SERNM

Genomics Education Partnership

Southeast Regional Node Meeting and Student Symposium FALL 2025

Date: November 14, 2025
Location: Virtual (Zoom & Discord)

Zoom Link:
https://uasystem.zoom.us/j/96926391457?pwd=T21BdERZalQ5ZkE4aFNlTC9MZkpadz09

Poster Session Access (Discord): (This link provides 24h guest access to the poster sessions)

https://discord.gg/SRMcuBcd

Program Schedule

Time (EST)	Session
12:00 PM – 1:00 PM	Poster Session Q&A (Discord)
All Day	Poster Presentations (Discord)
1:00 – 1:10 PM	Welcome & Opening Remarks
1:10 – 1:40 PM	Keynote Speaker - Chinmay Rele, University of Alabama *Network Evolution: How Networks Evolve and Constrain Sequence Evolution*
1:40 – 3:40 PM	Oral Presentations

Keynote Presentation (Zoom Nov 14, 2025 1:10 pm EST)

Chinmay Rele
University of Alabama
Genomics Education Partnership

Network Evolution: How Networks Evolve and Constrain Sequence Evolution

Oral Presentations (Zoom Nov 14, 2025 1:40-3:40 pm EST)

1:40 PM – Julia Vasconcellos (University of Alabama)
Examining the Insulin Signaling Pathway via Annotation of *Lnk* in *Drosophila subobscura*, Referenced from Model Organism *Drosophila melanogaster*

Abstract: Julia Vasconcellos, Logan Cohen, Laura Reed: *Drosophila melanogaster* is a model organism due to its short lifespan and shared conserved genes and pathways in humans; one of these is the insulin signaling pathway, which can be studied in fruit flies and be applied to other organisms. The lymphocyte adapter gene *(Lnk)* regulates inflammation and cell migration pathways. *Lnk* was annotated in the organism *Drosophila subobscura*, referenced from the model organism *D. melanogaster.* This annotation can advance understanding of *Lnk* in not only various fruit fly species, but also in human medical practices. The alignments for the putative *Lnk* ortholog have minimal gaps and high similarity, making it likely to be an ortholog. The genetic neighborhoods of *Lnk* are conserved in both fly species, although the gene is found on the negative strand in *D. subobscura* and the positive strand in *D. melanogaster*. There are the same number of isoforms in both species, although there is more variation between isoforms in *D. subobscura.* This annotation also examines each isoform completely, so the differences between each and between *D. melanogaster* can be compared and analyzed. Determining the level of gene conservation between the two species is essential for understanding the function of *Lnk.* This annotation will broaden applications and knowledge of the insulin signaling pathway in all organisms.

1:47 PM – Seema Soti (University of Alabama)
Gene model for the ortholog of *Sdr* gene in *Drosophila arizonae*

Abstract: Seema Soti, Logan Cohen, Laura K. Reed: *Sdr* (Secreted Decoy of Insulin Receptor) is a negative regulator of insulin signaling and is crucial for preserving *Drosophila's* nervous system and function. During the development of the embryo and larva, it is expressed in glial cells, where it controls insulin signaling and neural support. The role of *Sdr* has been studied in other stages of flies but its role in adult flies is not explored well. This study used *Drosophila melanogaster* as the reference species to build a gene model for the *Sdr* ortholog in *Drosophila arizonae* to determine its genomic structure and evolutionary conserved portions. The result shows that *D. arizonae Sdr* ortholog is a single isoform that maintains the same exon number, order, and overall structure as its *D. melanogaster*. Synteny analysis between *D. arizonae* and *D. melanogaster* revealed that the position of *Sdr* and one of its neighboring genes (*CG14861*) are conserved supporting that these genes are orthologs. Minor genetic variations such as short indels cause slight deviations in the dot plot on *D. arizonae* which represents genomic rearrangements rather than modifications in gene function. These findings indicate that *Sdr* has been conserved across species throughout *Drosophila* evolution. From this work, *D. arizonae* could be a suitable model for understanding the evolutionary genetics of insulin-related signaling. However, further study of *Sdr* is important to illustrate how neural regulatory genes and insulin signaling pathways are conserved across Drosophila evolution.

1:54 PM – John Powell and Sade Henry (Georgia State University)
High impact of undergraduate research in extracurricular programs on student success.

Abstract: John Powell, Sade Henry, VR Falkenberg: Undergraduate research experiences and extracurricular laboratory-training programs serve as high-impact educational practices that substantially elevate student success across academic, professional, and personal domains. Through programs such as EXCITE, Extra Curricular Instrument Training Experience, students gain structured exposure to laboratory etiquette, safety, measurement accuracy, analytical techniques, and scientific software competencies that form the foundation of evidence-based inquiry. The program's no-pressure, hands-on learning environment fosters confidence, supports skill acquisition, and creates strong mentoring and peer networks that reinforce persistence in STEM pathways. Engagement in research projects—including UV-Vis dye analysis, alkaline water characterization, chromatography, and renewable adsorbent experiments—enhances students' ability to identify patterns, construct logical arguments, and understand the necessity of empirical evidence. Participants report strengthened critical thinking, deeper academic curiosity, and clearer alignment between scientific training and long-term professional goals, particularly for pre-medical students seeking to integrate research with future clinical practice. Overall, this presentation demonstrates that structured undergraduate research and extracurricular training programs significantly improve student competencies, scientific identity, and motivation. This ultimately contributes to greater academic performance, preparedness for advanced study, and long-term career success.

2:01 PM – Chipper K. Johnson (Auburn University)
Manual Curation of the PRDM9 Gene in the Diamond-backed Terrapin (*Malaclemys terrapin pileata*)

Abstract: Johnson, Chipper K., Havard, Logan G., Stevison, Laurie S: PRDM9 is a rapidly evolving protein that directs meiotic recombination hotspots and plays a critical role in ensuring accurate chromosome segregation and genetic diversity. While PRDM9's function is well-established in mammals, the gene is completely absent in birds and crocodilians, and at least 10 documented losses have occurred across vertebrates. Understanding PRDM9 evolution in non-avian reptiles—representing over 12,000 species—has been hindered by low-quality genome assemblies and poor gene annotation. Here, we present a detailed manual curation of the PRDM9 gene model in the diamond-backed terrapin, *Malaclemys terrapin pileata*. Initial examination revealed the automated annotation as part of the reference genome lacked the KRAB domain, which is one of four canonical PRDM9 domains. It also exhibited unusual truncation in the beginning of the sequence. To generate an improved gene model, we performed tBLASTn searches using both human PRDM9 (NP_001297143) and painted turtle (*Chrysemys picta bellii*, XP_065429976.1) protein sequences against the *M. t. pileata* genome. The painted turtle query provided superior alignment metrics and identified genomic sequence extending approximately 11.5 kb beyond the original annotation. We extracted the expanded genomic region and used GeneWise with the complete *C. p. bellii* PRDM9 protein sequence to predict exon structure. The predicted protein was validated using InterProScan, confirming restoration of the missing KRAB domain. Manual refinement in NCBI Genome Data Viewer with six-frame translation identified the correct start and stop codons, validated canonical splice sites (GT-AG dinucleotides), assigned intron phases, and incorporated RNA-seq coverage data. The finalized gene model comprises ten exons, and the translated protein sequence contains all expected PRDM9 domains including KRAB, SSXRD, and zinc finger arrays. This work demonstrates how manual curation can correct automated annotation errors in poorly assembled genomic regions, particularly near chromosome ends where PRDM9 is frequently located. Accurate PRDM9 gene models are essential for understanding recombination evolution and have practical relevance for evolutionary biology and conservation genetics in reptiles.

2:08 PM – Naomi Jordan and Sahasra Maddu (Mercer University)
Exploring "rolled" (rl) in *D. Eugracilis* and *D. Elegans*

Abstract: Naomi Jordan, Sahasra Maddu, John Stanga: The gene *rolled* (rl) in the species *D. melanogaster* encodes the mitogen-activated protein (MAP) kinase, a core component of the RAS/MAPK pathway. It is inactivated by the phosphatases *PTP-ER* and *Mkp3*. It phosphorylates a diverse set of downstream cytoplasmic and nuclear effectors, which impact cell fate decisions in a wide array of tissues. In *D. Melanogaster*, this gene is concise, easily studied, and appears to be vital to the regulation of the RAS/MAPK pathway. The Pathways Project Walkthrough was used to discover findings on *rolled* (rl) in the exploration of *D. eugracilis* and *D. elegans.* The UCSC Genome Browser allowed us to find the genomic neighborhood and gene structure. BLAST searches were conducted to identify the genomic location. The Gene Record Finder provided further details regarding isoforms, coordinates, and protein

information. In *D. elegans*, there was no significant similarity found in the blastp search results for the closest upstream gene symbol and protein sequences of the genomic neighborhood. *D. eugracilis* has a confusing and difficult arrangement that leads to a variety of possibilities for the genomic annotation of several species.

2:15 PM – Emie Kate Vandiver (University of Alabama)
A Multi-Ortholog Analysis of *Pdk1* Across *Drosophila*

Abstract: Emie K. Vandiver, Logan K. Cohen, Laura K. Reed: The insulin/TOR signaling pathway is a conserved pathway across many species that regulates growth, metabolism, and aging. When this pathway is disrupted, it can have serious consequences and cause various metabolic syndromes. *Pdk1* is a key kinase in the insulin signaling pathway, and it is also involved in various other biochemical pathways across species. *Drosophila melanogaster* is a good model organism to study biochemical interactions due to their fundamental genetic and molecular similarities with humans. Learning the evolution of this pathway could give medical researchers insights into human disease implications. In this multi-ortholog analysis of *Pdk1* across 32 species of *Drosophila*, a synteny analysis will be done in the immediate genomic neighborhood of *Pdk1.* The synteny of *Pdk1* and its genomic neighborhood is relatively conserved across species, but the synteny is not as conserved in some phylogeny. In the species *D. kikkawai* the synteny is not very conserved. Using *D. melanogaster* as a reference species, a series of domain analysis will be performed to see if the structural domains of *Pdk1* are conserved in *D. kikkawai*, even though the synteny is not.

2:22 PM – Aneh Njoh (University of Alabama)
Challenges in Annotation Viewed Through Reconciliation of *Insulin-like peptide* (*Ilp*) Gene Orthologs in *Drosophila albomicans*

Abstract: Aneh Njoh, Logan Cohen, Laura K. Reed: Gene annotation is the process of identifying the structural and functional components of genes from sequence data, through comparative and computational methods. *Insulin-like peptide* (*Ilp*) genes in *Drosophila* play key roles in growth, metabolism, and reproduction, yet ortholog identification across species remains difficult due to rapid sequence divergence and incomplete evidence. Using the Genomics Education Partnership (GEP) workflow, independent student annotations of *Ilp1*, *Ilp2*, *Ilp3*, *Ilp5*, *Ilp7*, and *Ilp8* were compiled through integration of RNA-Seq data, BLAST homology searches, multiple sequence alignments, and computational gene predictions. Among 13 initial annotations, 62% contained errors in exon boundaries, splice sites, or ortholog assignments, which were resolved through reconciliation. This process refined *Ilp* gene models from *Drosophila albomicans* and produced a gene set suitable for subsequent comparative and functional analyses. This protocol can be adapted to other scientific questions and provides a scalable approach for improving annotation accuracy and enhancing publicly available genomic databases.

2:29 PM – Elizabeth Wasson (University of Alabama)
Comparative Multi-Ortholog Analysis of *chico* Reveals Evolutionary Trends in *Drosophilla*

Abstract: Elizabeth Wasson, Logan Cohen, Laura K. Reed: The Insulin/*Tor* signaling pathway plays an important role in growth and metabolism, with the gene *chico* acting as a key intermediate. Studying genes within this pathway can provide insight into human health and our understanding of Metabolic Syndrome. *Drosophila melanogaster* is an ideal model organism for use in this investigation because it possesses many genes orthologous to the human Insulin/Tor signaling pathway due to common ancestry with humans. This study is a multi-ortholog analysis of the gene *chico* within the 32 species of *Drosophila* by analyzing manually annotated orthologs across a 32 species phylogeny Our analysis includes DN/DS, Multiple sequence analysis as well as domain analysis. We hypothesize that after running this analysis we will be able to better understand and identify conserved and functionally significant gene expression patterns as well as changes in the gene throughout evolution. The results of this analysis will provide insights into the evolutionary trends of the Insulin/*Tor* signaling pathway, improving our understanding of how insulin signaling evolves across different species and deepening our knowledge of *chico* and its role in homeostatic regulation.

2:36 PM – Stephen Denham, Preet Jani, Evan Smith, and Ian Garcia (Mercer University)
Analysis of *Ptp61F* in 4 Species of Flies

Abstract: Stephen Denham, Preet Jani, Evan Smith, Ian Garcia, John Stanga: The research done was to explore the conservation of genes and their pathway across species. The main focus was on annotating the Ptp61F gene in D.

hydei, D. bipectinata, D. albomicans and D. guanche as the ortholog of Ptp61F in Drosophila melongaster, which plays a role in the insulin signaling pathway. Using tools like GEP UCSC Genome Browser, BLAST, and the Gene Record Finder this research identified the coding sequences and genomic neighborhood of Ptp61F. The analysis confirmed collinearity through alignment and comparison scores as well as the conserved gene orientation. The project determined that each of the different species has 5 isoforms (4 unique isoforms), and through examination of the dot plot and protein analysis generated by the GEP Gene Model Checker it was determined that the isoforms and their orthologs have similar structure. This analysis contributes to the further understanding of the evolutionary conservation of metabolic pathways of the genome of varying species.

2:43 PM – Tori del Cid (University of Alabama)
Evolutionary Changes in Synteny Around the Pten Locus Across *Drosophila* Species

Abstract: Tori del Cid, Logan K. Cohen, Laura K. Reed: The Insulin/Tor pathway is a key signaling network that regulates metabolism and growth in many eukaryotic species. The *Phosphatase and Tensin Homolog (Pten)* gene acts as a negative regulator of this pathway. Studying genes within this network provides insight into the mechanisms underlying metabolic syndromes. *Drosophila* species serve as an effective model for this research because many of their genes are orthologous to those in humans. This study examined changes in synteny within the genomic neighborhood of *Pten* across various *Drosophila* taxa. Specifically, the four closest upstream genes (*Rsf1*, *REPTOR-BP*, *Mob3*, and *CG4953*) and the four closest downstream genes (*Fundc1*, *Ror*, *CG31717*, and *bsk*) were analyzed. It was hypothesized that species more distantly related to *D. melanogaster* would display greater divergence in *Pten*'s genomic neighborhood. The results supported this hypothesis: starting with *D. pseudoobscura*, notable rearrangements were observed, including the insertion of genes such as *l(2)SH0834* in *D. virilis*, *D. novamexicana*, *D. grimshawi*, and *D. busckii*. These findings suggest that *Pten* plays an evolutionarily dynamic role within the Insulin/Tor pathway. The observed divergence across *Drosophila* species provides insight into how pathway regulation and genomic organization may have evolved over time.

Oral Presentations (Breakout Room 1 Nov 14 2:50 pm)

2:50 PM – Alison Thome (University of Alabama)
Orthology of Rheb in *Drosophila ficusphila*

Abstract: Alison Thome, Logan Cohen, Laura Reed: The insulin signaling network regulates glucose uptake and metabolism to maintain homeostasis through energy balance and sugar control. Within this pathway, *Ras homolog enriched in brain* (Rheb) plays a critical role by activating mTORC1, thereby promoting cell growth, protein synthesis, and metabolic regulation. As diabetes and other metabolic disorders affect millions of individuals worldwide, studying regulator genes such as Rheb is essential for understanding the evolution and function of key modulators that could better medical treatment. Using the model organism *Drosophila Melanogaster*, which has a well-established genome and conserved insulin signaling components, we can investigate the evolutionary conservation and function of these genes. In this study, synteny in the Rheb ortholog in Drosophila *Ficusphila* was examined using gene annotation to construct a gene model. As a result, it was found Rheb in *Drosophilia Fiscusphila* Is highly conserved, with all upstream, downstream, and target genes exhibiting orthology. Because the insulin signaling pathway in Drosophilia is similar to humans, these findings provide valuable insight into the specific role of Rheb as well as evolutionary patterns underlying its regulation.

2:57 PM – Ayush Pathak (University of Alabama)
Gene model for the ortholog of *slmb* in *Drosophila miranda*

Abstract: Ayush Pathak, Logan Cohen, Laura K. Reed: The *supernumerary limbs (slmb)* gene plays a crucial role in the regulation of biological processes, particularly as a key player in the regulation of proteins and development. *Drosophila*, as an established model organism for genetic studies, can offer insights into the proteomics and phylogenetic standing of *slmb*. We employed gene annotation to construct a gene model for the ortholog of *slmb* in *D. miranda*, using *D. melanogaster* as the model organism. By identifying homologous genomic neighbourhoods in both species, we narrowed down the location of *slmb* in *D. miranda*, identifying a putative ortholog which was corroborated using the Basic Local Alignment Search Tool (BLAST) and synteny analysis. This allowed us to isolate the location of the coding exons for this gene. Our analysis indicates that the gene structure in *D. melanogaster*-with two unique isoforms and nine coding exons-is largely conserved in *D. miranda,* with one exon in

the PB isoform absent. Once the composition of *slmb* is better understood across the *Drosophila* genus, the gene's conserved function would be more clear, which can improve our knowledge of genetic diseases.

3:04 PM – Lauren Mack (University of Alabama)
Investigating the orthologs of *Ilp5* in *Drosophila*

Abstract: Lauren Mack, Laura Reed, Logan Cohen: The gene *insulin-like peptide 5 (Ilp5)* encodes a peptide involved in the insulin signaling pathway, activating insulin receptor binding. It is a part of many processes, such as female mating and sleeping behaviors. *Drosophila* is used to study sleep disorders and provide insights into insulin activity and expression in other similar species. With this in mind, we annotated the ortholog of Ilp5, comparing *D. rhopoloa* to *D. melanogaster*, the model organism. Synteny analysis showed a conserved neighborhood, with genes *I-2* and *CG43897* being upstream and genes *CG32052* and *Ilp4* being downstream in both *D. melanogaster* and *D. rhopoloa.* This conservation further supports the idea that *Ilp5* is conserved across *Drosophila* species. Comparing genomic neighborhoods allows us to find a better potential location for *Ilp5*, finding the appropriate coding exons for this gene. When BLASTing the two sequences against each other and comparing start and stop codons, the coordinates brought us to multiple accessions in D. *rhopoloa*. In doing research, there is a triplication of the gene in *D. rhopoloa* that was not present *in D. melanogaster.* In annotating, we looked to discover why this occurred, whether it was random chance or an evolving variation. Finding the conservation of *Ilp5* across multiple *Drosophila* species can help understand the true function of the gene, which can be used to improve the genetic understanding of insulin expression in humans.

3:11 PM – Avery Fantl (University of Alabama)
Annotation of the rictor Ortholog in *Drosophila yakuba*

Abstract: Avery Fantl, Logan Cohen, Laura Reed: Metabolic syndrome increases the risk of diabetes, cardiovascular disease, and stroke through impaired insulin signaling and abnormal lipid regulation. The *rictor* gene encodes a core component of the mTORC2 complex, a critical branch of the insulin and TOR signaling pathway which governs cell growth and energy homeostasis. Since the *Drosophila* species share many conserved metabolic pathways with humans, they serve as effective comparative models for studying the evolution and function of this gene. The project aimed to locate and annotate the ortholog of *rictor* in *Drosophila yakuba* using *Drosophila melanogaster* as a reference sequence. A tblastn search identified a single orthologous region on chromosome X (scaffold NC_052526) with 100 percent query coverage, 77.66% percent identity, and an E-value of 0.0. This interval (12,602,410 to 12,610,879 bp) contained one predicted transcript (XM_039375441) supported by RNA-Seq data and gene prediction evidence. The neighboring genes, *Hs3st-B* and *CG7992* upstream, *VAV* and *CG8010* downstream, displayed conserved order and orientation relative to *Drosophila melanogaster*. The Gene Model Checker also confirmed twelve coding exons forming the two isoforms, *rictor-PA* and *rictor-PB*, with no alignment discrepancies. The results demonstrate strong conservation of *rictor* between *Drosophila yakuba* and *Drosophila melanogaster*. Understanding how *rictor* and related genes evolve across *Drosophila* species enhances insight into insulin pathway regulation and may clarify how disruptions in mTOR signaling contribute to metabolic disorders in humans. Future comparative annotations across additional species could reveal lineage-specific changes in gene structure or expression that impact metabolic adaptation.

3:18 PM – Evan Luu (University of Alabama)
Gene Analysis of *Inr* and Surrounding Genomic Neighborhood in *Drosophila*

Abstract: Evan Luu, Logan Cohen, Laura K. Reed: The insulin signaling pathway is an important pathway that regulates growth and metabolism in *Drosophila melanogaster*. This pathway is mediated by Insulin like receptors which translate signals from insulin like peptides. The interactions between *Inr* and the surrounding genomic neighborhood in model organism *Drosophila melanogaster* were studied to further understand the role of *Inr* in the insulin signaling pathway as a whole. Furthermore, a synteny analysis of *Inr* in *Drosophila Melanogaster* and *Drosophila Obscura* was done to see changes in the genomic neighborhood of Inr in the ortholog. Two genes immediately upstream, *E2F1* and *Archease*, and two genes immediately downstream, *CG15498* and *slou,* were compared. The overall genomic neighborhood was conserved; however, there was a gene duplication of *slalom* which appeared immediately downstream of *Inr* in *D.obscura*. Furthermore, after using BLAST to find the approximate coordinates of the ortholog, it was found that there were eleven CDs in the ortholog while only ten in the model organism. One hypothesis is that this was due to an exon splitting into two different coding regions. These results indicate that *Inr* is a highly conserved gene due to its role as a receptor and translator in different

species that plays a key part in the insulin signaling pathway. These studies provide insight that will help our understanding of not only simplistic insulin signaling pathways, but also for more complex insulin pathways such as in humans.

3:25 PM – Ty Hawkins (University of Alabama)
Gene Model of *Sdr* in *Drosophila eugracilis*

Abstract: Ty Hawkins, Logan Cohen, Laura K. Reed: The *Sdr* (secreted decoy of the insulin receptor) gene plays an important role in regulating insulin signaling and growth. It works by producing a secreted form of the insulin receptor that binds insulin-like peptides, helping control growth rate, metabolism, and stress responses. A synteny analysis of *Sdr* in *D. Melanogaster* and *D. Eugracilis* was conducted with the goal of producing a gene model of the *Sdr* ortholog in the latter species. The gene was located in *D. Eugracilis* and showed well conserved synteny with a percent identity of 80. The genomic neighborhood identified the downstream genes *CG14861* and *RpL10Aa* as orthologous. The closest upstream gene was identified as a non-orthologous insertion, but orthology continued upstream. These results suggest that the role of *Sdr* in regulating insulin signaling is critical, therefore conserved across *Drosophila* species. Understanding this conservation could help researchers study how insulin regulation contributes to differences in body size, metabolism, and lifespan among insects. This research could also contribute to broader studies on aging and metabolic diseases, since insulin pathways are conserved in many organisms, including humans.

3:32 PM – Kailee Aldag (University of Alabama)
Lnk in *D. obscura* Annotation

Abstract: Kailee Aldag, Logan Cohen, Laura Reed: Lymphocyte adapter gene or *Lnk* functions within the insulin signaling pathway as an adaptor for the insulin receptor, stabilizing its interaction with the substrate. It works to regulate lifespan, metabolism, and stress responses. *Drosophila Melanogaster* is an ideal model organism due to its short lifespan and the conservation of genes and pathways it shares with humans. It was therefore used as the reference species when annotating *Lnk* in *Drosophila Obscura*. The ortholog of the target gene in *D. obscura* was likely found and supported by the following lines of evidence. There were high percent identity and few gaps. The genomic neighborhood was conserved between the two species, though there were a few differences. The genes were on opposing strands of DNA and while some genes had less isoforms in the target species, all unique isoforms were conserved. By annotating all isoforms, the differences and conservation between *Drosophila melanogaster* and *Drosophila obscura* can be thoroughly examined. This allows for increased understanding of the function of *Lnk* in *Drosophila* species and in a variety of others, including humans. This annotation will permit increased knowledge and implementation of its effects on the regulation of metabolism and stress responses.

Oral Presentations (Breakout Room 2 Nov 14 2:50 pm)

2:50 PM – Belle Haynes (University of Alabama)
Gene model for the ortholog of *InR* in *Drosophila bipectinata*

Abstract: Belle Haynes, Logan Cohen, Laura Reed: Many metabolic conditions affecting growth and development arise from mutations in the *Insulin-like receptor* gene (InR), which enables glucose uptake and energy production in the insulin signaling pathway. To properly understand *InR*'s function, we must analyze its origins. *Drosophila* has established experimental lines dating back to the early 1900s, making it an exceptional model organism for analyzing the evolution and function of biological pathways. Consequently, we carried out gene annotation to assemble a gene model for the *InR* ortholog in *Drosophila bipectinata,* using *Drosophila melanogaster* as the model organism. Analyzing synteny enabled the construction of genomic neighborhoods in both species. In *D. melanogaster*, the genes *Archease* and *E2f1* were located upstream of *InR*, and the genes *CG15498* and *slou* were located downstream. All genes in the neighborhood were positively oriented, and this model was conserved in *D. bipectinata*. Applying this analysis refined the coding exon and splice junction locations. Two additional coding exons were identified in *D. bipectinata*, codons 2 and 3 in the gene model, compared to *D. melanogaster*, which reflects a need for deeper analysis. To fully characterize *InR* composition, findings must be validated across a larger fraction of *Drosophila* species. Humans and *Drosophila* share many conserved metabolic pathways, including glucose metabolism, so a better understanding of the full function of *InR* could provide more answers about where metabolic conditions originate and why they occur.

2:57 PM – Katie Osburn (University of Alabama)
Gene Model for the Ortholog of *Ilp5* in *Drosophila miranda*

Abstract: Katie Osburn, Logan Cohen, Laura Reed: Insulin-like peptide (*ILP*) is an endocrine hormone that regulates metabolism, growth, reproduction, stress resistance, and lifespan. Investigating genes in the insulin/*TOR* signaling pathway provides insight into metabolic regulation and the genetic basis of human disorders, such as Metabolic Syndrome. *Drosophila* serves as an ideal model organism for studying various types of *ILP* due to its genetic tractability and its common ancestry with humans, which is reinforced by its numerous genes orthologous to the human insulin/*TOR* pathway. This study focuses on *Ilp5*, a hormone analogous to human insulin, to analyze its genomic context and evolutionary conservation. The synteny of *Ilp5* across two *Drosophila* subgenera was examined through gene annotation and bioinformatic analysis. Using *Drosophila melanogaster* as a reference species, a gene model was constructed for the *Ilp5* ortholog in *Drosophila miranda*. Synteny analysis compared the two upstream, nested genes, and the two downstream genes surrounding *Ilp5* to evaluate conservation across species. The approach assessed changes in *Ilp5*'s genomic neighborhood over evolutionary time, allowing for the identification of analogous genomic regions and the putative location of *Ilp5* in *Drosophila miranda*. It was found that the *Ilp5* genomic neighborhood is highly conserved across the two species, which reflects strong functional and evolutionary constraints within the maintained insulin/*TOR* signaling pathway. This study provides insight into how genomic neighborhood conservation influences gene function, thereby advancing understanding of the evolution of insulin signaling and metabolic regulation across species.

3:04 PM – Maddy Carden (University of Alabama)
InR Orthologs in *D. biarmipes*

Abstract: Maddy Carden, Logan Cohen, Dr. Laura Reed: The insulin-like receptor (*InR*) gene regulates cell growth and survival by controlling cell number and size during development, thereby influencing overall body and organ size. Activation of the insulin signaling pathway by *InR* is central to metabolism, glycolysis, and fatty acid synthesis. Given its critical biological functions, the hypothesis is that the *InR* gene in *Drosophila melanogaster* would be highly conserved in the target species *Drosophila biarmipes*. To test this, an examination of conservation through analyses of synteny and protein sequence alignment between the two species was conducted. Synteny analysis revealed that the genomic neighborhood surrounding *InR* is largely conserved, except for the downstream gene *Slou*, which is located on the positive strand in *D. biarmipes* but on the negative strand in *D. melanogaster*. Protein alignment showed over 80% sequence similarity with fewer than 5% gaps. The only structural difference identified was an additional coding exon at the 5′ end of the *D. biarmipes* sequence, resulting in eleven coding exons compared to ten in *D. melanogaster*. These findings indicate that while *InR* is highly conserved across *Drosophila* species, subtle structural differences, such as the additional exon in *D. biarmipes*, may reflect evolutionary adaptations in gene regulation or developmental timing. This underscores how comparative genomics can not only confirm conservation of key pathways but also uncover the genetic changes that drive phenotypic diversity.

3:11 PM – Sydney Young (University of Alabama)
Lpin Isoforms in *Drosophila*

Abstract: Sydney Young, Logan Cohen, Laura K. Reed: Lipin (*Lpin*) plays a role in lipid metabolism and is highly conserved amongst species. *Drosophila* is often used as a model organism in genetic studies because it can provide insights to further understanding the mechanisms, genetic function, and phylogenetic structure of *Lpin* in species. A manual gene annotation was conducted for the ortholog of *Lpin* in *D. bipectinata*, using *D. melanogaster* as the model organism. In doing so, the orthologous gene *Lpin* was located in *D. bipectinata*. Further, the coding exons of *Lpin* in both species were located and isolated. In *D. melanogaster, Lpin* has 11 isoforms, differing by the coding sequence of 14 different CDS's. *D. bipectinata* appears to have 6 isoforms but when coordinates were refined, there are only unique 4 isoforms of the gene. The difference in the isoforms is due to the uniqueness of CDS's 5 and 6 in *D. melanogaster* which only differ by a single protein. Whereas in *D. bipectinata*, this variability does not exist when coordinates are refined, and coding sequences are determined. In humans, the different isoforms of *Lpin* each perform a different function within lipid metabolism. Understanding the variability across isoforms in *Drosophila* species can allow for better understanding of how *Lpin*, though highly conserved, can be found as different isoforms in many species, each with a possibly varying function.

3:18 PM – Tara Casey (University of Alabama)
Gene model for the ortholog of *InR* in *Drosophila novamexicana*

Abstract: Tara Casey, Logan Cohen, Laura K. Reed: The insulin signaling pathway is a central regulator of growth and metabolism, with disruptions contributing to conditions such as diabetes and metabolic syndrome in humans. The *Insulin-like receptor (InR)* acts as a positive regulator in this pathway, and functions by binding 3 insulin-like peptide ligands to regulate cell number and cell size during development. It also plays a role in life-span determination and may be involved in the regulation of other neuroendocrine signaling pathways. To investigate the evolutionary conservation of *InR*, a gene model was constructed for its ortholog in *Drosophila novamexicana*, using *Drosophila melanogaster* as the reference species. Through manual comparative annotation using the GEP Pathways Annotation Workflow and BLAST tools, the identified conserved genomic neighborhoods were identified, and the intron-exon structure and coding regions were refined using evidence from RNA-Seq data and gene prediction models. The annotation revealed the presence of an additional coding exon in *D. novamexicana* that is not present in *D. melanogaster*. This discovery suggests that *InR* may have undergone structural modification in this species, potentially reflecting adaptive changes in insulin signaling. Such a difference is notable given the evolutionary distance between these species, and supports the idea that *InR* is functionally significant enough to have been refined over time. This work contributes to a broader effort to characterize insulin signaling genes across the *Drosophila* genus, which can be applied beyond *Drosophila* to help improve our understanding of the conservation and function of *InR* and related genes in humans.

3:25 PM – Kyle VanderWeit (University of Alabama)
Conservation of Rheb between *D. melanogaster* and *D. rhopaloa*

Abstract: Kyle VanderWeit, Logan Cohen, Laura Reed: The *Rheb* gene from *Drosophila rhopaloa* was annotated against *D. melanogaster's Rheb* sequence using the Genomics Education Partnership (GEP) Pathways Project Annotation guidelines. *Rheb* encodes a Ras homolog enriched in brain that activates the kinase *mTOR*, which plays a key role in signal transduction for the insulin signaling pathway. *D. melanogaster Rheb* sequence served as the reference when identifying the ortholog in *D. rhophaloa* tblastn analysis. Scaffold NW_025335034 was the best match with a 96.7% percent identity, an E-value of 9e-66, and strong evidence of synteny across genomes. Neighboring genes CG12746, CG2931, CRMP, and CG2926 are present in both genes, although on different strands. Both species also contain A and B isoforms of *Rheb*. Both isoforms contain identical coding sequences and five exons. The coordinates for *D. rhopaloa Rheb* are 3,409,130-3410,016 for scaffold NW_025335034. The gene model checker is used to validate this position for exon alignment, reading frame, acceptor and donor sites, and start and stop codons. This confirmed conservation between both species. There is a minor variation at a GC splice donor site in exon 4 of *D. rhopaloa*. The results show that *Rheb* is a highly conserved gene between *D. melanogaster* and *D. rhopaloa*. This supports conservation, while highlighting the evolutionary and biological importance of the insulin signaling pathway in *Drosophila*.

3:32 PM – Emma C. Zur – (The University of Alabama)
Investigating Evolutionary Changes in the *InR* Genomic Neighborhood in Drosophila

Abstract: Emma C. Zur, Logan K. Cohen, Dr. Laura Reed: The Insulin signaling pathway plays an essential role in growth and metabolism, with the gene *InR* acting as a critical receptor in this process. *InR* functions at the core of the insulin signaling cascade, enabling insulin binding and receptor activity that initiate several downstream pathways controlling processes such as cell growth, energy balance, and metabolic regulation. Because *InR* is orthologous to several human genes, including *INSR*, *IGF1R*, and *INSRR,* it provides valuable insight into human health and diseases such as diabetic neuropathy and glucose metabolism disorders. This study examines synteny in *InR* across two subgenera of *Drosophila*, *D. melanogaster* and *D. ficusphila*, by analyzing the evolutionary changes in its genomic neighborhood. The synteny analysis includes the two most upstream genes, *slou* and *CG15498*, and the two most downstream genes, *E2F1* and *Archease*. The experimental hypothesis analyzes the conservation of the genomic neighborhood surrounding *InR* between the two species, reflecting the evolutionary importance of maintaining gene order near functionally critical loci. The findings of this study will help clarify how genomic context influences the evolution patterns of insulin signaling components across *Drosophila* species. More broadly, understanding the conservation of *InR* and its neighboring genes can reveal how selective pressures preserve essential metabolic pathways over millions of years. These insights demonstrate how comparative genomics and bioinformatics not only illuminate the molecular history of life but also inform our understanding of the genetic foundations of human health and disease.

Poster Presentations (Discord)

(Available asynchronously all day; presenters online for Q&A from 12:00 PM – 1:00 PM EST)

Sundus Shahzad (Georgia State University)

Evolution of the *Leptopilina boulardi* Wasp Venom *Cytochrome C* Gene

Abstract: Krishi Agarwal, JoJo Min, Abigail Serrano-Carpio, Sundus Shahzad, Nefertari Edwards, and VR Falkenberg: Bioinformatic analysis of wasp venom genes has implications for understanding complex human diseases like Alzheimer's and Cancer. Evolutionary relationships between wasp venom genes and host (Drosophila) immune responses have already been tied to key signaling pathways, including inflammatory pathways such as JAK-STAT. Our bioinformatic analysis identified evolution at amino acids in exons 2, 3, and 4 in the *LB_CYC* gene in *Leptopilina boulardi*, a species of wasp that has evolved to override the host immune response. The instances of evolution will be key in further investigation of the special ability of *L. boulardi*-17 to resist complete encapsulation.

Joy Dubem Iroegbu (University of Alabama)

Gene model for the ortholog of *Ilp7* in *Drosophila persimilis*

Abstract: Joy D. Iroegbu, Logan K. Cohen, Laura K. Reed: The insulin signalling pathway is essential for metabolic regulation in many animal species, affecting their growth and development and contributing to metabolic disease conditions when perturbed. A key component in this pathway is the Insulin-like peptide 7 (*Ilp7*), which binds to the insulin receptor to activate the insulin signalling network, allowing cellular glucose uptake and energy production. Given the importance of *Ilp7* in metabolic and energy regulation, it is important to examine its conservation across species. This project annotated the gene model for the *Ilp7* ortholog in *Drosophila persimilis*, using *Drosophila melanogaster* as the reference organism because it is well-studied. Synteny analysis showed that the two of the *Ilp7* genomic neighbours in *D. persimilis* maintains conserved synteny with *D. melanogaster*. However, they are all oriented in the opposite direction to their orthologs in *Drosophila melanogaster*, indicating a likely local inversion event in this region and requires further investigation to confirm. In addition, a single intervening gene, *Prot-A,* is inserted between *Ilp7* and its conserved upstream neighbour. Nonetheless, BLAST comparison supported orthology, showing 70.50% identity across 94% of the sequence with a highly significant E-value of 3e-57. Further refining of intron-exon boundaries with splice-junction and RNA-seq coverage evidence identified an alternatively spliced *Ilp7* transcript in *D. persimilis,* which has two coding exons, alongside a transcript similar to *D. melanogaster's Ilp7* that has three coding exons. The analysis also revealed one distinct insertion region in the second exon of the novel isoform. Altogether, these *in silico* findings demonstrate that while *Ilp7* is largely conserved, differences in splicing may contribute to species-specific variations in its function within the insulin signalling network.

Access Posters & Discussion: https://discord.gg/SRMcuBcd
(This link provides 24h guest access to the poster sessions)