transthyretin-like protein TTR-53 for phagocytosis*

Dylan Suriadinata, Bianca Guerra, Riley Harrison, Julia Frondoni, Gabriela S. Paredes-Devalillo, Charlotte Kommini, Ann M. Wehman
Texas A&M University

Phagocytic cargos expose lipids to signal for engulfment, which is important for tissue homeostasis and immune responses. The transthyretin-like protein TTR-52 recognizes phosphatidylserine (PtdSer) for receptor-mediated phagocytosis but is not required for all engulfments in Caenorhabditis elegans. We discovered that a related protein, TTR-53, also promotes phagocytosis and localizes to the surface of phagocytic cargos. By disrupting PtdSer and phosphatidylethanolamine (PtdEth) asymmetry, we find evidence that TTR-53 may function as a bridging molecule for PtdEth rather than PtdSer. Thus, PtdEth exposure is also likely to promote phagocytosis and TTR-53 can be used to identify undiscovered functions of PtdEth asymmetry.

Talk_5G. *The Evolution of SNHG14: Understanding the Development of a Disease-Relevant Polycistronic Transcription Unit in Placental Mammals*

Alasdair Taylor, Scott V Dindot
Texas A&M University

The small nucleolar host gene 14 (*SNHG14*) is an imprinted polycistronic transcription unit that encodes a complex array of coding and noncoding genes, including the SNURF and SNRPN protein-coding genes and six different C/D box small nucleolar RNAs (SNORDs) located in the introns of a long noncoding host gene. The *SNHG14* SNORDs include *SNORD64*, *SNORD107*, *SNORD109A*, *SNORD116*, *SNORD115*, and *SNORD109B*. *SNORD115* and *SNORD116* are organized as arrays of tandemly repeated units, and *SNORD109A* and *SNORD109B* share identical sequences but are 240 kb away from each other, highlighting the structural complexity of this locus. *SNHG14* is associated with several clinically distinct neurodevelopmental disorders, including Prader-Willi syndrome, Angelman syndrome, and duplication 15q syndrome; however, the functions of the *SNHG14* genes are poorly understood. The highly complex genomic structure and epigenetic regulation of *SNHG14* have hindered the investigation of the locus among different species, particularly the evolution of the locus and conservation among placental mammals. Using 64 high-quality genome assemblies representing the major clades of placental mammals, we show that the sequential order of genes encoded by *SNHG14* have remained remarkably conserved throughout placental mammalian evolution, but the organization has not. We made custom annotations of *SNHG14* for each species using EGAPx and LiftOff and then determined the sequence identities, order, copy number, and conservation of each hosted gene using Geneious and MUSCLE. We found that rapidly evolving clades such as murid rodents and shrews have lost several SNORDs, potentially limiting their use as model systems. Although the *SNORD116* and *SNORD115* gene sequences are largely conserved across species, the genes are highly copy number variable, ranging from a single copy in some species to over 1000 copies in others. Overall, our findings support prior studies indicating that *SNHG14* evolved in a common ancestor of

placental mammals and show that although the overall organization of *SNHG14* is conserved, it has been subject to extensive genomic rearrangements and copy number expansions.

Talk_3P. ***Phylogeography of a forest generalist bird reflects glacial expansion and sex-biased dispersal***

Swapnil S. Boyane, Javier E. Colmenares-Pinzón, Ethan F. Gyllenhaal, Ari A. Rice, María C. Tocora, Ben D. Marks, Joseph D. Manthey
Texas Tech University

Although the field of phylogeography has allowed us to gain a strong sense of how genetic diversity is distributed across landscapes for a wide range of taxa, avian studies tend to focus on specialist taxa and those with clear patterns of morphological variation. Here we collected whole genome resequencing data across the tropical region of Africa for a widespread forest generalist bird species with little described geographic variation, the Yellow-whiskered Greenbul (*Eurillas latirostris*). Despite their weak morphologic divergence, we recovered three strong genetic clusters corresponding to three known Pleistocene forest refugia, one montane and two lowland. The break between the two lowland populations in central and west Africa corresponded to a known gap in forest habitat, but the break between the central lowland and eastern highland populations did not appear to correspond to such a gap. Demographic modeling suggested that the central population—now distributed throughout central Africa—had both a larger effective population size and acted as a stronger source of migrants for the populations to its east and west than vice-versa. Although many aspects of this system were consistent with common phylogeographic patterns globally, two aspects were unusual for avian systems: apparent capture of mitochondria of the eastern population by the expanding edge of the central population and reduced sex chromosome divergence among all populations. Both patterns suggest male-biased dispersal, a phenomenon thought to be uncommon in birds. Due to the rarity of reduced sex chromosome divergence in avian genomic studies, we used population genetic simulations to demonstrate that male-biased dispersal alone is sufficient to produced comparably low ratios of sex chromosome to autosome divergence. Together, our data reflects the importance of sampling widespread, cryptic taxa to fully understand the early stages of speciation, and the role life history can have on phylogeographic inference.

Talk_1U. ***Fusions of autosomes with sex chromosomes are disfavored in mammals***

Maximos Chin, Matthew Marano, Kenzie G. Laird, Michelle M. Jonika, Heath Blackmon
Texas A&M University

Fusing autosomes with sex chromosomes is hypothesized to be advantageous because it can resolve sexual antagonism at autosomal loci. Here, we evaluate the patterns and frequency of autosome sex chromosome fusions across mammals. We test whether fusions involving sex chromosomes are overrepresented in mammals using a comprehensive dataset including 950 mammalian species and novel extensions to stochastic mapping. Our research combines empirical data analysis with simulation studies to estimate the proportion of fusions involving sex chromosomes. Contrary to initial expectations, we find a paucity of fusions that join autosomes and sex chromosomes. We consider alternative evolutionary pressures that might influence the prevalence of fusions involving sex chromosomes, such as dosage compensation, meiotic sex chromosome inactivation, and structural characteristics of mammalian sex chromosomes. Our findings suggest that while sexual antagonism may contribute to the fixation of fusions with sex chromosomes, the fusion process is intricately linked with broader evolutionary dynamics, demonstrating the complex and likely countervailing selection pressures acting on structural

mutations like fusions joining an autosome and a sex chromosome. Our study underscores the need for targeted genomic studies that could distinguish among the possible forces that disfavor fusions of autosomes with sex chromosomes.

Talk_6G. ***Endangered and Endemic Beetle Genomic Study***

Sean Chien, Jen-Pan Huang, Heath Blackmon
Texas A&M University

Habitat fragmentation, driven by natural events, human activities, and environmental changes, disrupts gene flow among populations, leading to genetic isolation. Isolation can result in reduced genetic diversity due to bottlenecks and genetic drift, diminishing populations' adaptive capacities and increasing extinction risks. High-quality reference genomes are essential for genomic studies addressing demography, adaptation, and population structure, thereby informing conservation strategies. This study presents a de novo genome assembly and population genomics analysis of *Cheirotonus formosanus*, an endangered and endemic beetle species from the mountain forests of Taiwan and *Dynastes grantii*, one of the largest and most charismatic beetles in North America. These genomic resources will offer insights into the evolutionary history of these beetles and accelerate future population genetics work that can provide a basis for scientifically informed conservation efforts.

Talk_7G. ***Population expression ceilings predict gene duplication sensitivity***

Iyer, S.K.*, Sanchez, S.M.*, Frohock, B.A., Groh, J.C., Agnihotri, A., Beckett, E.L., Bigham, C., Dermott, E., Fiorito, A.E., Jones, R.C., Mourao, N., Perks, K.M., Smith, S.R., Syed, B., Pierce, J.T. (* Authors contributed equally)
University of Texas at Austin

Many genetic disorders are caused by gene duplication, but it is hard to know which genes are sensitive or tolerant to duplication. To identify factors that predict gene duplication sensitivity, we transformed 47 orthologs of human 21st chromosome genes one at a time in the nematode Caenorhabditis elegans. More than half caused developmental, behavioral, or reproductive deficits as extra copies. Interestingly, most overexpression-sensitive genes displayed a ceiling in expression across wild C. elegans, as though individuals with higher levels are selected against in nature. This model extended to independent worm studies including those on genes that cause overexpression phenotypes when derepressed in microRNA mutants. The model also generalized to humans. We found that duplication-sensitive genes that cause severe medical conditions (e.g. *APP*, *PCSK9*, *PMP22*, and *SNCA*) display a ceiling of expression in a healthy population. Likewise, about half of 1,048 genes contained within duplication-sensitive copy-number variant regions also display expression ceilings. Conversely, the vast majority of 1,029 example duplication-tolerant genes do not display expression ceilings. To empirically test our ceiling hypothesis, we are currently conducting quantitative tests and behavioral screenings in worms, to assess if ramping up or down the number of copies of human 21st chromosome genes around their ceiling threshold, results in an overexpression phenotype. Additionally, we are developing computational methods to further identify genes with hard vs soft ceilings, explore expression floors to predict haploinsufficient genes, and study combinatorial gene expression interactions for worm and human genes. Altogether, our model suggests that genes sensitive to copy number variations may be predicted by population expression patterns observed in genetically diverse, healthy members of a species.

Talk_8G. ***A Genomic and Morphological Assessment of the Pinyon Deermouse, Peromyscus truei (Cricetidae: Neotominae)***

Javier E. Colmenares-Pinzón, Caleb D. Phillips, Robert D. Bradley, Joseph D. Manthey
Texas Tech University

The Pinyon Deermouse, *Peromyscus truei*, is a widely distributed Cricetid rodent inhabiting the western United States. The taxonomy of this species has been contentious, with populations historically oscillating between subspecies and species status. Currently accepted but outdated hypotheses recognize 11 subspecies, distinguishable by limited phenotypic traits. However, Cytochrome-b analyses reveal that these subspecies are not monophyletic and instead suggest the species comprises two highly divergent haplogroups, likely representing distinct species.
To address these taxonomic and evolutionary questions and assess conservation implications, we expanded from single-marker analyses to whole-genome sequencing, complemented by a geographically extensive multivariate morphometric study. We generated the first chromosome-level genome assembly for the species, revealing genomic stability compared to other Peromyscus species. Genome-wide analyses across the species' range reveal population structure, with some genetic clusters potentially shaped by geographic barriers such as rivers and mountains. Multivariate analyses of 35 craniodental and external measurements partially align with these genetic patterns. The only threatened subspecies*, P.* truei comanche, emerges as genetically distinct and isolated, with reduced genetic diversity and higher levels of homozygosity compared to neighboring populations. These findings reinforce its conservation status and underscore the need for targeted management strategies. However, its stable effective population size in recent times and relatively low genetic load offer promising prospects for its long-term survival.

Talk_9G. ***Disentangling the roles of selection and drift in the origins of microproteins: a case study using the chromosomal distribution of human genes encoding microproteins***

Matthew Marano, Claudio Casola
Interdisciplinary Doctoral Program in Ecology and Evolutionary Biology
Texas A&M University

De novo gene birth is a widespread process of novel gene formation and play a major role in the origin of small ORFs (sORFs) encoding microproteins. It has been reported that nearly 56% of the 7,264 recently annotated human microproteins-encoding sORFs have originated through de novo gene birth. These de novo sORFs encode 'evolutionary untested' microproteins; how such proteins integrate in the well-established cellular networks without causing havoc is unclear. Two main hypotheses, the 'continuum' and 'preadaptation' models, have been introduced to explain the evolutionary success of de novo genes. However, these models have not been tested in the context of major evolutionary forces, i.e. natural selection and genetic drift. We propose a novel evolutionary framework to thoroughly test these models and identify the impact of selection and drift in de novo gene birth. Here, we focus on intragenomic regions with varying effective population size (Ne) to determine the influence of selection vs. drift. In particular, we aim to test the formation of de novo sORFs between human sex chromosomes and autosomes, which are known to have different Ne. Our analyses of 4,101 human de novo sORFs revealed that the chromosome X contained fewer sORFs than any autosome, after correcting for chromosomal length. We further inspected if this result could stem from other differences between chromosome X and autosomes. For instance, chromosomes with an average higher GC-content should harbor more sORFs because stop codons are AT-rich. In addition, small upstream ORFs (uORFs) are

expected to be found more often in chromosomes containing more annotated genes. Because de novo uORFs represent ~50% of all small de novo genes, gene density is likely playing a major role in the chromosomal distribution of de novo ORFs overall. We thus generated a linear model accounting for the GC-content, the gene count and the total length of each chromosome, all as fixed effects, to compare de novo sORF content on each chromosome. The adjusted $r2 = 0.8978$ indicates that a majority of the variance in de novo sORF counts across chromosomes can be predicted by the model parameters. The X chromosome maintains the lowest proportion of de novo sORFs compared to each autosome in this model. These results indicate lower rates of de novo gene formation/retention in low-Ne chromosomes, supporting the preadaptation model for de novo gene birth. We also excluded that the lower mutation rate of the X chromosome vs, autosomes contributed to these differences in de novo sORFs, because the increased mutation rates in the autosomes would negatively affect the rate of de novo sORF formation by increasing the frequency of disabling mutations (stop-gain, frameshift, splice mutations). These findings represent the first analysis of microprotein-encoding gene birth in the context of selection, drift, and de novo gene evolutionary models.

Talk_10G. ***A comprehensive multi-omics analysis to assess the strain-dependent effects of dietary vitamin A and fat intake on the liver of female mice***

Marianny Alvarado-Gonzalez, Yuta Matsuno, Younkyung Kim, Jeniffer Aguilan, Samuel Rosean, Simone Sidoli, Loredana Quadro & Masako Suzuki
Texas A&M University

Early life adverse environmental exposures, such as macro- and micronutrient imbalance of mothers or obese pregnancies, can increase both mother and offspring health risks later in life. Often the diets consumed in communities suffering from food insecurity consist of higher macronutrient content with limited dietary micronutrient intake, which can allow these individuals to meet a satisfactory energy intake but still suffer from micronutrient deficiencies. Micronutrients, such as vitamin A (VA), are essential for proper functioning and healthy development. They are crucial in gestation as they are involved in homeostasis, signaling, and cell differentiation, among other biological functions associated with metabolic pathways after postnatal development. We hypothesize that dietary VA status modifies the effect of a high-fat diet (HFD) consumption, and genetic variations modulate the effect since our preliminary mouse study showed significant strain-dependent variations in VA status.

This study aims to elucidate how dietary VA-fat intake and genetic background contribute to liver multiome and retinoid status alterations in female mice before mating. Therefore, to achieve this we tested the effect of our dietary contents in four semi-purified diets: 5 IU/g VA - 10 % fat (Control), 5 IU/g VA - 60 % fat, 25 IU/g VA - 10 % fat, and 25 IU/g VA - 60 % fat, on two inbred mouse strains (C57BL/6J and DBA/2J). Eight-week-old female mice of C57BL/6J, and DBA/2J strains were randomly assigned to 5 IU/g VA - 10 % fat (n=10) or 25 IU/g VA - 10 % fat (n=10) for 6 weeks to reach the desired starting VA status while monitoring their body weight and food intake weekly. Each group was further divided into 10 % fat (n=5) or 60 % fat (n=5) containing the previously assigned VA concentration. The daily body weight changes and average food intake per cage were measured for 2 weeks.

As expected, we observed a significant body weight increase by HFD feeding in both strains where only in C57BL/6J the 60 % fat diet-fed mice have a significant difference which is VA

independent. In addition, a smaller liver size (body weight-adjusted) was observed among the HFD-fed mice, with only DBA/2J showing differences independent of VA status. Nevertheless, when liver Retinyl Esther (RE) was quantified, it showed a strain and VA-independent increase of liver RE levels in HFD-fed mice. Currently, the analysis of proteome, transcriptome, and metabolome datasets tries to elucidate the mechanisms of how dietary intake and genetic background influence female mice metabolism to establish a relationship to offspring phenotypes later in life when a secondary dietary intervention is performed. Initial inferences from our analysis entail an association with the 60 % fat diets (B & D) driving significant differential expression of strain-dependent proteins and metabolites when compared to the control diet that comply with an adjusted p-value < 0.05. Furthering the comprehensive multi-omics analysis highlights the potential alteration of expression and pathways due to the strain-specific response and effect of VA and fat contents.

Talk_11G. *Somatostatin is reduced in the frontal cortex of an Angelman syndrome pig model*

Ashley Coffell, Sarah Christian, Scott V. Dindot
Texas A&M University

The ubiquitin-protein ligase E3A (*UBE3A*) gene is one of only a few genes subject to genomic imprinting in a cell-type specific manner. *UBE3A* is imprinted with maternal-allelic expression in central nervous syndrome (CNS) neurons and biallelically expressed in all other cell types. The loss of the maternally inherited *UBE3A* allele causes Angelman syndrome, a rare neurodevelopmental disorder characterized by profound developmental delay, cognitive impairment, motor incoordination, an ataxic gait, reduced speech, and a uniquely happy disposition. It remains unclear how the cell type-specific expression of genes are dysregulated in the Angelman CNS, where *UBE3A* expression is absent in neurons and haploinsufficient in other cell types. Using single nuclei RNA-sequencing, we identified 3,812 dysregulated genes across 10 cell-type clusters in the frontal cortex of neonatal pigs (Sus scrofa) with a deletion of the maternal *UBE3A* allele. Most of the dysregulated genes were detected in neuronal subtypes. We further found that the somatostatin (SST) gene — a secreted neuropeptide involved in GABAergic inhibition — was downregulated in inhibitory neurons of the cortex, persisting throughout development. SST protein levels were also reduced in the circulating serum, suggesting it could be used as a potential biomarker for disease-modifying therapies for Angelman syndrome. Overall, these findings provide greater clarity on the genes affected by the loss of *UBE3A* expression in neurons, advancing our understanding of the molecular pathways affected in this devastating disorder.

Talk_12G. *Mutations in the androgen receptor gene and other sex development key genes are associated with equine disorders of sex development*

Hailey Anderson, Sam Stroupe, Rytis Juras, Brian Davis, Terje Raudsepp
Texas A&M University

Disorders of sex development (DSDs) occur when there is disagreement of chromosomal, gonadal, or anatomical sex. Although many cases of DSDs are reported in horses, the genomic basis of equine DSDs is not well understood, and most of the causative genes remain unidentified. The androgen receptor (AR) gene is composed of eight exons and encodes for the AR protein, which plays a critical role in male sexual development by regulating gene expression in response to androgen signaling. Loss-of-function mutations in the AR gene are associated with several diseases, including androgen insensitivity syndrome (AIS) in which 64,XY individuals are female-

presenting. More than 1000 AR gene variants in humans contribute to AIS, while few AR gene variants are described in horses. In this work, we aim to advance the understanding of DSDs in horses by exploring the genomic basis of these conditions and identifying key sex development genes involved, focusing on AR and other critical genes involved in sexual differentiation.

To achieve this, a comprehensive investigation was initiated into the genomics of 88 equine DSD cases, all determined to be chromosomally normal by karyotype analysis. These cases were categorized into three clinical phenotypes: 64,XX X-monosomy-like females, 64,XX intersex, and 64,XY *SRY*-pos female-like. The genomic analysis was conducted using short-read data-based variant VCF files of all DSD cases and ~200 control horses. We developed and employed a pipeline in-house to investigate a set of 80 candidate genes, filtering for mutations of high to moderate effect and for homozygosity for alternate alleles with <1% frequency.

Missense, nonsense, frameshift, or indel mutations were found in 15 sex development key genes in 25 DSD cases. Notably, seven novel mutations were found in the AR gene in seven of the nineteen (37%)64,XY *SRY*-pos female-like horses. These mutations, located in exons 1, 3, 4, and 7, represent four out of the eight exons in the AR gene, and impact all major functional domains of the AR protein. The structural impacts of these mutations on protein folding are still under investigation. In addition, a hypothesis-free, genome-wide analysis is underway to identify additional potential variants that may contribute to these equine DSD cases, which were not captured in the initial candidate gene selection.

Talk_2U. *Examining the Role of TOR Signaling in the* Saccharomyces cerevisiae pgm2Δ *mutant*

Micaiah M. Wetzold, David P. Aiello
Austin College

In *Saccharomyces cerevisiae*, phosphoglucomutase (PGM) is an enzyme that catalyzes the interconversion of glucose-1-phosphate (G1P) and glucose-6-phosphate (G6P). Loss of *PGM2*, the major isoform of PGM, results in phenotypic defects when grown on galactose. The phenotypic defects of *pgm2*Δ include high accumulation of calcium, high accumulation of G1P, altered levels of carbohydrate metabolites (G1P and G6P), and no growth on galactose containing cyclosporin A, a calcineurin inhibitor. These phenotypes indicate *pgm2*Δ has defects in calcium homeostasis. To identify a link between carbohydrate metabolism and calcium homeostasis, our lab compared RNA sequencing data between wild-type and *pgm2*Δ yeast strains to identify significant changes in gene expression. Genes with roles in autophagy were found to have increased expression in the *pgm2*Δ mutant. Autophagy is the recycling of nutrients in the cell through the degradation of unnecessary or broken components and can be induced by the inactivation of TOR signaling in low nutrient environments. TOR signaling is an important pathway that uses nutrient sensing to regulate growth and stress responses, and altered TOR signaling has been implicated in cancer, metabolic diseases, and neurodegenerative diseases. This study aims to examine the role of TOR signaling in the viability of the *pgm2*Δ mutant. I hypothesize that altered TOR signaling negatively regulates the viability of *pgm2*Δ through the hyperactivation of autophagy. I further hypothesize that upregulated autophagy in pgm2Δ is unnecessarily recycling cellular resources and thus contributing to the phenotypic defect when metabolizing galactose. To test these hypotheses, TOR signaling related gene knockouts were constructed in conjunction with *pgm2*Δ. These genes included *TOR1*, *EGO1*, *GTR1*, *GTR2*, *SCH9*, *FPR1*, *SNF1*, and *ATG8*. The loss of genes directly

involved in the TOR signaling pathway, *TOR1*, *EGO1*, *GTR1*, and *GTR2*, did not significantly alter the viability of *pgm2*Δ on galactose. Initially, this did not support the hypothesis; however, when the galactose media contained either rapamycin or caffeine, *pgm2*Δ growth was significantly reduced by these gene knockouts. This data suggests a role for TOR signaling in the viability of *pgm2*Δ yeast.

Talk_1F. ***Neo-sex chromosome evolution in treehoppers despite long-term X chromosome conservation***

Daniela Palmer Droguett, Micah Fletcher, Ben Alston, Sarah Kocher, Diogo Cabral-de-Mello, Alison Wright
The University of Texas at Arlington

The organization of the genome into multiple chromosomes is a fundamental feature of genome function and evolution that impacts key processes like recombination and inheritance of co-adapted loci. Sex chromosomes (X and Y in male heterogametic systems) begin as an identical pair of autosomes but often evolve extreme differences in gene content and expression because of their distinct inheritance patterns. In some lineages, this results in a gene-rich X chromosome and a degenerate – or even missing – Y chromosome. These highly differentiated X and Y chromosomes are thought to be an 'evolutionary trap' that acts as a dead-end for sex chromosome evolution. However, karyotypic rearrangements like chromosomal fusions may alter the trajectory of sex chromosome evolution by bringing autosomal loci into sex-linkage, allowing for sex-specific genome adaptation. Here we investigate the role of X-autosome fusions in shaping the evolutionary trajectory of treehopper sex chromosomes. Treehoppers predominantly have XX/X0 sex chromosome systems in which the Y chromosome has been lost. However, cytological analyses indicate the presence of treehopper species with XX/XY sex chromosomes. Using comparative genomic data, we find that treehoppers exhibit dynamic chromosomal rearrangements that are largely confined to the autosomes while the X remains shielded from such changes, consistent with long-term evolutionary conservation of the X chromosome throughout much of insect evolution. However, we also find departures from this general trend in which X-autosome (X-A) fusions underlie the formation of neo-XX/XY sex chromosome systems. Here we study the evolutionary forces driving X-A fusions to test whether such transitions may contribute to genome adaptation by promoting the resolution of sexual antagonism. We conduct comparative analyses across species with independently evolved neo-sex chromosomes to investigate whether such fusions have convergently linked the ancestral treehopper X to the same autosomal region. Together, these results contribute to elucidating the impacts of large-scale genome rearrangements in sex chromosome evolution and genomic adaptation.

Talk_2F. ***Sequencing for Everyone: Single Molecule Sequencing in the Classroom***

Brian Teague, Danielle Palow
Trinity University

Insights from modern genetics often depend on genome-scale datasets and analyses, and these insights and methods are taking an increasingly central place in undergraduate genetics education. While genomics studies were initially restricted to research laboratories due to their difficulty and expense, recent developments have brought modern genomics within the reach of undergraduate teaching laboratories. This talk will describe our introduction of single-molecule sequencing in both lower- and upper-division laboratory courses at Trinity. The lower-division

course is an inquiry-based experience where students study the bean beetle microbiome to learn about phylogenies, taxonomies, species diversity and community structure. The upper-division course is a full-fledged course-based undergraduate research experience, where students develop, execute, and present their own genomics-based study. These experiences point toward a generalizable template for integrating authentic research and modern genomics into undergraduate education, helping students learn genetics by doing it.

Talk_3F. ***A bacterial expression cloning screen reveals single-stranded DNA-binding proteins as potent desicco-protectants***

Jonathan D. Hibshman, Courtney M. Clark-Hachtel, Kerry S. Bloom, and Bob Goldstein
Southern Methodist University

Desiccation kills most cells. Some proteins have been identified to help certain cells survive desiccation, but many protein protectants are likely to be unknown. Moreover, the mechanisms ensuring protection of key cellular components are incompletely understood. We devised an expression-cloning approach to discover further protectants. We expressed cDNA libraries from two species of tardigrades in E. coli, and we subjected the bacteria to desiccation to select for survivors. Sequencing the populations of surviving bacteria revealed enrichment of mitochondrial single-stranded DNA-binding proteins (mtSSBs) from both tardigrade species. Expression of mtSSBs in bacteria improved desiccation survival as strongly as the best tardigrade protectants known to date. We found that DNA-binding activity of mtSSBs was necessary and sufficient to improve the desiccation tolerance of bacteria. Although tardigrade mtSSBs were among the strongest protectants we found, single-stranded DNA binding proteins in general offered some protection. These results identify single-stranded DNA-binding proteins as potent desicco-protectants.

Talk_P4. ***The Equine Pangenome: Improvements in Structural Variant Detection and Genotyping for Horses***

Sam Stroupe, Jonah N. Cullen, Sian A Durward-Akhurst, Jessica Petersen, Ted Kalbfleisch, Molly McCue, Brian W. Davis
Texas A&M University

Variant discovery traditionally relies on aligning short sequence reads to a linear reference genome. However, when these reads differ significantly from the reference, it can result in imprecisely mapped or unmapped reads and ultimately lead to less accurate genotyping, referred to as “reference bias”. As a replacement for linear references, pangenomes can help to mitigate these inherent limitations by representing haplotypes from multiple individuals. Pangenome graphs are particularly informative in regions with variability in genome structure such as copy number variation, deletions, insertions, inversions, and complex rearrangements. This structural variation is almost always missed in the traditional approach due to breed or individual genomic content that is not present in the linear reference genome. As a reference, pangenomes are a graph-based approach that retains the variation across many representative haplotypes allowing multiple populations, breeds, and species to be represented simultaneously. To demonstrate the value of pangenomics for equine genetic research, we built containerized workflows to build and evaluate pangenome graphs, as well as align short-read sequences using the “personalized pangenome” approach. The pangenome method shows a clear improvement in mapping quality compared to using a linear reference genome. Previously documented examples of structural variation were accurately detected and genotyped as validation of this methodology. Additionally, both breed and

haplotype specific novel structural variation of potential phenotypic impact was identified. Pangenomics offers a clear way forward and progress towards characterization of variation associated with phenotypes and heritable disease and understanding of genome evolution.

Talk_13G. ***High Quality Alpaca Genome VicPac4 and Oligo-FISH Reveal a Satellite Sequence Specific to South American Camelids***

Mayra N. Mendoza, Brian W. Davis, Terje Raudsepp
Texas A&M University

The alpaca (*Vicugna pacos*), a native species to the high-altitude Andean regions, is the most important fiber producer among the South American camelids. We recently developed a high quality, chromosome-level alpaca reference genome, VicPac4. The assembly is based on integrated data of PacBio HiFi long-reads, Hi-C chromosome conformation capture, and optical genome mapping (OGM), achieving a scaffold N50 of 75.40 Mb with a total of 523 scaffolds. This includes chromosomes with complex repetitive regions, such as telomeric sequences and nucleolus organizer regions (NORs) unidentifiable in previous assemblies. However, three large scaffolds of 5 Mb, 8 Mb, and 10 Mb, containing NORs and telomeres, remained chromosomally unassigned. To incorporate these sequences, single-stranded oligonucleotide hybridization probes, targeting unique sequences within the 3 scaffolds, were designed by KromaTiD Inc., and used for oligo-FISH (Oligonucleotide Fluorescence in situ Hybridization). The results showed that the three scaffolds map to the same place in 8 to 10 autosomes in South American camelids (alpacas, vicuñas, llamas, and guanacos), whereas no hybridization signals were detected in Old World camelids (dromedaries and Bactrian camels) or other mammals (horse, cat, dog, cattle). These findings suggest that the three large unassigned scaffolds contain sequences unique to South American camelids that are overlapping and potentially misassembled. Manual inspection identified a dynamic 267 bp tandemly repeated motif positioned between NOR clusters and the p-arm telomere. All unassigned scaffolds containing these satellite repeats were concatenated into a single ~60 Mb scaffold in VicPac4. We show that oligo-FISH can complement genome assembly by assigning complex and repetitive sequences to specific chromosomes. Characterization of these South American camelid-specific satellite sequences offer valuable insights into comparative organization and evolution of camelid genomes.

Talk_14G. ***Telomere-to-Telomere References and Pangenomes for Domestic Dog***

Sarah Fross, Sam Stroupe, Anna Kukekova, Hannes Lohi, Jeffrey Schoenebeck, Brian W. Davis
Texas A&M University

Personalized pangenomes are increasingly used in human healthcare due to recent advances led by the Human Pangenome Reference Consortium. Our efforts build upon these advances by utilizing multiple representative reference-quality genome haplotypes aligned to one another to identify normal and deleterious variation in domestic animals. We present the current iteration of the Domestic Dog pangenome and assembly methodology, which implements advances made in our work in Equids. The resulting genome graph leads to better accuracy when examining structural variation over entire chromosomes for breed association and extends the utility of genomes sequenced using short read approaches. Applying personalized pangenome methods, assessment of short read variant discovery shows a decrease in reference bias for domestic dog breeds and Canidae both represented and absent from the pangenome compared to linear haploid references. Utilizing fibroblast-derived cell lines, the application of pangenomes is enhanced by the addition of telomere-to-telomere (T2T) haplotypes from various dog breeds,

allowing a high-resolution understanding of the structural differences with the species. Currently composed of 27 dog breeds, the Domestic Dog pangenome provides greater than 250 megabases of novel diversity represented by 65 haplotypes from haploid and diploid assemblies.

Talk_15G. *Transgene removal using DNA repair*

Joseph S. Romanowski, Keun Chae, Kevin M. Myles, Zach N. Adelman
Texas A&M University

Site-directed nucleases such as homing endonucleases and programmable CRISPR/Cas systems have revolutionized the field of genetics by enabling site-specific insertions or deletions through DNA double-strand break (DSB) repair. In the field of mosquito vector control, gene editing by these tools has inspired a new wave of population control approaches that aim to prevent disease transmission. Though much DSB repair studies have been done in humans, mice, fruit flies, and yeast, less has been performed in disease vector mosquitoes like Aedes aegypti, an organism in which site-specific gene editing has become commonplace. Here, we report a scalable, high-throughput platform for studying DSB repair by delivering CRISPR/Cas9 and I-*SceI* to Aedes aegypti embryos, capable of measuring single-strand annealing (SSA), non-homologous end joining (NHEJ), and microhomology-mediated end joining (MMEJ) repair outcomes. We find CRISPR/Cas9 can delete up to 8.6-kbp of transgene by SSA repair with 684-bp direct repeat sequences to restore wild-type alleles in the *kynurenine 3-monooxygenase* (*kmo*) locus. We also report a 4-fold increase in SSA/indel ratios when I-*Sce*I was used to induce the DSB compared to CRISPR/Cas9. Further, we found that enriched indel events were attributed to the MMEJ repair pathway and conclude that it is the dominant form of repair in *Aedes aegypti* at CRISPR/Cas9 DSBs.

Talk_16G. *Transcriptomic analysis of the stable fly brain and genetic control approaches*

Tyler Chan, Zachary Adelman
Texas A&M University

Stable flies are an economically significant pest of livestock both in the US and globally, and they are also vectors of disease. Increased insecticide resistance has been documented in stable fly populations, highlighting the need for genetic and other methods of controlling stable fly populations. However, both stable fly sexes have a painful bite and must take a blood-meal before mating, which makes sterile insect technique (SIT) less than optimal for large releases. Transcriptomic analysis of the stable fly brain before and after blood meals reveals potential targets for reducing biting behavior, and microinjections of embryos shows potential for genetic sexing strains of stable fly.

Talk_17G. *DirectRepeateR: An R package for annotating direct repeats in genome assemblies*

Megan Copeland, Andres Barboza, Joseph Romanowski, Zach Adelman, Heath Blackmon
Texas A&M University

Exploring the role of natural selection on the distribution and abundance of direct repeats in eukaryotic genomes is critical for understanding their evolutionary impact. Direct repeats can be used by the single-stranded annealing repair pathway, impacting genome integrity. We developed DirectRepeateR, a software package designed to detect and annotate direct repeats in genome assemblies. The tool operates on a de novo basis, enabling the identification and annotation of direct repeat sequences. To demonstrate the value of our software, we investigate whether the Aedes aegypti genome's distribution of direct repeats is consistent with selection against having

direct repeats in regions where the mutagenic effects of the single-stranded annealing pathway would impact coding sequences. Our results suggest that selection has acted against direct repeats that flank or overlap with protein-coding DNA sequences.