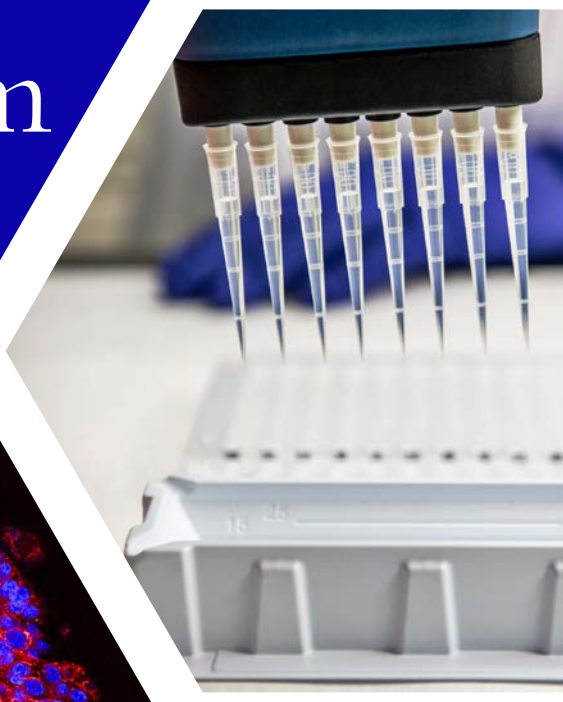
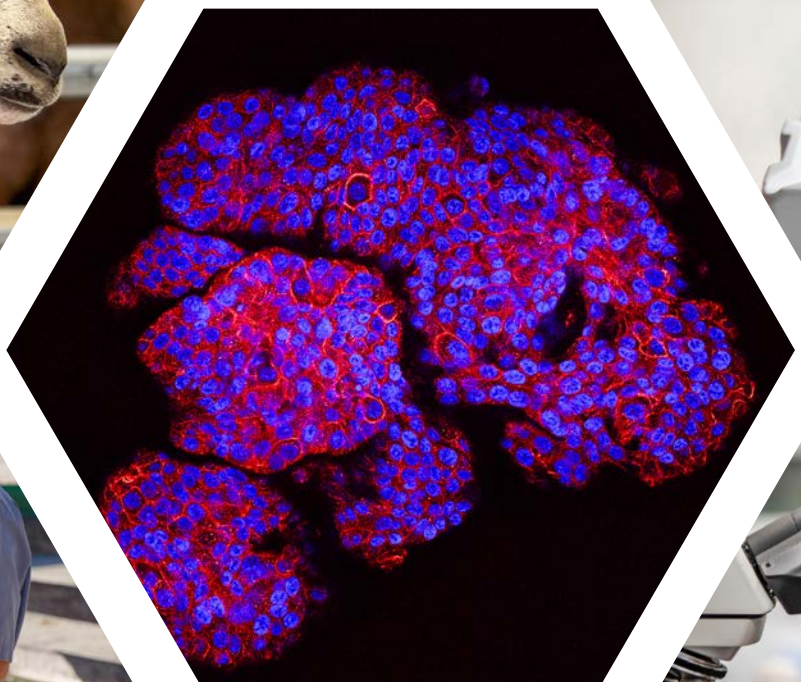




39th Annual Symposium

May 28, 2026

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Welcome from the Chair

Welcome to the 39th Annual Symposium of the Department of Animal and Avian Sciences! This event is a cherished tradition that gives us time to share our research with one another. It's also an opportunity for our graduate students to practice their presentation skills, and a well-deserved celebration for everyone at the end of the academic year.

We have a lot to be proud of as a department, and the research findings presented today are indicative of the many accomplishments our faculty and students have made over the past year. Our research portfolio remains strong and our graduate program continues to attract outstanding students.

A great deal of effort went into planning and preparing for this event. The members of the Annual Symposium committee - Sunoh Che, Heewon Seo, Bishal Bhattachan, Adriana Kempen, Michael Mobley, Ashley Montalvan, and Jonathan Stephanoff - have done an excellent job planning the agenda and preparing the proceedings for this event. No celebration is complete without good food and drinks, so I am grateful to the members of the departmental Social Events committee - Peter Chamberlain, Paul Vaughan, Ashley Montalvan, Andy Schiffmacher, Heewon Seo, Pablo Villafranco, and Zhengguo Xiao - for organizing today's refreshments and tonight's barbecue. Most of all, I thank all the graduate students for their research efforts and the time they devoted to preparing their presentations.

Your attendance and support of today's event is greatly appreciated. Thanks for making our Annual Symposium one of the best days of the year.

Sincerely,

Adele M. Turzillo, Ph.D.
Professor and Department Chair

Invited Speaker

Dr. Martin J. Zuidhof

Dr. Martin Zuidhof is a professor of poultry systems modeling and precision feeding in the Department of Agricultural, Food and Nutritional Science at the University of Alberta. He is internationally recognized as the first to develop a transformative precision feeding system that controls individual feed intake in group-housed chickens, achieving exceptional flock uniformity with body weight coefficients of variation routinely below 2%. This innovative system has opened new avenues to improve broiler breeder and layer management, optimize pullet body weight and composition for lifetime reproductive efficiency, and partition dietary energy among maintenance, growth, and reproduction. It has also become a powerful research platform, eliminating confounding body weight variation to better elucidate physiological and metabolic mechanisms underlying reproductive success in poultry, while enabling high-quality research with free-run birds and directly addressing societal concerns about animal confinement.

Dr. Zuidhof's unique skill set spans broiler breeder nutrition, precision feeding, development of linear and nonlinear mixed models, and biologically meaningful nonlinear mathematical models. His work has contributed to reduced nutrient excretion and a deeper understanding of foraging and feeding behavior patterns in modern poultry systems. Most recently, Dr. Zuidhof served as President of the Poultry Science Association during the 2024–2025 term, providing strategic leadership to the international poultry science community.

As a teacher, he emphasizes mastery of subject matter, critical questioning, and experiential learning. He actively integrates insights from industry and research partners so that students develop not only strong technical knowledge but also informed opinions grounded in real-world challenges.

Program

39th Annual Symposium

May 28, 2026
Department of Animal and Avian Sciences
Animal Sciences/Agricultural Engineering Building
Concourse and Lecture Hall (Room 0408)

8:00 **Breakfast**

8:30 **Welcome and Opening Remarks** - Dr. Adele Turzillo, Department Chair and Dr. Sunoh Che

8:35 **Precision Feeding and Data-driven Animal Management** - Dr. Martin J. Zuidhof, PhD, Professor, Department of Ag, Food & Nutrition, University of Alberta

9:35 **Break**

9:45 **Oral Presentations** (12 minutes each, 3 minutes Q&A)

- 9:45 **Differentiation and regulation of neonatal calf Th2 cells in vitro** - Usman Abubakar
- 10:00 **Effects of guanidinoacetic acid on breast myopathies, and gene expression in the pectoralis major muscle of broilers** - Bishal Bhattachan
- 10:15 **Differences in Testicular Morphology Associated with Sperm Mobility Phenotypes in Broiler Breeder Roosters** - Arianna Bond
- 10:30 **Iron import via transferrin receptor 1 is essential for early postnatal development and browning of white adipose tissue** - Tamseel Fatima
- 10:45 **Developmental regulation of intestinal CTR1 and hepatic ATP7A in perinatal copper homeostasis** - Pratibha Poudel
- 11:00 **Effect of egg storage duration on broiler breeder embryonic gene expression** - Paige Meisner
- 11:15 **Effects of fasting and semi-purified diets on hypothalamic mRNA expression in broiler chicks** - Michaela Riedel

11:45 **Staff Member of the Year Award** - Presented by Dr. Adele Turzillo

12:00 **Lunch**

12:30 **Poster Presentations**

2:15 **Break**

2:30 **Oral Presentations** (12 minutes each, 3 minutes Q&A)

- 2:30 **Region-specific transcriptomic profiles and extracellular remodeling in ovine caruncular and intercaruncular endometrium** - Sonika Neupane
- 2:45 **Branched chain amino acid degradation induces lipid oxidation and TCA cycle metabolism in cultured myoblasts** - Caitlin Ryan
- 3:00 **Synergistic antimicrobial and immunomodulatory effects of Lactiplantibacillus plantarum and berry pomace extracts against Avian Pathogenic E. coli** - Kanchan Thapa
- 3:15 **Cross-species in vivo proteomics reveals a conserved interactome for the lysosomal heme transporter HRG1** - Xuedi Zhang
- 3:30 **Elongating conceptuses rely on non-canonical TCA cycle metabolism to supply biosynthetic precursors within the physiologically low-oxygen intrauterine environment in pigs** - Joe Cain

4:15 **Awards Reception** - Dr. Sunoh Che, Dr. Zhengguo Xiao, and Dr. Adele Turzillo

4:30 **Barbecue Dinner** - Families welcome to attend

Oral Presentation Abstracts

Graduate Students

Differentiation and Regulation of Neonatal Calf Th2 cells In vitro
Presenter: Usman Abubakar
Advisor: Zhengguo Xiao

Neonates face significantly higher morbidity and mortality rates from infectious diseases than adults, accounting for over 30% of newborn deaths. In calves, approximately 66% of early morbidity and all first-year mortality occur within the first month of life and are primarily due to gastrointestinal infections. These infections are driven by enteric parasites like gastrointestinal nematodes and bacteria like *Escherichia coli*; as well as respiratory pathogens such as bovine respiratory syncytial virus (BRSV). Despite this high susceptibility, the mechanisms underlying neonatal immune dysfunction remain incompletely understood. Protection against infection is primarily mediated by the adaptive immune system, in which B cells produce antibodies and T cells coordinate immune responses. CD8+ T cells target intracellular pathogens such as viruses by killing infected cells. In contrast, CD4+ T cells orchestrate immune responses against both intracellular and extracellular pathogens, including viruses, bacteria, and parasites. Upon activation, CD4+ T cells differentiate into specialized functional subsets that direct immune responses by producing cytokines that enhance B cell antibody production and promote pathogen clearance. Among these, Th1 responses are typically associated with immunity to intracellular pathogens, while Th2 responses support antibody-mediated immunity and the expulsion of extracellular pathogens. Given that effective protection against extracellular pathogens relies heavily on CD4+ T cell-mediated immunity, particularly Th2 responses, understanding how these pathways are regulated in cattle is critical. Previously, our lab demonstrated that adult bovine CD4+ T cells exhibit limited IL-4 protein expression even under canonical Th2-polarizing conditions and instead predominantly display an IFNγ-biased or mixed Th0 phenotype, challenging the classical paradigm of T helper 2 (Th2) differentiation defined by interleukin-4 (IL-4) production. These findings highlight fundamental differences between bovine and murine/human Th2 biology and raise critical questions regarding the development and functional identity of Th2 responses in cattle. However, whether these unconventional Th2 characteristics observed in adult cattle are already established in early life or are further constrained by neonatal immune immaturity remains unknown. Therefore, we aim to determine whether developmental constraints shape neonatal CD4+ T cell differentiation and whether the atypical Th2 phenotype observed in adult cattle is established early in life or emerges during immune maturation. To investigate Th2 differentiation in neonatal calves, we will isolate naïve CD4+ T cells ($CD4^{+}CD25^{-}$) and culture them under the three-signal model of T cell activation with established Th2-polarizing conditions. Differentiated cells will be assessed using intracellular cytokine staining and transcriptional profiling to define their functional phenotype. These findings will provide critical insights into neonatal immune programming and inform strategies to enhance protective immunity and improve vaccine efficacy in early life.

Effects of guanidinoacetic acid on breast myopathies, and gene expression in the pectoralis major muscle of broilers
Presenter: Bishal Bhattachan
Advisor: Sunoh Che
Co-authors: Sarai Celestine, Randolph Mitchell

This study evaluated the effects of guanidinoacetic acid (GAA) supplementation on the prevalence of woody breast (WB) and spaghetti meat (SM) and gene expression in the *pectoralis major* muscle of broilers. We hypothesized that GAA, a precursor of creatine, may influence muscle energy metabolism and susceptibility to myopathies. A controlled experiment was conducted using Ross 708 broilers (42 birds × 36 pens, total n = 1512), assigned to two dietary treatments: a control group (18 pens) and a GAA-treated group at 0.08%

(18 pens) under commercial-like conditions. Body weight and feed intake were recorded at four production stages, while myopathy scores were assessed at 6 and 7 weeks through visual and tactile evaluation. *Pectoralis major* muscle samples from control and GAA-treated birds were collected for transcriptomic analysis, including principal component analysis (PCA), to assess gene expression differences between treatments. Results indicated that GAA supplementation significantly increased body weight and feed intake at 7 weeks ($p = 0.03$ and $p = 0.01$, respectively), while FCR and myopathy prevalence were not significantly affected (SM: $p = 0.089$; WB moderate: $p = 0.901$; WB severe: $p = 0.105$). PCA and PERMANOVA showed no overall differences in gene expression between treatment groups. However, differential gene expression analysis revealed that, at week 6, GAA supplementation increased the expression of genes associated with cell proliferation and tissue repair (*SKA1*, *SPARC*, *EPX*). By week 7, the upregulation of *HPGD* and *RhoV* suggested reduced inflammatory signaling and cytoskeletal remodeling. These complementary findings suggest that GAA may modulate muscle energy and tissue remodeling, potentially affecting myopathy development, even in the absence of measurable prevalence changes. This study highlights the complex molecular effects of nutritional interventions and identifies gene expression changes that may help develop future mitigation strategies to reduce broiler breast myopathies.

Differences in Testicular Morphology Associated with Sperm Mobility Phenotypes in Broiler Breeder Roosters

Presenter: Arianna Bond
Advisor: Tom Porter
Co-authors: Paige Meisner, Ricardo Sierra Arroyo, Kuan Ling Liu, Diane Hildenberger, Isaac Harford, Kristen Diehl

The objective of this study was to quantify testicular morphology in roosters with high and low sperm mobility (HM and LM, respectively) and to determine if high oleic soybean meal could alter sperm dynamics. Broiler breeder roosters were randomly allocated to the standard broiler breeder commercial diet or high oleic soybean diet (n=28) experimental groups at 21 weeks of age. Semen was collected twice a week and assessed for sperm concentration and mobility. Testes were collected from HM and LM roosters at 35 weeks of age from each diet (n=5). The right testis was weighed, fixed in 10% formalin, and sectioned for histological analysis of the seminiferous tubules (ST) (ST area, ST diameter, lumen width, and epithelial thickness). Semen metrics, testis weight/diameter, and ST parameters were analyzed by a one-way (diet), two-way (diet; mobility), and three-way ANOVA (diet; mobility; ST location), respectively. The birds fed a high oleic soybean diet had higher sperm mobility (0.57 ± 0.017 AU) than the birds fed a standard soybean diet (0.52 ± 0.01 AU). The weight of the left testes was less in LM birds (13.17 ± 0.9 g) than HM birds (18.64 ± 1.39 g). The ST area was greater in HM birds (0.081 ± 0.004 mm^2) than LM birds (0.069 ± 0.001 mm^2). The ST epithelium thickness was greater in HM birds (95.68 ± 1.28mm) than LM birds (90.77 ± 1.33 mm) and it was also greater in the internal region (96.55 ± 1.17 mm) than the external region (89.90 ± 1.34 mm). The ST diameter was greater in the external region (322.75 ± 4.40 mm) than the internal region (305.48 ± 4.07 mm). The lumen width was greater in birds fed a high oleic diet (120.05 ± 2.83 mm) than the birds fed a standard soybean diet (110.59 ± 2.52 mm) and it was also greater in the external region (127.03 ± 2.92 mm) than the internal region (102.84 ± 2.15 mm). High oleic soybean meal improved sperm mobility and increased ST lumen width. The low mobility phenotype was associated with substantially lower left testes weight, smaller ST area, and smaller ST epithelial thickness. ST location influenced ST diameter, lumen width, and epithelial thickness. Future directions include analysis of differences in genetic or hormonal regulation of testicular growth and function.

Iron import via transferrin receptor 1 is essential for early postnatal development and browning of white adipose tissue

Presenter: Tamseel Fatima
Advisor: Byung-Eun Kim
Co-authors: Yasmin A. Mejia-Guevara, Yining Liu, Ashton Trey Belew, Evan Ying, Najib-El Sayed

Iron (Fe) is essential for adipose tissue development and thermogenic function, yet the mechanisms linking Fe availability to adipogenesis and browning remain poorly understood. Adipose tissue

consists of white, brown, and beige depots, with beige adipocytes representing a key therapeutic target for alleviating metabolic disorders. Fe uptake is facilitated by transferrin receptor 1 (TfR1), and while Fe is known to support mitochondrial biogenesis and browning of inguinal white adipose tissue (iWAT), its precise molecular role in thermogenic signaling and postnatal adipose development has remained unresolved. To investigate the role of Fe in iWAT browning, we employed dietary Fe-deficient and adipose-specific TfR1 knockout ($TfR1^{adi/adi}$) mice. RNA sequencing of Fe-deficient iWAT following β3-adrenergic stimulation (CL316,243) revealed an Fe-dependent thermogenic gene subset enriched for cAMP response elements (CRE) rather than canonical iron response elements. Further, Fe deficiency impaired intracellular cAMP generation in response to both CL316,243 and direct adenylyl cyclase stimulation, blunting PKA-CREB-driven thermogenic programs. Mechanistically, Fe deficiency induced expression of Adcy3-at, which suppresses full-length ADCY3 function, thereby reducing cAMP production and thermogenic capacity. In parallel, we assessed TfR1's contribution to postnatal adipose development across key developmental stages (P3–P30). $TfR1^{adi/adi}$ mice exhibited progressive iWAT atrophy coinciding with loss of TfR1-knockout adipocytes, while TfR1 expression peaked in iWAT at P13 which aligns with the reported postnatal beiging window between P10 and P20. BAT maintained consistently high TfR1 expression from P6 to P14, revealing depot-specific dependencies on TfR1. Importantly, Fe supplementation at P3 and P10 rescued both iWAT development and CL316,243 responsiveness, directly linking Fe availability to postnatal adipose remodeling and thermogenic competence. Together, these findings identify Fe and TfR1 as critical regulators of postnatal adipogenesis and thermogenic signaling, uncovering a previously unrecognized molecular link between Fe status, cAMP production, and the browning capacity of iWAT.

Developmental regulation of intestinal CTR1 and hepatic ATP7A in perinatal copper homeostasis
Presenter: Pratibha Poudel
Advisor: Byung-Eun Kim
Co-authors: Yuan Yee Lee, Yining Liu, Irene Ki

Copper (Cu) is an essential micronutrient required for enzymatic activity, ATP synthesis, and tissue development. Mutations in Cu transporters disrupt Cu homeostasis, causing Menkes or Wilson's disease, underscoring the need for regulated Cu transport. The high-affinity Cu transporter CTR1 mediates dietary Cu uptake in intestinal epithelial cells (IECs), yet how its subcellular localization is dynamically regulated across developmental stages, metabolic demands, and systemic Cu status to maintain whole-body Cu homeostasis remains unclear. In the fetal stage, hepatic Cu levels and ATP7A, an ATP-dependent Cu exporter, peak and decline postnatally, suggesting liver-driven Cu supply before dietary intake begins. However, the mechanisms of fetal hepatic Cu storage, postnatal mobilization, and intestinal CTR1 response remain unclear. We hypothesize that CTR1 localizes basolaterally in fetal IECs to import maternal Cu and shifts apically after birth for dietary uptake. To test this, we performed age-dependent immunofluorescence (IF) of CTR1 in mouse intestine and, since constitutive intestinal CTR1 knockout (KO) is postnatally lethal, we generated tamoxifen-inducible, intestine-specific CTR1 KO mice (Villin-CreERT2) to study intestinal CTR1 function in adults. CTR1 deletion elevated CCS protein in the intestine, indicating local Cu deficiency; however, 10 days of CTR1 loss did not induce Cu deficiency in liver, heart, or brain, suggesting compensatory mechanisms or existing Cu stores use. IF across developmental stages revealed CTR1 in a largely sub-apical vesicular pattern at postnatal days 0 and 10, transitioning to dynamic intracellular trafficking in adults. To explore ATP7A's role in developmental Cu regulation, we characterized its hepatic expression across the perinatal period. ATP7A displayed broad punctate staining at embryonic day 18.5, primarily in albumin-positive hepatocytes, which declined by postnatal day 5 and became restricted near hepatic veins by P14, while Kupffer cells and sinusoidal endothelial cells showed no dramatic changes. These findings suggest coordinated, stage-dependent regulation of intestinal CTR1 trafficking and hepatic ATP7A expression during the perinatal-to-adult transition, advancing our understanding of systemic Cu homeostasis and Cu-related disorder.

Effect of egg storage duration on broiler breeder embryonic gene expression
Presenter: Paige Meisner
Advisor: Tom Porter
Co-authors: A. Bond, R. Sierra Arroyo, B. Kamkrathok, P. Sinpru, and K. Diehl

Pre-incubation egg storage is a standard practice in commercial poultry production, yet extended storage durations are associated with declining hatchability and increased early embryonic mortality during the first three days of incubation. Previously, targeted multiple reaction monitoring-based lipidomic and metabolomic profiling identified storage- and mortality-associated yolk biomarkers. The objective of this study was to evaluate the transcriptional and metabolic responses associated with egg storage in broiler breeder embryos. Fertilized Cobb broiler breeder eggs were stored for either 2 or 10 days at 12 C and then incubated at 37.5 C. Yolk and embryo samples were collected on day 3 of incubation (n=8/storage duration). RNA expression data was analyzed using one-way ANOVA with storage duration as the main effect. Reverse transcription-quantitative PCR (RT-qPCR) was performed to evaluate mRNA levels of 15 genes associated with fatty acid metabolism, oxidative stress, cellular transport and signaling, and cellular differentiation between storage duration groups. Seven genes were significantly ($p<0.05$) up-regulated in the 10-day storage condition, implicating shifts in mitochondrial fatty acid oxidation (carnitine palmitoyltransferase 1A), oxidative stress (glutathione peroxidase 7), cellular transport (beta tubulin and clathrin heavy chain), and early developmental signaling (inhibitor of DNA binding 2 and polo-like kinase 1). These results indicate that some but not all of the genes analyzed for mitochondrial fatty acid metabolism, oxidative stress, cellular transport and signaling, and cellular differentiation were affected by egg storage. It remains to be determined whether any of the genes whose expression was affected by storage results in embryonic mortality. Future integration of metabolomic datasets may help provide biologically informed strategies for improved hatchability in commercial poultry production.

Effects of fasting and semi-purified diets on hypothalamic mRNA expression in broiler chicks
Presenter: Michaela Riedel
Advisor: Tom Porter
Co-authors: Parama Bhattacharjee and Nishanth Sunny

Provision of feed after hatching induces a metabolic switch in chicks, where there is a shift from hepatic lipolysis during embryonic development to *de novo* lipogenesis after hatch. Delayed feeding (DF) delays the metabolic switch and alters gene expression in the hypothalamus—a neuroendocrine organ responsible for appetite and control of feed intake. Our lab has shown that hypothalamic mRNA expression of neuropeptide y (*NPY*) increases after 48 hours (hr) DF, which is a neuropeptide driving feed intake. Furthermore, our group previously reported that DF increased thyrotropin-releasing hormone receptor mRNA expression in the pituitary gland. While the effects of DF have been studied on the hypothalamus, the effects of specific dietary macronutrients have not been studied. The objectives of this study were to determine the effects of DF and specific dietary macronutrients on hypothalamic mRNA expression. Ross 708 broiler chicks were separated into 7 treatment groups (n=8/group): day of hatch (DOH), fully fed (FF), fasted (DF), and fed semi-purified (SP)-complete, SP-dextrin, SP-casein, and SP-corn oil. FF chicks were fed *ad libitum*, while the SP diets were orally gavaged every 8 hr for 48 hr and consisted of 85% of its respective macronutrient on an isocaloric basis. Gene expression was measured using reverse transcription-quantitative-PCR and normalized to phosphoglycerate kinase 1 before being statistically analyzed by ANOVA (SAS Version 9.4). The following hypothalamic genes that regulate metabolism and feed intake were analyzed: *NPY,* deiodinase 2 (*DIO2*), and thyrotropin-releasing hormone (*TRH*). Genes downstream from hypothalamic *TRH* expressed in the liver—deiodinases 1 and 3—were measured and normalized to β-actin. No significant changes in hypothalamic *TRH* mRNA were found in DF chicks compared to FF chicks. There was a significant increase ($P<0.05$, relative to FF) in hypothalamic *NPY* and *DIO2* mRNA. *DIO1* and *DIO3* showed decreased and increased mRNA expression in the liver, respectively. We conclude that fasting newly hatched chicks alters the thyrotropic axis and the regulation of feed intake by the hypothalamus. However, none of the SP-diets given by oral gavage mimicked the FF treatment group. Ongoing research is evaluating the effects of SP diets provided in a crumble form *ad libitum*.

Region-specific transcriptomic profiles and extracellular remodeling in ovine caruncular and intercaruncular endometrium
Presenter: Sonika Neupane
Advisor: Heewon Seo
Co-author: Joe Cain

The ovine placenta utilizes specialized structures called placentomes that act as the primary sites of maternal-fetal exchange during pregnancy. Each placentome is formed by the extension of tortuous cotyledonary villi into the caruncular endometrium (CE). The mechanisms that regulate this invasion and limit it specifically to the CE, remain poorly understood. We hypothesize that the cellular and extracellular matrix (ECM) components of the endometrium selectively permit invasion into the CE during placentomal development. In the present study, transcriptomic and histological analyses were performed to identify possible mediators of this regulation. Total RNA was extracted from paired caruncular and intercaruncular endometrial (IE) samples collected from ewes on Days 32-34 of gestation. Bulk RNA-seq analysis identified 1407 differentially expressed genes (DEGs; Padj< 0.05, log2FC≥ 1). Of these DEGs, 713 were upregulated in the CE and 694 were upregulated in the IE. Functional enrichment analysis using Gene Ontology indicated that these DEGs were predominantly associated with cell–cell signaling and ECM organization. KEGG pathway analysis further revealed enrichment of pathways related to ECM–receptor interaction, integrin signaling, and focal adhesions, in the CE. These data indicate dynamic crosstalk between cells of the CE and cotyledon, and interactions with the ECM during cotyledonary invasion. Uterine sections from ewes on Days 18-34 of gestation were collected and stained. PAS staining revealed that the basement membrane of the syncytial epithelium remains intact in the IE but is breached at the leading front of invading cotyledonary villi. Additionally, a distinct band of PAS stain was detected at the basal stroma of the CE where it appears to delineate the maximum possible extent of cotyledonary invasion. Masson's trichrome staining detected differences in ECM composition and density in the sub-epithelial stroma between the CE and IE. This variation suggests that differential collagen depositions may establish a permissive microenvironment for invasion, similar to the ECM-dependent regulation of invasion observed in human implantation. Collectively, these results indicate a crucial role for region-specific cell-cell and cell-ECM interactions in facilitating the development of placentomes.

Branched chain amino acid degradation induces lipid oxidation and TCA cycle metabolism in cultured myoblasts
Presenter: Caitlin E. Ryan
Advisor: Nishanth E. Sunny

Elevated plasma branched chain amino acids (BCAAs; Valine, Leucine, Isoleucine) and changes in their degradation networks interact with lipid and mitochondrial metabolism in insulin resistant muscle, yet the mechanism remains unknown. We hypothesize that increased BCAA degradation induces lipid oxidation and tricarboxylic acid (TCA) cycle metabolism via AMP-activated protein kinase (AMPK). Mouse C2C12 myoblasts were given increasing concentrations (0, 50, 100mM) of 3,6-dichloro-benzo[b] thiophene-2-carboxylic acid (BT2) for 3 days to induce BCAA degradation. Myoblasts were seeded (500,000 cells/well) in low-glucose (5 mM) DMEM containing 250μM 2:1 $^{13}C_{18}$ Oleate:$^{13}C_{16}$ Palmitate and 2mM of 5-Aminoimidazole-4-carboxamide ribonucleotide (AICAR; AMPK activator) for 5 hrs before collection in 100μL cold methanol for gas chromatography–mass spectrometry. Intracellular BCAAs (μg/500,000 myoblasts ± SEM; Isoleucine; 0μM BT2; 0.61±0.06 vs. 100 μM BT2; 0.44±0.05 $p = 0.06$) and their corresponding ketoacids (ng/500,000 myoblasts ± SEM; α-keto-β-methylvalerate (KMV); 0μM BT2; 1.57±0.16 vs. 100 μM BT2; 1.20±0.08 $p = 0.07$) trended lower with increased BT2, indicating higher rates of BCAA degradation. Lower levels of intracellular branched chain keto-acids following BT2 priming were significantly correlated with higher M+2 Citrate enrichment (APE; atom percent excess) arising from ^{13}C fatty acids (e.g., M+2 Citrate vs. KMV; r (21) = -0.67, $p \leq 0.001$), suggesting induced lipid oxidation with higher BCAA degradation. This induction resulted in higher enrichments (APE) of M+1, M+2, and M+3 isotopomers of multiple TCA cycle intermediates, showing a general induction of mitochondrial TCA cycle metabolism (α-ketoglutarate; M+1; 0μM BT2; 0.81±0.18 vs. 100μM BT2; 1.50±0.25 ; M+2;

0μM BT2; 5.76±0.58 vs. 100μM BT2; 8.36±0.87 ; M+3; 0μM BT2; 1.58±0.38 vs. 100μM BT2; 4.26±0.63, $p \leq 0.05$). Interestingly, AMPK activation in myoblasts via AICAR enhanced BT2-mediated induction of lipid oxidation and TCA cycle metabolism (Citrate M+2 (APE); 100μM BT2 + No AICAR; 30.81±1.19 vs. 100 μM BT2 + 2mM AICAR; 37.75±1.29 $p \leq 0.001$). Priming myoblasts to induce BCAA degradation results in higher mitochondrial lipid oxidation via AMPK. Modulation of BCAA degradation could be a strategy to enhance mitochondrial lipid oxidation and TCA cycle function in myoblasts.

Synergistic antimicrobial and immunomodulatory effects of *Lactiplantibacillus plantarum* and berry pomace extracts against Avian Pathogenic *E. coli*

Presenter: Kanchan Thapa
Advisor: Debabrata Biswas
Co-authors: Anna Phan, Susan Lin

Lactiplantibacillus plantarum (LP) is a well-characterized probiotic with demonstrated antimicrobial and immunomodulatory properties relevant to poultry health. Berry pomace extract (BPE), a polyphenolic plant-derived byproduct, exhibits intrinsic antimicrobial activity and selectively promotes growth of beneficial microorganisms, consistent with prebiotic functionality. The combination of LP and BPE as a synbiotic formulation represents a promising antibiotic alternative strategy against Avian Pathogenic *Escherichia coli* (APEC), a major extraintestinal poultry pathogen with recognized zoonotic implications. This study evaluated the *in vitro* antimicrobial efficacy of LP and BPE against APEC and their potential to alter interaction of the pathogen with host macrophages. Inhibitory and bactericidal concentrations of BPE against APEC were determined. LP was grown in BPE supplemented media to obtain cell-free culture supernatants ($CFCS^{BPE}$). APEC growth kinetics, survival, stress-response, and virulence-associated gene expression were assessed following treatment with $CFCS^{BPE}$ or BPE independently. BPE demonstrated an MIC of 1 mg GAE/mL against APEC and enhanced LP growth at 0.5 mg GAE/mL, supporting its prebiotic potential. $CFCS^{BPE}$ reduced APEC counts by >3 log CFU/mL within 24h and achieved complete elimination by 48h ($p<0.001$). These effects were accompanied by significant downregulation of virulence-associated (*iss, fyuA*), outer membrane (*ompC*), quorum sensing (*luxS*), stress-response (*rpoS*), and cell wall biosynthesis (*murD*) genes ($p<0.05$). Further, bacterial membrane integrity and structural alterations were visualized via confocal and scanning electron microscopy. The HD-11 cells were employed to assess the interaction of host macrophage in the presence of LP or BPE. LP pre-treatment significantly enhanced macrophage bactericidal activity ($p<0.05$) without altering phagocytic uptake efficiency. LP and BPE differentially modulated the expression of pro-inflammatory (IL-1β, IL-6, IL-8) and anti-inflammatory (IL-10) cytokines. Collectively, these findings demonstrate the combined antimicrobial and host immunomodulatory capacity of LP and BPE, supporting their development as antibiotic-free intervention strategies for control of APEC in poultry production.

Cross-Species *In Vivo* Proteomics Reveals a Conserved Interactome for The Lysosomal Heme Transporter HRG1

Presenter: Xuedi Zhang
Advisor: Iqbal Hamza
Co-authors: Vijaya Pandey, Jean-Martin Harder, Joshua MacDermott, David Bodine, Ute Hellmich, James Wohlschlegel, Iqbal Hamza

Heme, an iron-containing biomolecule, serves as the prosthetic group for proteins and enzymes involved in many essential biological pathways across all living organisms. Due to its hydrophobicity and cytotoxicity, heme transport and trafficking must be tightly regulated. Using *Caenorhabditis elegans*, we identified the first metazoan heme importer/transporter, HRG-1/SLC48A1, which mediates heme uptake in the worm intestine. In mammals, HRG1 is required for heme-iron recycling in macrophages to sustain new red blood cell production. Given the hydrophobicity and cytotoxicity of free heme, HRG1 likely transports heme by forming ternary complexes with other proteins. Here, we identify the *in vivo* HRG1 interactome using cross-species proteomic analyses combined with functional screening. By

integrating data from transgenic mice, *C. elegans*, and mammalian cells, we reveal a comprehensive list of HRG1 interactors. By assessing their impact on HRG1 expression, localization, and function in *C. elegans*, *Saccharomyces cerevisiae*, and mammalian cell lines we identify ATP-binding cassette transporter ABCB6 as a prominent HRG1 interactor. Using biochemical, cellular, and complementary structural analyses, we demonstrated that HRG1 and ABCB6 forms a stable complex on lysosomal membranes. Our findings provided a functional framework for heme trafficking mechanisms through HRG1-ABCB6 protein complexes.

Post-Doctoral Associates

Elongating conceptuses rely on non-canonical TCA cycle metabolism to supply biosynthetic precursors within the physiologically low-oxygen intrauterine environment in pigs
Presenter: Joe Cain
Advisor: Heewon Seo

Pig conceptuses elongate rapidly through extensive cellular proliferation, migration, and morphological change. Tricarboxylic acid (TCA) cycle flux provides biosynthetic precursors for synthesis of lipids, nucleotides, and amino acids. However, during the peri-implantation period of pregnancy, the low-oxygen intrauterine environment slows electron transport chain (ETC) activity, resulting in the accumulation of NADH and the depletion of NAD^+, stalling upstream oxidative TCA cycle reactions and reducing the generation of biosynthetic intermediates. There is biological precedence for the use of non-canonical metabolic strategies such as reverse TCA cycle reactions to maintain TCA cycle flux and redox balance in low-oxygen conditions, but these pathways have yet to be examined in the porcine conceptus trophectoderm. In the present study, conceptuses from Days 11 to 17 of pregnancy were collected and subjected to LC-MS/MS. After Day 11, concentrations of pyruvate, citrate, and succinate decreased, while concentrations of lactate and fumarate increased, indicating a metabolic shift in response to low oxygen availability. When porcine trophectoderm cells (pTr2) were cultured with low oxygen (5% O_2), or with antimycin to inhibit ETC function, an increase in the NADH/NAD^+ ratio was detected, suggesting that low-oxygen levels within the intrauterine environment generate a reductive force capable of reversing TCA cycle flux. Isocitrate dehydrogenase 1 (IDH1) catalyzes the interconversion of isocitrate into αKG in either the forward or reverse direction of the TCA cycle. ATP citrate synthase (ACLY) irreversibly catalyzes the reverse conversion of citrate into oxaloacetate and acetyl-CoA. Immunoreactive IDH1 and ACLY were detected in conceptus trophectoderm during the peri-implantation period, which suggests that pig conceptuses can reverse TCA cycle flux. Consistent with these findings, *ex vivo* cultures of conceptuses from Day 15 of pregnancy demonstrated that antimycin-mediated inhibition of the ETC causes accumulation of succinate, which is the end-product of the reverse TCA cycle in mammals. Collectively, these results indicate that pig conceptuses likely utilize non-canonical TCA cycle activity to fulfill biosynthetic demands as they elongate in challenging redox conditions.

Poster Presentation Abstracts

Graduate Students

Molecular signatures and machine learning driven stress biomarkers for rainbow trout aquaculture and climate adaptation
Presenter: Youssef Ali
Advisor: Mohamed Salem
Co-authors: Ali Ali, Guglielmo Raymo, Asutosh Dalei

Climate-induced stressors pose significant threats to fish growth, survival, and ecological stability. Identifying reliable molecular biomarkers is crucial for improving stress management and acclimation strategies. This study employed a comprehensive transcriptomic analysis to examine stress responses in rainbow trout (Oncorhynchus mykiss) exposed to five distinct environmental stressors—high and low temperatures, crowding, salinity, and low water quality (characterized by reduced dissolved oxygen and elevated CO2)—over six hours. A total of 21,580 differentially expressed transcripts (DETs)were identified, including 16,959 unique DETs. Heat stress and salinity induced the most pronounced transcriptomic responses, with most DETs being stressor-specific, highlighting distinct physiological acclimation mechanisms. Only 39 DETs were consistently regulated across all stress conditions. Key DETs associated with heat stress were further analyzed using machine learning models to evaluate their predictive potential in distinguishing control and heat-stressed fish from natural Redband trout populations. The logistic model tree (LMT) classifier demonstrated the highest accuracy with a set of 234 DETs. When the dataset was reduced to 50 or 2 DETs, the Random Forest model achieved optimal classification, consistently identifying two heat shock protein transcripts, hsp47 and hspa4l, as primary predictors across both short- and long-term stress responses. In contrast, core DETs shared across stressors exhibited limited predictive power, achieving only 52.78% classification accuracy. These findings underscore the specificity of molecular signatures to individual stressors and highlight the potential of transcriptomic biomarkers for monitoring climate-induced stress in fish populations. The study recommends the integration of these biomarkers into selective breeding programs and conservation strategies to enhance fish resilience and welfare in the face of environmental change.

A calcium-associated transitional stromal state emerges during intestinal mesenchymal remodeling in preweaned piglets
Presenter: Hammed Ayansola
Advisor: Younggeon Jin

Postnatal intestinal development depends on coordinated communication between epithelial and stromal cells, yet the transcriptional dynamics in intestinal mesenchymal stromal cells (iMSCs) during preweaning stages remain undefined in piglets. We investigated whether early postnatal iMSCs undergo temporal changes in niche factor expression that shift stromal support from epithelial proliferation to differentiation. Jejunal iMSCs were isolated from mixed-sex piglets at postnatal Days 0, 7, and 21 (n = 4 per group) and evaluated using enteroid coculture assays, RNA sequencing, and targeted validation. Coculture studies showed that Day 0 iMSCs promoted the formation of large, cystic spheroidal enteroids (suggesting a high proliferative niche), coinciding with peak *RSPO3* expression. In contrast, Day 7 iMSCs supported multibudded enteroids (higher pro-differentiation niche), corresponding with elevated *BMP4* expression. Day 21 iMSCs promoted mixed enteroid growth morphology, accompanied by increased expression of *SFRP1* and *GREM1*, consistent with a more regulated stromal niche. Aligning with the functional data, KEGG and GSEA analyses revealed major transcriptional changes in Day 7 iMSCs compared with Day 0, with enriched calcium signaling and SMAD-pathway activation, including upregulation of calcium-responsive channels (*TRPA1*, *CACNA1I*, and *P2RX7*). To test whether calcium modulation is involved in this transcriptional switch during early postnatal intestinal development in piglets, Day 7 iMSCs were treated with the calcium channel inhibitor SKF-96365 (SKF, 5

μM, 2 h). Following the treatment, SKF significantly decreased *BMP4* and increased *RSPO3* and *WNT5A* in Day 7 iMSCs, reversing the stromal niche expression patterns observed between Day 0 and Day 7 iMSCs (q-value ≤ 0.05). These results identify Day 7 as a transitional stromal state during early postnatal intestinal remodeling, associated with calcium signaling and the emergence of pro-differentiation profiles in iMSCs. Such transcriptional shift precedes the establishment of a more balanced stromal niche required by Day 21. Together, the findings support a model linking calcium channel-dependent signaling in iMSCs to epithelial maturation and provide a novel approach for future studies aimed at improving early neonatal gut maturation and resilience.

Role of metabolic pathways providing acetyl-CoA in the differentiating granulosa cells
Presenter: Taiwo Bello
Advisor: Emilia Przygrodzka
Co-Author: Juliana Sand

Progesterone (P4) is a steroid hormone synthesized by the corpus luteum (CL), an endocrine gland formed after ovulation from remnants of the ruptured ovarian follicle (OF). This differentiation is driven by the Luteinizing Hormone (LH)/Protein Kinase A (PKA) signaling pathway. Activation of PKA triggers the transcriptional and metabolic reprogramming required for the CL formation. Preliminary results showed increased chromatin opening in bovine granulosa cells (GC) treated with a PKA activator, suggesting activation of epigenetic machinery. Acetyl-CoA (AcCoA) serves as the acetyl group donor for histone acetylation and hence is considered an essential epigenetic regulator. AcCoA is also a fundamental precursor for *de novo* cholesterol synthesis for P4 production. ATP-citrate lyase (ACLY) and AcCoA synthetase short-chain family member 2 (ACSS2) supply cytosolic AcCoA. Herein, we hypothesize that PKA signaling facilitates luteal differentiation by metabolic reprogramming that upregulates AcCoA-producing pathways, thereby enhancing cholesterol availability for P4 synthesis and nuclear protein acetylation for chromatin remodeling. To test our hypothesis, GC and luteal cells (n=2-6 per group) were isolated from bovine OF (2-5 and 6-9mm) and mid-luteal phase CL. Bovine GC isolated from 2-5mm OF (n=4) were cultured in the presence or absence of PKA activator (Forskolin) for 24h. Data were analyzed using one-way ANOVA or student's t test. The content of ACLY and ACSS2 progressively increased ($P<0.05$) in GC to luteal cells, suggesting an enhanced AcCoA availability. Alongside this, increased content of Cytochrome P450 Family 11 Subfamily A Member 1 (CYP11A1) and Steroidogenic Acute Regulatory Protein (STAR), and decreased Cytochrome P450 Family 19 Subfamily A Member 1 (CYP19A1) ($P<0.05$) was observed, indicating transition from estradiol to P4 synthesis in luteal cells. Forskolin elevated ($P<0.05$) P4 secretion, the content of ACLY, and acetylated histone H3 (lysine 9 and 27) in GC. Immunofluorescence analysis demonstrated an increase in cytoplasmic and nuclear localization of ACLY in Forskolin-treated GC. These results suggest that PKA signaling stimulates AcCoA supply to enhance lipid synthesis and chromatin remodelling, both essential for proper secretory function and genetic reprogramming of differentiating GC.

Macronutrient-specific initiation of metabolic switch in newly hatched chickens
Presenter: Parama Bhattacharjee
Advisor: Nishanth Sunny
Co-authors: Michaela Riedel, Caitlin Ryan, Tom Porter

The embryonic to post-hatch transition in chickens is characterized by a dynamic metabolic shift from reliance on yolk lipid oxidation during embryogenesis to rapid activation of hepatic *de novo* lipogenesis after hatch. Although this switch is broadly attributed to the provision of the starter diet immediately after hatching, the specific contribution of individual dietary macronutrients to initiating this metabolic switch remains unclear. We hypothesized that dietary carbohydrates alone are sufficient to initiate this metabolic shift in post-hatch chickens. Newly hatched Ross 708 chickens (n=8/group) were assigned to one of the 8 dietary treatments for the 48-hrs post-hatch: fasted (Fas), starter diet (SD), or one of the semi-purified diets, including complete diet or diets enriched in dextrin (Dex), casein (Cas), or corn oil (Oil). The oil diet could not be incorporated into a solid diet and was administered by oral gavage, with a corresponding gavage control group (GC). A cellulose-enriched diet (Cel) was also provided *ad libitum* to measure metabolic changes associated with feeding behavior initiation, independent of caloric intake. Plasma, liver, and skeletal muscle metabolites were quantified using gas chromatography-mass spectrometry, and hepatic gene expression

was assessed by qPCR analysis. Plasma ketone (β-hydroxybutyrate and acetoacetate) concentrations were significantly lower in Dex compared to Cas and Oil ($P \leq 0.03$) but were comparable to SD and Com, indicating robust suppression of lipid oxidation. Conversely, plasma pyruvate and lactate concentrations were highest in Dex and comparable to SD and Com, but significantly higher in Cas and Oil, indicating enhancement of carbohydrate utilization. Similar metabolic patterns were observed in liver and muscle tissues. Dextrin treatment upregulated hepatic lipogenic gene expression (*SCD1*, *ELOVL6*; $P \leq 0.05$) but downregulated lipid oxidation gene expression (*CPT1A*, *PPARα*; $P \leq 0.05$) compared to Cas and Oil treatments. These findings demonstrate that dietary carbohydrate (dextrin) alone is sufficient to initiate the post-hatch metabolic transition in broiler chicks. These results could have implications for optimizing early nutritional strategies to support neonatal growth and development and reduce post-hatch morbidity and mortality rates.

Mechanisms of mammalian hemozoin formation
Presenter: Indira Bhattacharya
Advisor: Iqbal Hamza
Co-authors: Katherine Arnott, Andrew Rock

More than 90% of body iron is recycled when senescent red blood cells (RBCs) are phagocytosed by macrophages in the spleen, liver, and bone marrow, collectively known as the reticuloendothelial system. After erythrophagocytosis, heme-iron is recycled for new RBC production via the heme transporter Heme Responsive Gene 1 (HRG1/SLC48A1), which transports heme from the phagolysosome into the cytosol. In HRG1-deficient mice, heme accumulates as hemozoin (Hz) within lysosomes that are enlarged by 10–100-fold. Hz was first described over 175 years ago in malaria patients, and its formation has been linked to various intracellular and extracellular factors. However, the in vivo mechanisms of hemozoin formation remain unclear. Here, we show that mammalian Hz formation depends on functional lysosomes and that this enigmatic heme-tolerance system is active in additional pathophysiological conditions. Hz formation was markedly attenuated with the lysosomotropic agent chloroquine and in a Niemann–Pick disease model where lysosomal function is impaired. While macrophages were essential for Hz formation, the crystals were also associated with cell-free extracellular vesicles and a diverse array of other immune cells. Parallel in vitro experiments indicate that inflammatory signals trigger Hz formation. We propose that genetic variation in HRG1, or pharmacological inhibition of heme transport, could substantially affect the progression of hemolytic disease.

The virus factories (VFs) of Infectious bursal disease virus (IBDV) increase in liquidity over time
Presenter: Andrew Brodrick
Advisor: Andrew Broadbent

Infectious bursal disease virus (IBDV), a double-stranded RNA virus of the *Birnaviridae* family, produces cytoplasmic replicative bodies, termed “virus factories” (VFs), that we have previously determined are biomolecular condensates driven by liquid-liquid phase separation (LLPS). Viral protein (VP)3 is a major component of IBDV VFs, and we identified the VP3 C-terminus to be an important modulator of the VF physical properties. Though we have previously reported that IBDV VFs grow over the course of an infection, a more detailed temporally resolved assessment of VF properties has yet to be performed. To address this, we utilized mNeonGreen (mNG)- tagged VP3 as a reporter for live cell imaging, and we measured the properties of IBDV VFs over time by confocal microscopy. Interestingly, unlike the analogous viroplasms formed by rotavirus (another double stranded RNA virus in the *Reoviridae* family), whose condensates “harden” or become less liquid over time, IBDV VFs exhibited increased liquidity at later timepoints as measured by fluorescence recovery after photobleaching (FRAP): At 8, 12, 16, and 24 hours post-infection (hpi), the mobile fraction was calculated to be xxxx, xxx, xxx, and xxx respectively. To further investigate the internal properties of the VFs, we employed fluorescence lifetime imaging microscopy (FLIM), a technique which spatially resolves fluorescence lifetime, a property influenced by the local microenvironment. Interestingly, we observed little change in fluorescence lifetime, with measured lifetimes homogenous within individual VFs and between different VFs, with behavior indicative of a single population of fluorescent molecules with lifetimes similar to literature values for mNG in solution (~3.1ns). Taken together, our data suggest that like rotavirus viroplasms, IBDV VFs experience an evolu-

tion in physical properties during an infection, but the course of this evolution has marked differences, revealing another distinction between the *Birnaviridae* and *Reoviridae*.

Evaluating the efficacy of inoculant application in short-stature and conventional corn silage on fermentation quality, nutritional value, and dairy cow performance
Presenter: Hannah Burchard
Advisor: Fabiana Cardoso
Co-author: Niraj Suresh

Corn silage is the most commonly used forage source for dairy cows due to its high energy availability. Due to this, short stature corn (STC) is a relatively new variety of corn that is being investigated as a potential alternative forage source. Short stature corn has been suggested to be efficient in harvesting, ensiling, and have a decreased lodging risk due to the sturdiness of the reduced sized stalk compared to conventional corn (CC). Previously seen, STC silage offers quality nutritional and fermentation characteristics, with potential advantages when treated with organic acids. However, inoculants have also been found to promote the quality of silage as it undergoes fermentation by using bacteria, such as lactic acid bacteria, to produce acids to reduce the pH of silage and protect against yeast and mold growth. The current study implements a 4 x 4 Latin square design, with 32 mid-lactation Holstein cows total, and 4 treatment diets- conventional corn silage with inoculant, conventional corn silage without inoculant, short stature corn silage with inoculant, and short stature corn silage without inoculant. The objectives of the study are to compare nutritional profiles between the two varieties of corn silage with or without the application of inoculants, determine the efficiency of animal performance and production, and evaluate digestibility. The particle size distribution was 25 and 20% on the upper sieves, 48 and 54% in the middle, 14 and 13% on the lower sieves, and 13% in the pan for STC and CC, respectively. Similar to previous studies, STC particle size distribution aligns with the goal values for each sieve, as described by Penn State Extension, with the greatest accumulation in the middle sieve for STC (48%). The DM % for STC and CC was 35.5% and 35%, respectively. As STC is a relatively new variety, little is known about its nutritional impact, particularly in combination when used with inoculants, compared to CC. This study aims to fill knowledge gaps of STC, as its potential economic benefits and compatibility with currently used standard equipment can benefit producers and management practices.

Sequence-level GWAS and fine-mapping to prioritize candidate genes for eight fertility traits in Holstein bulls
Presenter: Jiarui Cai
Advisor: Li Ma

Fertility is a key determinant of dairy herd sustainability, yet its genetic improvement remains challenging because of low heritability, strong environmental influence, and unfavorable correlations with production traits. Leveraging large-scale genomic and phenotypic resources, we analyzed eight daughter-centered fertility traits in 49,930 Holstein bulls using 11.29 million high-quality imputed sequence variants. Genome-wide association analysis was performed with SLEMM-GWA, and candidate loci were further refined by Bayesian fine-mapping with BFMAP. Across traits, 53 significant peaks in GWAS were detected ($P < 5 \times 10^{-8}$), of which 15 are novel findings, together with11,835 fine-mapped SNPs ($P < 5 \times 10^{-5}$). Functional characterization indicated that the strongest candidates were more consistent with proximal regulatory mechanisms, along with a smaller subset of deleterious missense variants (SIFT/CADD score) was also retained. Gene Enrichment analyses highlighted pathways related to PI3K–Akt signaling, Hedgehog signaling, focal adhesion, and cytoskeletal organization and integration with ChromHMM, CattleGTEx and FAEMI annotation further supported the biological relevance of prioritized loci. As a representative example of deeper regional resolution, follow-up of the BTA18 55–60 Mb hotspot prioritized 4 lead-centered blocks spanning 56.29–57.87 Mb, consistent with a locally complex architecture rather than a single isolated signal. Motif disruption analysis provided additional support for a cis-regulatory interpretation of this region. Overall, these results indicate that dairy cattle fertility

traits are shaped largely by local regulatory variation and provide a refined set of biologically supported candidate loci and hotspot regions for future functional validation.

Ketone synthesis and utilization during embryonic and neonatal development in chicken
Presenter: Jasmin Celedon
Advisor: Nishanth Sunny
Co-author: Parama Bhattacharjee

Ketones (beta-hydroxybutyrate[BHB], acetoacetate, acetone) are byproducts of lipid metabolism and are an alternative energy source during periods of fasting, prolonged exercise, and pregnancy. While normal ketogenesis by the liver provides oxidative and synthetic substrates to various peripheral tissues, higher levels of ketones are associated with inflammation and metabolic dysfunction. Unlike most mammalian species, embryonic development in chickens is characterized by circulating ketone levels (2-5mM) which far exceed conditions of clinical ketosis in multiple species. Circulating ketones in the chicken embryo rapidly decrease to 0.25-0.5mM, as soon as the hatchling starts feeding and switches to carbohydrate metabolism. My overall goal is to profile the tissue specific differences in ketone synthesis and utilization, to in turn determine whether hepatic ketogenic insufficiency will impair healthy embryonic myogenesis. Towards this goal, in objective 1, I will characterize ketogenic and ketolytic gene expression (ACAT1, HMGCS2, HMGCL, BDH1B, BDH2, SLC16A1, SLC16A7, OXCT1) profiles in the liver and muscle during embryonic (day 12, 14, 16, 18) and post-hatch (day of hatch and 2 days post hatch) stages in chicken. In objective 2, I will validate a shRNA-based strategy to downregulate the expression of HMGCS2, to determine whether suppression of ketogenesis will impair myogenesis. To validate the downregulation of ketones via suppression of HMGCS2, three sets of lentiviral vector-based shRNAs will be tested for their transduction efficiency. For this, 1 mg of shRNA will be injected into a capillary beneath the eggshell membrane on embryonic day 10, followed by tissue (liver, muscle) collection on embryonic day 14. Alterations in ketogenic and ketolytic metabolites, gene and protein expression will be evaluated using gas-chromatography mass-spectrometry, qPCR and western blots respectively. These studies will help us identify how the liver vs. muscle crosstalk to aid efficient ketogenesis and ketolysis will in turn contribute to the healthy embryonic muscle development in chicken.

Loss of e-cadherin in intestinal stem cells promotes enhanced epithelial repair after colitis injury
Presenter: Jiecheng Chen
Advisor: Younggeon Jin
Co-authors: Bereket Girma, Lauren Kim, Ellie Kim, Rachel Phan

Inflammatory bowel disease (IBD) is characterized by chronic mucosal inflammation and impaired epithelial regeneration. Repeated injury cycles deplete the intestinal stem cell (ISC) pool and disrupt barrier function, yet current therapies targeting inflammation alone are insufficient to restore the mucosal epithelium, contributing to disease relapse and increased surgical risk. E-cadherin, a transmembrane protein central to epithelial cell adhesion and integrity, is well characterized in cancer biology, but its specific role in $Lgr5^{+}$ ISC-driven regeneration following colitis injury remains poorly understood. We hypothesized that E-cadherin loss in $Lgr5^{+}$ ISCs promotes epithelial expansion and accelerates mucosal healing after injury. To test this, we employed two complementary approaches. In a genetic loss-of-function model, tamoxifen-inducible, $Lgr5^{+}$-specific homozygous or heterozygous E-cadherin knockout was induced at peak DSS colitis (day 8; 100 mg/kg tamoxifen for three consecutive days) in Lgr5-CreERT x $Cdh1^{fl/fl}$ mice. In a translational engraftment model using the same colitis protocol, DSS-colitis mice received rectal administration of transiently E-cadherin-knockdown organoids or control organoids at peak disease symptoms. Homozygous E-cadherin knockout significantly expanded the regenerative area and increased Ki-67^{+} proliferating cells within the regenerative zone compared to heterozygous and wild-type controls. Consistent with these findings, mice receiving E-cadherin knockdown organoids showed markedly greater re-epithelialization and mucosal coverage than controls, confirming the pro-regenerative effect of E-cadherin reduction in a therapeutically relevant context. Together, these results demonstrate that targeting E-cadherin in $Lgr5^{+}$ ISCs enhances epithelial regeneration and supports its modulation as a promising strategy to restore mucosal integrity in IBD.

Presenting a General Computational Pipeline for Finding Insertion Sites
Presenter: Ray Gao
Advisor: Jiuzhou Song
Co-authors: Qunhao Niu, Longbin Yang

Precise identification of insertion sites is essential when working with complex transgenes, GFPs, and genomic insertions, yet current methods are often labor-intensive, costly, and lack generalizability. In animal research, genetically engineered models are widely used to study gene function, disease, and therapies, making accurate mapping critical for understanding effects on nearby genes, confirming phenotypes, and avoiding unintended disruptions. Here, we present a general computational pipeline for identifying insertion sites across heterogeneous genomic datasets. The workflow integrates preprocessing, de novo assembly, insertion mapping, statistical modeling, and significance testing into a unified framework. By reconstructing novel genomic regions from short-read sequencing data, the method detects insertions without relying on reference genomes, making it well-suited for unknown or complex constructs. Statistical modeling evaluates the frequency and distribution of insertion events to distinguish true signals from background noise, while providing confidence estimates and prioritizing biologically relevant sites. Within the pipeline, we use the Wasserstein distance to quantify the similarity between observed and expected insertion patterns, enabling systematic comparison of candidate sites. Together, this approach provides a versatile and cost-effective solution for insertion-site identification. We validated the pipeline using four independent single-end chicken DNA sequencing datasets, each generated at varying sequencing depths and containing a GFP insertion at the same known genomic location. Across all datasets, the pipeline consistently identified and closely approximated the correct insertion site, demonstrating robustness to differences in sequencing coverage. Notably, the pipeline successfully assembled and identified the GFP insertion sequence at as low as 17x genome coverage. Performance remained stable across sequencing depths, indicating reliable detection even under suboptimal conditions. These results highlight the pipeline's consistency, accuracy, and broad applicability across diverse genomic datasets. Overall, this work establishes a scalable and species-agnostic framework for insertion-site discovery, with potential to streamline analysis workflows and improve reliability in studies involving large genomic modifications.

Regulators of inter-organ heme signaling
Presenter: Sandeepan Ghosh
Advisor: Iqbal Hamza
Co-authors: Sohini Dutt, Xiaojing Yuan, James Wohlschlegel

Heme, an iron-containing organic ring, acts as an essential co-factor in numerous proteins. Since heme is a hydrophobic and cytotoxic molecule, it must be transported in a well-controlled manner through membranes via specific intra- and inter-cellular pathways. However, the molecular components of heme trafficking remain poorly defined. Our previous studies in *Caenorhabditis elegans* uncovered HRG-7, an aspartic protease homolog, that mediates inter-organ heme signaling between the intestine and extra-intestinal tissues. Intestinal HRG-7 functions as a secreted signaling factor during heme starvation and is regulated through DBL-1, a BMP5 homolog secreted from neurons. Intestinal expression of *hrg-7* is regulated via the transcription factor SMA-9. Here, we identify *hrg-11.1*, and its paralogs *hrg-11.2, hrg-11.3* and *hrg-11.4* as additional components of the HRG-7 mediated inter-organ heme communication network. Loss of *hrg-11* leads to a heme deficiency signal in the heme sensor strain, phenocopying loss of *hrg-7*. *hrg-11* mutants have significantly lower HRG-7 protein level compared to wildtype. Loss of *hrg-11* results in mislocalization of HRG-7 and lower heme levels in muscle and neurons. *hrg-11.1* and *hrg-11.2* mutants show a heme-dependent growth, phenocopying *hrg-7* mutants. Depletion of either *hrg-7* or *hrg-11* paralogs in *hrg-1* heme importer mutants results in lethality, which are rescued with heme. *hrg-1* mutants show elevated HRG-7 even at excess heme that was suppressed in *hrg-11* mutants. Intestine-specific loss of *hrg-11* significantly depletes HRG-7 protein abundance, phenocopying systemic *hrg-11* loss. Knockdown of either *hrg-7* or *hrg-11* causes AMsh glia to over-migrate and reduces the number of GABAergic synapses, phenotypes that are rescued by heme. Collectively, these results strongly support a role for *hrg-11* in regulating HRG-7 secretion, stability, and inter-organ heme signaling function.

Modeling the spillover of avian influenza viruses from wild birds into poultry using primary chicken and turkey intestinal organoids
Presenter: Jyothsna Girish
Advisor: Andrew Broadbent
Co-authors: Matthew Quintanilla, Daniel Sung, Declan Kehlbeck, Younggeon Jin, Kristen Diehl, Andrew Broadbent

Spillover of avian influenza viruses (AIV) from wild aquatic waterfowl into domestic poultry occurs frequently, where infection can be respiratory, or enteric. Spillover into turkeys has cost the US millions of dollars, however, our understanding of how AIVs interact with turkey cells is limited compared with chickens, as there are fewer resources available to dissect the molecular and cell biology of infection. To fill this knowledge gap, and compare how AIVs behave and evolve following spillover into different poultry species, we developed primary apical-out intestinal organoids from both turkeys and chickens that contained diverse intestinal cell types, including epithelial, goblet, Paneth, and enteroendocrine cells. Next, we demonstrated, for the first time, that both chicken and turkey intestinal organoids supported infection with the low-pathogenicity avian influenza (LPAI) strain A/mallard/Minnesota/AI09-2749/2009 (H6N8) that was previously isolated from a mallard duck. Immunofluorescence microscopy (IFM) confirmed viral antigen in discrete organoid cell populations, and viral replication kinetics were quantified using reverse transcription quantitative PCR (RT-qPCR) and tissue culture infectious dose-50 ($TCID_{50}$) assays. Replication dynamics were further compared with the well-characterized LPAI strain A/turkey/Wisconsin/1966 (H9N2). Ongoing studies are aimed at evaluating viral tropism by IFM and characterizing host transcriptional responses in both species using RT-qPCR and bulk RNA sequencing. Future work will sequence viruses recovered after organoid infection to identify potential species-associated adaptations. We hope the primary apical-out turkey intestinal organoids will provide a valuable platform for studying host–virus interactions and may serve as a broadly useful tool for the avian virology community.

Stromal-dependent sodium butyrate stimulation of neonatal pig enteroid growth revealed by AI-guided organoid screening
Presenter: Bereket Girma
Advisor: Younggeon Jin

Neonatal intestinal development depends on coordinated stromal-epithelial interactions within the intestinal niche. Short-chain fatty acids derived from the gut microbiota, particularly butyrate, serve as a primary energy source for colonocytes and support intestinal barrier integrity. Although sodium butyrate increases epithelial cell proliferation in neonatal piglets in vivo, direct application to isolated porcine intestinal epithelial cells fails to recapitulate this effect, suggesting that stromal context may be required for the proliferative response. To address this gap, we established a neonatal piglet enteroid-mesenchymal (E+M) co-culture system and employed a high-throughput, AI-guided image analysis platform based on convolutional neural network segmentation to quantitatively assess organoid area, budding complexity, and morphological expansion over a 10-day culture period. Sodium butyrate elicited a robust, dose-dependent, and stromal-dependent proliferative response: low (0.05 mM) and mid (0.2 mM) doses significantly increased organoid area and budding complexity in E+M co-cultures ($p < 0.0001$), whereas enteroid-only monocultures showed no comparable expansion. In contrast, other tested metabolites, including lactate, nicotinamide, and spermidine, promoted epithelial growth independent of mesenchymal presence, confirming that the stromal requirement is specific to butyrate and is not a generalizable feature of metabolite-driven epithelial expansion. Transcriptomic profiling of butyrate-treated intestinal mesenchymal cells revealed selective enrichment of lipid-centered metabolic pathways, including fatty acid biosynthesis, fatty acid metabolism, cholesterol metabolism, and associated PPAR and AMPK signaling programs. Key induced genes included SCD, FASN, ACSL3, SREBF1, ABCA1, ABCG1, and the niche ligand WNT2B, pointing to coordinated metabolic reprogramming alongside reinforcement of mesenchyme-derived epithelial support signals. Lipid droplet accumulation further confirmed active lipid biosynthesis in butyrate-treated mesenchymal cells at the cellular level. Together, these findings support a model in which sodium butyrate reprograms stromal lipid metabolism and niche signaling to indirectly promote epithelial proliferation through mesenchyme-dependent mechanisms. This study

establishes a scalable, AI-assisted ex vivo platform for interrogating metabolite-niche interactions and identifies butyrate as a stromal-dependent enhancer of neonatal intestinal epithelial expansion.

Bovine intestinal induced intraepithelial T lymphocytes activation, and their regulation by intestinal epithelial cells
Presenter: Akanksha Hada
Advisor: Zhengguo Xiao

Gastrointestinal (GI) diseases in cattle pose significant challenges to animal health and cause substantial economic losses. Intraepithelial T lymphocytes (T-IELs) reside between intestinal epithelial cells (IECs) that form one of the largest T cell compartments in the body, where they balance pathogen defense with immune tolerance. Induced T-IEL subsets, including TCRαβ+CD8αβ+ and TCRαβ+CD4+ populations, produce pro-inflammatory cytokines such as IFNγ and TNFα, and regulatory cytokines including TGFβ and IL-10. However, activation properties of individual bovine T-IEL subsets remain unexamined. Moreover, IECs and T-IELs express complementary ligand-receptor pairs that may modulate T-IEL effector function, but whether these interactions functionally affect T-IEL cytokine production has not been demonstrated. We hypothesized that TCR signaling activates bovine T-IELs, and that IECs regulate their pro-inflammatory cytokine production. To test this, we isolated T-IELs from bovine jejunum, sorted CD8αβ+ and CD4+ subsets by FACS, and examined their activation and regulation by primary bovine IECs. Unexpectedly, TCR stimulation activated both subsets (CD25 upregulation) yet simultaneously suppressed IFNγ and TNFα while TGFβ remained unchanged and IL-10 increased in CD4+ T-IELs, suggesting an intrinsic regulatory program upon TCR engagement. IEC co-culture imposed a further layer of suppression, reducing IFNγ and TNFα in CD8+ T-IELs and IFNγ in CD4+ T-IELs under both unstimulated and stimulated conditions. Transwell experiments showed that CD8+ T-IEL suppression requires direct cell-cell contact, while CD4+ T-IEL TNFα regulation might also involve IEC-derived soluble factors. Monocyte co-culture did not suppress CD8+ T-IEL cytokines, confirming IEC specificity. Since T-IELs and IECs are constantly exposed to luminal microbial products, we tested whether LPS could disrupt this regulatory interaction. Both subsets expressed TLR4 mRNA, but LPS did not alter their cytokine production, and IEC-mediated suppression persisted during LPS challenge. These findings demonstrate that bovine T-IELs have intrinsic regulatory capability, and IECs actively regulate T-IEL pro-inflammatory output that withstand microbial challenge, highlighting potential for developing targeted therapeutics for GI diseases in both cattle and humans.

Impacts of thermal stress on rainbow trout *Onchorynchus mykiss* and their microbial communities
Presenter: Christopher Joung Kim
Advisor: Mohamed Salem
Co-author: Guglielmo Raymo

The rainbow trout *Oncorhynchus mykiss*, is a widely cultivated freshwater fish with a strong contribution to sustainable aquaculture initiatives. Despite its broad range globally, their performance and health in aquaculture is highly sensitive to environmental stressors, particularly temperature fluctuations. Thermal stress can be disruptive of host physiology and alter interactions with associated microbial communities, having potential consequences for growth and immunity. It is well established that microbiomes serve a variety of functions, including metabolic processes, production of essential nutrients, pathogen colonization resistance, and immune system development. Characterizing these communities and their genetic content enables inference of adaptive strategies and functional roles in supporting host responses to environmental stress. This study investigated the impacts of elevated water temperature on aquaculture-grown rainbow trout and their gut microbiota. A prebiotic dietary intervention was implemented to assess nutritional mitigation of heat stress through analyses of diet temperature interaction effects on taxa and functional enrichment. Microbial communities were characterized by utilizing deep whole metagenomic sequencing of fecal samples for taxonomic and functional profiling using a species-specific, proprietary microbial genome atlas. Terminal sampling was conducted to assess host responses, including liver bulk RNA sequencing to characterize transcriptomic changes and

broad patterns of gene expression associated with thermal exposure. Correspondingly, wild redband rainbow trout populations from diverse environments in Idaho were surveyed to contextualize bacterial community structure and variation under natural conditions. Together, this work provides an integrated view of the influence of thermal stress on host-microbial dynamics in rainbow trout, highlighting shifts in microbial composition and functional understanding of host transcriptional responses. Findings may contribute to a broader understanding of environmental stress in aquaculture systems to inform strategies for genetic selection, stress mitigation, and aquaculture management.

Establishing *in vitro* systems to model fetal bovine mammary development
Presenter: Thomas Podles
Advisor: Andrew Schiffmacher
Co-authors: Hannah Burchard, Mai Zarrinkar

The mammary gland is a unique organ system that relies on cellular plasticity to drive drastic remodeling of mammary tissue to accommodate a variety of roles during distinct physiological stages. Multipotent cells are responsible for this high degree of plasticity, and while the presence of true mammary stem cells in the adult gland is a subject of debate, such a population certainly exists in the fetus. Therefore, we hypothesize that understanding fetal mammary development is critical for advancing bovine mammary stem cell research. Our main objective is to develop an in vitro system modelling fetal bovine mammary development to benefit animal health and production. Immunolabelling of TP63 and cytokeratin 5 reveals basal/luminal segregation occurs in the mammary sprout with basal TP63 localization and luminal cytokeratin 5 localization by 90 days of gestation. Similarly, fluorescent in situ hybridization demonstrates expression of early mammary (*TBX3, PTHLH)*, basal (*TRP63*), and luminal (*SOX9, NOTCH1, GATA3*) specifiers in the bovine mammary epithelium with segregation occurring by 90 days. Four cell lines were generated using isolated fetal mammary epithelia and propagated over 7 passages. We confirmed that all cell lines expressed early mammary (*TBX3, PTHLH*), basal (*SNAI2)*, and luminal (*SOX9, GATA3)* specifiers via qPCR. Two cell lines (BOV131 and BOV140) demonstrated an upregulation of luminal specifier *SOX9* when cultured in media containing FGFs and Horse serum, with and without Wnt3a and Rspo1, suggesting differentiation capability. When cultured in 3D conditions, BOV131 showed similar TP63 and E-cadherin immunolabelling patterns as in vivo. In all, we have been able to confirm the feasibility of our in vitro fetal bovine mammary epithelial cell models to be used in future genetic or mechanistic studies.

Functional redundancy underpins gut-microbiome composition across genetically and geographically isolated sub-populations of rainbow trout
Presenter: Guglielmo Raymo
Advisor: Mohamed Salem
Co-authors: Ridwan Ahmed, Ali Ali, Rafet Al-Tobasei

Current cataloging of bacterial taxa inhabiting the Rainbow Trout gut microenvironment remains incomplete and the impact on feed efficiency and nutrient assimilation remains underexplored. The *Rainbow Trout Gut Microbial Atlas (RTGMA)* addresses this gap through a comprehensive genomic survey of bacterial communities inhabiting the trout gut across geographically and genetically distinct trout populations. We report 62 putative novel bacterial symbionts recovered from a highly diverse collection of trout lineages including two USDA-ARS selectively bred cohorts for high and low fillet yield, three European hatchery populations, various wild Pacific Northwest populations, two genetic lines optimized for alternative feed digestion as well as *Flavobacterium* resistant genetic cohort. Constructing metagenome-assembled genomes (MAGs) refined with Hi-C proximity ligation data and axenic isolates, we have curated a database of 455 non-redundant bacterial genomes dispersed across 74 taxonomic orders, with pronounced representation from Lactobacillales, Bacteroidales, and Enterobacterales—core fermenters central to energy extraction and gut homeostasis. Comparative functional genomics reveals a conserved suite of carbohydrate-active enzymes (CAZymes) driving carbon turnover across all host populations, including GH13 starch backbone cleavage, CE4 and GH23 chitin degradation, and GH109

mucin oligosaccharide utilization. Strikingly, these key functions are carried out by taxonomically distinct microbial actors in each population, underscoring functional redundancy as a stabilizing force in microbiome composition. This suggests that trout maintain critical digestive functions despite variable microbial taxonomy. By defining the functional core of the trout gut microbiome, the RTGMA establishes a genomic framework for rational microbiome engineering in aquaculture. These insights pave the way for the design of precision prebiotics and probiotics that promote nutrient assimilation, feed efficiency, and growth performance across diverse production settings.

HRG1/SLC48A1 as a Genetic Modifier of Erythropoietic Protoporphyria
Presenter: Andrew Rock
Advisor: Iqbal Hamza
Co-author: Audrey Belot

The heme transporter HRG1/SLC48A1 plays an essential role in heme recycling by reticuloendothelial system macrophages during the turnover of senescent red blood cells (RBCs). Recent findings suggest a role for HRG1-mediated heme import during (RBC) maturation. To investigate this, we examined a disease model characterized by heme deficiency. Erythropoietic Porphyria (EPP) is an inherited disorder caused by mutations in ferrochelatase (FECH), the enzyme catalyzing the final step in heme biosynthesis. Loss of FECH activity results in accumulation of the heme precursor protoporphyrin IX (PPIX) in RBCs and other tissues leading to photosensitivity and oxidative stress. To assess the role of HRG1-mediated heme import in this context, we utilized the *FECH*^{m1pas} mouse, which carries a hypomorphic mutation of FECH. These mice were modified to either lack *HRG1* (*HRG1 KO*) or overexpress HRG1 (*Rosa26* $^{HRG1\text{-}GFP}$). Loss of *HRG1* reduced mean corpuscular hemoglobin (MCH) and increased cell death in early erythroid progenitors while accelerating PPIX accumulation in erythropoietic tissues. Conversely, HRG1 overexpression reduced stress erythropoiesis and improved MCH when exogenous heme was provided. Together, these findings identify HRG1 as a genetic modifier of EPP and imply heme import as a critical determinant of erythroid maturation under instances of heme deficiency.

Alterations in the content and cellular localization of acetyl-CoA-related enzymes in the aging ovary
Presenter: Juliana Sand
Advisor: Emilia Przygrodzka
Co-authors: Kendra Clark, Taiwo Bello

Ovarian aging is associated with diminished ovarian reserve and a decline in the function of somatic ovarian cells, which are critical for oocyte development and steroid hormone production. Acetyl-CoA-producing enzymes connect cellular metabolism to acetyl-CoA production and protein acetylation, processes that are essential for lipid homeostasis and regulation of protein activity. However, the role of these enzymes in ovarian function and aging has not yet been investigated. This study aimed to determine age-related changes in ovarian morphology and in the content and cellular localization of proteins that provide acetyl-CoA. Ovarian sections from mice (n=3 per group) at different ages [21 days, 3-, and 12-month (mo)] were analyzed using hematoxylin and eosin (H&E) staining to assess the distribution of ovarian follicles (OF) and corpora lutea (CL). Immunofluorescence (IF) staining was performed to evaluate the cellular and subcellular localization of proteins involved in acetyl-CoA production [*i.e.,* ATP citrate lyase (ACLY) and acyl-CoA synthetase short-chain family member 2 (ACSS2)]. Protein extracts from mice ovaries (n=4-6 per group) at different ages (21 days, 3-, 12-, and 17-mo) were analyzed using western blotting to determine the content of the above-mentioned proteins. Results were analyzed using one-way ANOVA with *post-hoc* Tukey's test. H&E analysis revealed a progressive reduction ($P<0.05$) in the number of different types of OF and CL with aging. The content of ACSS2 and ACLY gradually increased with age ($P<0.05$), reaching a maximal level in the ovary of 17-mo-old mice. ACLY and ACSS2 were predominantly localized in the cytoplasm of granulosa (GC), theca (TC), and luteal cells (LC), with signal intensity decreasing with age progression in both OF and CL. Both enzymes were primarily present in the GC surrounding the oocyte. ACSS2

was more abundant in the GC of young (21-day, 3-mo-old) mice compared to ACLY. ACLY staining increased in the stroma of 12-mo-old mice, especially multinucleated giant cells, a hallmark of ovarian aging. ACSS2 staining was elevated in the CL of 12-mo-old mice. Our findings indicate that ACLY and ACSS2 regulate steroidogenic cells and cells involved in inflammation and fibrosis in the aging ovary, providing a potential basis for strategies to enhance steroid hormone production and reduce tissue stiffness in aging females.

Effect of sodium sulfite or sodium acetate on feed intake and milk production in lactating dairy cows
Presenter: Anand Tiwari
Advisor: Richard Kohn

Sodium sulfite and sodium acetate are preservatives for foods that may also affect rumen fermentation. This study evaluated effects of sodium sulfite and sodium acetate in TMR fed to lactating Holstein cows. 32 multiparous Holstein cows (174 ± 41 days in milk; 40 ± 6 kg milk/d) were used in a replicated 4 × 4 Latin square design with 8 squares and four 21-d periods. Four original dietary groups were used: bicarbonate, bicarbonate + sulfite, acetate, and acetate + sulfite. One square was comprised of 4 rumen fistulated cows, and two squares (8 cows) received a double dose of sulfite when assigned a treatment containing sulfite, resulting in 3 sulfite levels (0, 0.45, and 0.9% of DM) with or without 1% acetate. Two cows were removed from the study after the second period due to illness. The mixed model (JMP 19.0.1) included fixed effects of period, sulfite level (0, 0.45, and 0.9% of DM), acetate (0 or 1% of DM), and sulfite × acetate, and random effects of cow and period × cow. DIM and baseline milk production were used as covariate. Cows in 0.45% sulfite had greater body weight (692 kg) vs 0% (674 kg) or 0.9% sulfite (676 kg; SE = 12.0; $P < 0.05$). Milk yield decreased ($P < 0.05$) with 0.9% sulfite (36.9 kg/d) vs control (39.1 kg/d) and 0.45% (37.9 kg/d, SE = 1.07). Sulfite affected energy-corrected milk (44.0, 42.9, and 41.3 kg/d for 0, 0.45, and 0.9%, respectively; SE = 1.10; $P < 0.05$), although pairwise comparisons were not significant. Dry matter intake was higher in 0 than 0.45 and 0.9% sulfite levels (28.8, 27.6, and 27.1 kg/d; SE = 0.79; $P < 0.05$). Acetate did not affect milk yield, DMI, ECM, milk fat %, protein %, or fatty acid % ($P > 0.05$). One block of 4 cannulated cows was used for rumen sampling during week 3 of each period. Individual VFA and total VFA were not affected by treatment, although period effects were detected. Day effects were observed only for ruminal redox potential (Eh), which was more negative on day 7 of each period compared with other sampling days ($P < 0.05$). Although a previous study showed that sodium sulfite delayed fermentation in vitro, fewer effects were observed in vivo.

Cross-platform profiling of alternative polyadenylation reveals post-transcriptional regulatory divergence between chicken embryonic stem cells and primordial germ cells
Presenter: Longbin Yang
Advisor: Jiuzhou Song
Co-authors: Qunhao Niu, Ray Rui Gao, Yanghua He, Paula Chen, Janet Fulton, Tom Porter, Jing Huang, Yunlong He, Zhihua Jiang, Bichun Li

Alternative polyadenylation (APA) is a major post-transcriptional mechanism that generates transcript isoforms with distinct 3′ ends and modulates mRNA stability, translation and miRNA-mediated regulation. However, its contribution to avian germline specification remains poorly defined. Here we performed an APA-centred analysis of the transition from chicken embryonic stem cells (ESCs) to primordial germ cells (PGCs) by integrating WTTS-seq, Oxford Nanopore long-read RNA sequencing and miRNA profiling across both sexes. WTTS-seq identified 12,843 genes with APA sites, including 11,732 protein-coding genes and 1,015 lncRNA genes, with ~60% of protein-coding genes harbouring more than one APA site. Both WTTS-seq and long-read analyses revealed extensive APA remodelling during the ESC-to-PGC transition, whereas sex-biased APA differences were comparatively modest. Cross-platform comparison showed substantial overlap in gene coverage (~8,000–10,000 shared genes) but only partial directional concordance, indicating that WTTS-seq and long-read sequencing capture complementary dimensions of transcript-end regulation. Functional integration showed that

APA was only partially coupled to other transcriptomic layers. Among 560 APA genes, 259 overlapped with differential expression whereas 301 did not, indicating that APA frequently acts independently of overall transcriptional output. Only 65 APA genes overlapped with alternative splicing changes, including 13 significant events, and 30 genes exhibited isoform switching, supporting a model in which APA primarily remodels the 3′UTR regulatory landscape rather than broadly altering coding structure. Motif analysis identified distinct PAS-associated signatures in concordant and discordant APA–DEG genes, including a miRNA-like motif matching gga-miR-1653 in discordant genes. This motif was linked to representative targets including FGFR2, OTUD3, PLA2G10, SBDS, SEPTIN8 and ZBED4**,** revealing both canonical and non-canonical relationships between APA, miRNA regulation and gene expression. Mechanistically, canonical PAS strength, GC content and UGUA emerged as major positive cis determinants of PAS usage, whereas cis–trans modelling supported context-dependent interactions between local sequence architecture and the 3′ end processing environment. Together, these findings establish a multi-platform, sex- and cell-type-resolved APA atlas in an avian germline system and identify APA as a pervasive and functionally important regulatory layer during early germline development.

Post-Doctoral Associates

Host Genetic and Gut Microbiome Interactions Influence Growth Traits and Improve Genomic Prediction in Rainbow Trout
Presenter: Ridwan Ahmed
Advisor: Mohamed Salem
Co-authors: Guglielmo Raymo, Rafet Al-Tobasei, Ali Ali, Tim Leeds

Host genetic variation plays a key role in shaping gut microbiome composition and function, influencing microbial abundance, diversity, and metabolic capacity. In turn, the microbiome can regulate host gene expression, reflecting a bidirectional host–microbiome relationship. Here, we investigated the genetic architecture of gut microbiome variation in rainbow trout and its association with growth-related traits. Differential abundance analysis (MaAsLin2) identified three lactic acid bacteria (LAB) taxa—*Lactococcus lactis*, *Lactobacillus crispatus*, and *Vagococcus fluvialis*—that were enriched in high muscle yield families. Genome-wide association studies (GWAS) were conducted using 3,608 SNPs following stringent quality control. Heritability estimates from REML showed moderate SNP-based heritability for LAB taxa (h^2 = 0.147–0.189), while a glycolysis pathway (ANAGLYCOLYSIS-PWY) showed lower heritability (h^2 = 0.097). Mixed linear model association identified a shared LD block ($r^2 > 0.95$) on chromosome 21 significantly associated with all three LAB taxa (FDR < 0.05). Lead SNPs explained ~6.4–6.5% of phenotypic variance and were annotated to *LOC110500605* (PTPRD). A distinct locus on chromosome 19 associated with the glycolysis pathway mapped to *COMMD8*. Importantly, incorporating microbiome features into genomic prediction models improved prediction accuracy by up to 15% compared to genomic- or pedigree-only models. These findings demonstrate that host genetics shapes gut microbiome composition and function and highlight a genetically structured host–microbiome axis influencing growth traits in rainbow trout, with direct implications for microbiome-informed genomic selection.

Thyroid hormones modulate the reproductive axis during egg production in turkey hens
Presenter: Boonyarit Kamkrathok
Advisor: Tom Porter
Co-authors: Kristen Diehl, Diane Hildenberger, Ricardo G. Sierra Arroyo, Arianna Bond, Paige Meisner

In avian species, reproductive activity is regulated by multiple neuroendocrine axes, including the gonadotropic axis, the lactotropic axis, and the thyrotropic axis, which are key to enhancing egg production in the turkey industry. The objective of this study was to determine the influence of circulating thyroid hormone (TH) levels on the reproductive axis during peak egg production. Sixty average egg

producing turkey hens (0.65–0.75 eggs per day) were assigned to 3 treatment groups: control (C), the TH synthesis inhibitor Lugol's Iodide (LI; 0.1%), and synthetic thyroxine (T4; 1 ppm), dosed in the water for 2 weeks starting at 35 weeks of age. At week 37, plasma samples were collected to measure progesterone, estradiol, and TH. Tissue samples were collected for RT-qPCR analysis of mRNA levels for candidate genes (n=16 hens/treatment). Data were analyzed using one-way ANOVA with the MIXED procedure in SAS. Among the plasma hormones measured, only T4 levels were elevated in the T4 group. Gene expression analysis revealed that T4 and LI treatments affected both the gonadotropic and thyrotropic axes. In the gonadotropic axis, T4 decreased hypothalamic GNRH and pituitary GNRHR mRNA levels. Hypothalamic PGR and ESR1 mRNA increased slightly in the T4-treated group, while ESR2 dramatically decreased. T4 elevated ESR1 expression 3-fold in the pituitary, whereas ESR2 mRNA decreased dramatically. In the thyrotropic axis, pituitary TSHB expression markedly increased in the LI group but was reduced 13-fold in the T4-treated group, showing a similar pattern to TSHR expression in the thyroid gland. THRB mRNA in the thyroid decreased 5-fold following T4 treatment. Moreover, THRA expression was significantly increased in the liver of the LI group. T4 increased DIO3 levels 10-fold in the hypothalamus but reduced pituitary DIO1 and DIO2. Levels of TSHR, TPO, and TG mRNA in the thyroid gland were all dramatically reduced by T4 treatment. Liver TTR expression was elevated by T4 treatment. These findings demonstrate that TH can modulate both the gonadotropic and thyrotropic axes, potentially playing a central role in coordinating reproductive and metabolic regulation during peak egg production in laying turkey hens.

Whole-Genome Sequencing and Structural Mapping Identify Genetic Diversity among Infectious Bursal Disease Virus Field Isolates from Delmarva

Presenter: Zubair Khalid
Advisor: Andrew Broadbent
Co-authors: Zubair Khalid, Sofia Egana-Labrin, Andrew Brodrick, Milos Markis, Shankar Mondal, Andrew Broadbent

The continual evolution of infectious bursal disease virus (IBDV) in the field complicates poultry health management. IBDV has a double-stranded RNA genome divided into two segments (A and B) that encodes five proteins, four on segment A and one on segment B. Previously, we investigated the evolution of Delmarva IBDV strains by sequencing two proteins, the polymerase (VP1), and the capsid (VP2), where we identified amino acid substitutions indicative of ongoing selection. Building on these results, we developed a cost-effective pipeline to sequence the complete IBDV genome from a subset of samples using long-read sequencing, in combination with both gene-targeted and whole-segment approaches. Translated amino acid sequences of all viral proteins were aligned to the reference strain (Del-E), and amino acid substitutions were mapped onto AlphaFold3-predicted protein structures using PyMOL. This analysis identified additional substitutions across the IBDV genome that were absent from the reference strain. In the multifunctional scaffolding protein (VP3), the substitution T44N was present in 10/12 (83%) sequences; in the protease (VP4), C168R/F occurred in 7/12 (58%) sequences; and in the non-structural protein (VP5), substitutions D31N, I74F, and P103S were present in 11/15 (73%) sequences. Together, these findings underscore the importance of continued surveillance to monitor IBDV evolution across the whole genome. Ongoing work includes phenotypic characterization to assess the potential consequences of the amino acid substitutions for pathogenicity, immunosuppression, and disease control.

Unveiling the Functional Landscape of RNA Editing Associated with Chicken Marek's Disease

Presenter: Qunhao Niu
Advisor: Jiuzhou Song
Co-authors: Longbin Yang, Yi Ding, John Dunn, Huanmin Zhang

Marek's disease virus (MDV) has evolved into more virulent strains and continues to threaten the global poultry industry. Adenosine-to-Inosine (A-to-I) RNA editing results in modifications to the mRNA sequence. Accumulating evidence has demonstrated that this type of RNA editing plays a crucial role in mediating

the cellular response to viral infections. Nevertheless, the role of RNA editing in the cellular response to Marek's disease (MD) remains unclear. In this study, we investigated A-to-I RNA editing in $CD4^+$ T cells during Marek's disease virus (MDV) infection between MD-resistant and susceptible chicken lines. We detected 642 A-to-I RNA editing events in $CD4^+$ T cells, most of them localized within genomic repeat elements—enriched in the CR1 family. We found the divergence in RNA editing and count between the two chicken lines with different infection status, suggesting that immune regulatory mechanisms influenced by RNA editing differ across genetic backgrounds and infections. Moreover, we found that ADAR expression has a correlation with RNA editing frequency. Furthermore, we identified 21, 42, 14, and 38 RESs A-to-I editing events that contribute to gene expression, amino acid sequences, alternative splicing, and miRNA-target binding, respectively. Comparative analyses identified 131 group-specific RESs and 21 RESs shared among groups. Functional enrichment of group-specific RES-associated genes pinpointed several MD-resistance pathways (e.g., MHC class I protein complex in $L6_3$-control). More important, we pinpointed two functional Line 6_3-specific RESs including chr6:26,600,122 and chr16:1,716,632 may play important role in the resistance formation of Line 6_3. Collectively, our findings reveal the distinct landscape of A-to-I RNA editing in $CD4^+$ T cells during MDV infection, providing novel insights into how RNA editing modulates MD resistance.

Effect of water deprivation on hypothalamic and renal water homeostasis gene expression in chickens selected for water efficiency

Presenter: Panpradub Sinpru
Advisor: Tom Porter
Co-authors: Boonyarit Kamkrathok, Gregory S. Fraley, Sara K. Orlowski-Workman, Rosie Whittle, Shawna L. Weimer, Tom Porter

Poultry production faces increasing challenges due to water scarcity driven by climate change, making genetic selection for water efficiency vitally important. This study aimed to investigate the effects of water deprivation (WD) on gene expression profiles related to hypothalamic and renal water homeostasis in high water conversion ratio (HWCR) and low water conversion ratio (LWCR) chicken lines. Birds from each line were raised with free access to feed and water in six pens per line (15 birds/pen). At 32 days of age, chickens from each line were assigned to two groups (3 pens/line/group): a control group with free access to water (0 h of WD) and an experimental group subjected to 12 h of WD. Six birds per group per line were humanely euthanized by cervical dislocation, and hypothalamic and kidney samples were collected for gene expression analysis. Total RNA was isolated, and target genes associated with water homeostasis were quantified using reverse transcription-quantitative PCR (RT-qPCR). In the hypothalamus, mRNA levels for *AVT*, *MT*, *ATP1A1*, *AQP1*, *AQP2*, *AQP3*, *NOS2*, *NPY*, *POMC*, *ORX*, and *MCH* were quantified. Levels of *ATP1A1* mRNA decreased in response to WD in both HWCR and LWCR lines. Interestingly, *AQP2* and *AVT* mRNA levels decreased following WD in the HWCR line but not in the LWCR line. In contrast, WD increased mRNA levels of *AQP3* in the LWCR line but not in the HWCR line. In the kidney, mRNA levels for *AQP1*, *AQP2*, *AQP3*, *AQP4*, *AQP7*, *AQP11*, *ATP1A1*, *ATP1B1*, *AVT*, *AVTR1B*, *AVTR2*, MT, *MTR*, *CLCNKA*, *REN*, and *AGT* were quantified. WD decreased mRNA levels for *ATP1A1* and *CLCNKA* in both lines. Interestingly, *AQP7*, *AVT*, and *AVTR2* mRNA levels decreased by WD in the LWCR but not in the HWCR line. In contrast, *AVTR1B* and *MTR* mRNA levels increased in the HWCR line but not in the LWCR line following WD. *MT* mRNA levels increased in the HWCR but decreased in the LWCR due to WD. Genetic selection for WCR altered mRNA levels for *AVT*, *AQP2*, and *AQP3* in the hypothalamus, as well as mRNA levels for *AQP7*, *AVT*, *AVTR2*, *AVTR1B*, *MT*, and *MTR* in the kidney in response to WD. These differential responses might explain a portion of the WCR differences between the HWCR and LWCR genetic lines.

Faculty

Faculty

Name	Rank	Appointment Percentage		
		Research	Teaching	Extension
Dr. Debabrata Biswas	Professor	70	30	
Dr. Andrew Broadbent	Assistant Professor	70	30	
Dr. Amy Burk	Professor		60	40
Dr. Fabiana DeFreitas Cardoso	Assistant Professor	15	15	70
Dr. Sunoh Che	Assistant Professor	15	15	70
Dr. Iqbal Hamza	Professor		20	
Dr. Christine Hakenkamp	Senior Lecturer		100	
Dr. Younggeon Jin	Assistant Professor	70	30	
Dr. Byung-Eun Kim	Professor	70	30	
Dr. Richard Kohn	Professor	60	20	20
Dr. Li Ma	Professor	70	30	
Dr. Kris Mayo	Lecturer		100	
Dr. Tom Porter	Distinguished University Professor	70	30	
Dr. Emilia Przygrodzka	Assistant Professor	70	30	
Dr. Mohamed Salem	Associate Professor	70	30	
Dr. Andrew Schiffmacher	Assistant Professor	70	30	
Dr. Heewon Seo	Assistant Professor	70	30	
Dr. Jiuzhou ‘John’ Song	Professor	70	30	
Dr. Nishanth Sunny	Associate Professor	70	30	
Dr. Lisa Taneyhill	Professor	80	20	
Dr. Adele Turzillo	Professor and Chair	34	33	33
Dr. Zhengguo Xiao	Professor	70	30	

Emeritus Faculty

Dr. John Doerr
Dr. Larry Douglass
Dr. Richard Erdman
Dr. Tom Hartsock
Dr. Carol Keefer
Dr. Ian Mather
Dr. Mary Ann Ottinger
Dr. Robert Peter
Dr. Joseph Soares
Dr. Mark Varner
Dr. Inder Vijay
Dr. Dennis Westhoff

DEBABRATA BISWAS

Professor, Foodborne Bacterial Infections and Safety

Education:

1994	B.S.	University of Dhaka
1998	M.S.	University of Tokyo
2001	Ph.D.	University of Tokyo
2002	PostDoc Fellow	Washington State University

Professional Experience:

2003-2009	Research Associate, Vaccine and Infectious Disease Organization, University of Saskatchewan
2009-2011	Research Associate, Center for Food Safety, Department of Food Science, University of Arkansas
2011-2017	Assistant Professor, Department of Animal and Avian Sciences, and Center for Food Safety and Security Systems, University of Maryland
2017-2021	Associate Professor, Department of Animal and Avian Sciences, and Center for Food Safety and Security Systems, University of Maryland
2021-Present	Professor, Department of Animal and Avian Sciences, and Center for Food Safety and Security Systems, University of Maryland

Teaching Responsibilities:

- ANSC 440/688J (Zoonotic Infections and Controls)
- ANSC 410/688M (Gut Microbiome and Its Role in Health and Disease)
- ANSC 399 (Special Topics of Animal Sciences)
- ANSC 699 (Special Topics of Animal Sciences)

Research Interests:

- Food safety, foodborne bacterial pathogens, pathobiology, and molecular microbiology.
- Alternative to antibiotics, natural farm animal growth promoters, probiotics, prebiotics, and vaccine

Significant Accomplishments:

- Developed a *Salmonella* auto-lytic vaccine for chicken using bacteriophage genes, holin and lysin, and submitted for patent
- Edited two books entitled “Safety and Practice for Organic Food” published by Elsevier and “Gut Microbiome and its impact on health and diseases” published by Springer Nature
- Authored or co-authored more than 100 refereed scientific publications, 18 book chapters and more than 120 abstracts presented at professional meetings
- Editorial board member for 8 reported journals and reviewer for more than 40 journals

Awards and Honors:

- USDA-NIFA-Organic Grant, 2025
- USDA-NIFA-Exploratory Grant, 2024
- MERCK Inc-Vaccine Research Grant-2023
- USDA-NIFA-Exploratory Grant, 2019
- USDA-NIFA-Organic Grant, 2018
- USDA-NIFA-Exploratory Grant, 2017
- Research Development Tier-1 Seed Grant, 2016
- Delmarva (DE, MD and VA) Grant, 2016 and 2018
- Maryland Agricultural Experimental Station (MAES) Award, 2012, 2014 and 2023
- University of Maryland Extension Award (UME) Award, 2013
- Young Investigator Award, Canadian Society of Helicobacter Research, Canada, 2005
- Postdoctoral Research Fellowship, Japanese Society for Promotion of Science, Japan, 2005
- Young Investigator Award, Campylobacter and Related Organisms, Baltimore, USA, 1999
- Japanese Government Scholarship for graduate study, University of Tokyo, Japan, 1996

ANDREW BROADBENT

Assistant Professor, Virology

Education:

2002	M.A.	Pathology, University of Cambridge, UK
2005	DVM	University of Cambridge, UK
2006	M.S.	London School of Hygiene & Tropical Medicine, UK
2010	Ph.D.	Microbiology & Immunology, Imperial College, London

Professional Experience:

2010-2014	Postdoctoral Visiting Fellow, Virology, NIAID, NIH, Bethesda, MD, USA
2014-2019	Research Fellow, Avian Virology, The Pirbright Institute, UK
2019-2021	Group Leader, Avian Virology, The Pirbright Institute, UK
2020-2021	Teaching Fellow, Immunology & Virology, University of Surrey, UK
2021-Present	Assistant Professor, Virology, Department of Animal and Avian Sciences, University of Maryland, College Park, MD, USA

Teaching Responsibilities:

- ANSC 101: Principles of Animal Science, co-instructor (2023), guest lecturer (2024- present)
- ANSC 340: Health Management of Animal Populations, instructor (2022-present)
- ANSC 440: Zoonotic Diseases and Control, co-instructor (2024-present)

Research Interest:

- Understanding the molecular basis underpinning the replication and pathogenesis of avian viruses of importance to the poultry industry, and to public health, with a view to improving control. Current projects are focused on infectious bursal disease virus (IBDV), avian reovirus (ARV), and avian influenza virus (AIV).

Significant Accomplishments:

- Awarded over $5.7 million in research funding as a Principal Investigator, including over $3.2 million at UMD
- Authored or co-authored 35 publications (1,126 citations; h-index:17; i10-index:27)
- Advised 3 postdoctoral research associates (PDRAs) in the UK, and 2 PDRAs and 1 faculty assistant at UMD
- Advised 2 PhD students in the UK, and 3 PhD students at UMD
- Advised 4 MS and 2 undergraduate students in the UK, and 17 undergraduate students at UMD
- Elected as Veterinary Virology Councilor at the American Society for Virology (ASV) (2022-2025)
- Elected to Virology Division at the Microbiology Society (2025-present)
- Member of the Board of Reviewers for Journal of General Virology (2020-present)
- Member of the Editorial Board of the Journal of Medical Microbiology (2017- present)

Awards and Honors:

- 2022-2026: Invited departmental seminar speaker at The Ohio State University, the University of Georgia, Cornell University, University of Pittsburgh School of Medicine, USDA Agricultural Research Service, University of Delaware, Wake Forest University, The Catholic University of America, University of Maryland School of Medicine, and the Institute of Marine and Environmental Technology
- 2015: Ebola Medal for Service in West Africa
- 2005-present: Member of the Royal College of Veterinary Surgeons, The Microbiology Society, the ASV, and the American Association of Avian Pathologists (AAAP)

AMY BURK

Professor, Equine Science
Director, ANSC Undergraduate Program

Education:

1995	B.S.	James Madison University
1998	M.S.	Virginia Polytechnic Institute and State University
2001	Ph.D.	Virginia Polytechnic Institute and State University

Professional Experience:

2001-2003	Lecturer, Department of Animal and Avian Sciences, University of Maryland
2003-2010	Assistant Professor, Department of Animal and Avian Sciences, University of Maryland
2010-2021	Associate Professor, Department of Animal and Avian Sciences, University of Maryland
2021-Present	Professor, Department of Animal and Avian Sciences, University of Maryland

Teaching Responsibilities:

- ANSC 105 Horse Care Practicum
- ANSC 232 Horse Management
- ANSC 237 Equine Reproduction
- ANSC 330 Equine Science

Extension Responsibilities:

- Provide statewide leadership in equine nutrition and pasture management Extension programming, with an emphasis on sustainable horse farming and environmental stewardship
- Vice-Chair of the Maryland Horse Industry Board, contributing to statewide leadership, policy advising, and strategic planning for Maryland's horse industry

Research Interests:

- Adoption and effectiveness of best management practices to reduce the environmental impact of horse farms, with an emphasis on nutrient management and pasture sustainability
- Impacts of grazing management tools, including grazing muzzles, on equine body condition, metabolic health, and welfare
- Evidence-based strategies to prevent and manage obesity in equids

Significant Accomplishments:

- Vice-Chair of the Governor-appointed Maryland Horse Industry Board
- Equine Studies Program featured in over 50 media articles
- Presenter of 100 invited presentations
- Hosted extension events educating an estimated 6,000 people.
- Extension Horse YouTube channel features 72 videos with 192,000 total views

Awards and Honors:

- 2024 Industry Service Award, National Association of Equine Affiliated Academics
- 2021: Integrated Research and Extension Award, AGNR, University of Maryland
- 2019: Youth Development Professional of the Year. MD 4-H Horse Program
- 2018: Outstanding Educator of the Year, AGNR Student Council, University of Maryland
- 2013: Excellence in Extension, AGNR Alumni Association, University of Maryland
- 2011: Agriculture Advocate Award, Sigma Alpha Sorority, University of Maryland
- 2008: Poffenberger Excellence in Teaching and Advising, AGNR, University of Maryland
- 2007: Outstanding Educator, Equine Science Society

FABIANA DE FREITAS CARDOSO

Assistant Professor, Dairy Cattle Management and Nutrition

Education:

2015	B.S.	Federal University of Lavras, BR
2018	M.S.	Federal University of Lavras, BR
2022	Ph.D.	University of Illinois, Champaign-Urbana, USA

Professional Experience:

2010-2018	Undergraduate Research Assistant, Federal University of Lavras, Department of Animal Sciences, Lavras, MG
2017-2017	Exchanged program at Purdue University, USA
2019-2022	Research Assistant, University of Illinois at Urbana-Champaign Department of Animal Sciences, Urbana-Champaign, IL
2023-Present	Assistant Professor, Department of Animal and Avian Sciences, University of Maryland USA

Teaching Responsibilities:

- ANSC 242: Dairy Cattle Management. Instructor
- ANSC 282: Grazing Management. Instructor

Extension Responsibilities:

- As an Extension Specialist, I work with Maryland's dairy industry to identify challenges and provide practical solutions. My focus is on dairy nutrition, sustainable farming, and forage management, helping farmers improve herd health, productivity, and efficiency while promoting environmentally responsible practices.
- Statewide producer engagement, workshops, on-farm visits, publications

Research Interests:

- Through applied research and hands-on education, I have developed extension programs that connect farmers with the latest knowledge and tools. Whether through one-on-one consultations, or collaborative projects, my goal is to bridge research and real-world application, ensuring dairy producers have the resources they need to improve their operations and secure long-term success.

Major Programs:

- Feed Safety & Microbial Contamination (2024–present)
- Dairy Nutrition & Management (2023–present)
- Forage & Silage Management (2023–present)

International collaboration:

- MOUs with Brazilian universities
- Study abroad course development

Significant Accomplishments:

- Total secured funding: ~$240,000+ (PI and Co-PI since 2023) at UMD
- 14+ peer-reviewed journal articles
- 25+ conference abstracts and presentations
- 10+ magazine and newsletter publications
- M.S. Advisor: 2 students (current)
- Ph.D. Committees: Multiple
- Associate Editor: Brazilian Journal of Animal Science
- Reviewer: multiple journals
- USDA-NIFA Review Panel (2024)

SUNOH CHE

Assistant Professor, Poultry Management and Veterinary Epidemiology

Education:

1996	D.V.M.	Chonnam National University, South Korea
2012	M.V.E.	Murdoch University, Australia
2019	M.S.	University of PEI, Canada
2022	Ph.D.	University of Guelph, Canada

Professional Experience:

1997-2000	Veterinary Officer, Damyang County Office, South Korea
2000-2006	Veterinary Officer, Animal and Plant Quarantine Agency, South Korea
2006-2007	Visiting Scholar, CSIRO Black Mountain Laboratory, ACT, Australia
2007-2010	Senior Veterinary Officer, Animal and Plant Quarantine Agency, South Korea
2010-2012	Graduate Research Assistant, School of Vet Med, Murdoch University, WA, Australia
2012-2016	Senior Veterinary Officer, Animal and Plant Quarantine Agency, South Korea
2016-2018	Graduate Research Assistant, Atlantic Vet College, University of PEI, PE, Canada
2019-2022	Graduate Research Assistant, Ontario Vet College, University of Guelph, ON, Canada
2022-2023	Post-doctoral researcher, Ontario Vet College, University of Guelph, ON, Canada
2024-Present	Assistant Professor, Department of Animal and Avian Sciences, University of Maryland

Teaching Responsibilities:

- ANSC 262: Commercial Poultry Management

Extension Responsibilities:

- Deliver applied research findings on managing commercial and backyard poultry to farmers, industry stakeholders, and the public, while assisting poultry producers in maintaining the health and productivity of their animals through data-driven approaches

Research Interests:

- Transcriptomic analysis of spaghetti meat and woody breast in broiler chickens across different production types
- Metagenomic analysis of cecal microbiome data comparing broiler chickens fed control vs. dietary additive–supplemented diets

Significant Accomplishments:

- Authored or co-authored 15 referred scientific publications, 21 abstracts presented at professional conferences, and 7 newsletters; Invited speaker at 5 events for academia and the poultry industry
- Secured funding from USPOULTRY and brought undergraduate and graduate students to IPSF and IPPE meetings (2025: 5 participants; 2026: 7 participants).
- Served as review panels for Canadian Poultry Research Council (2026), Animal Health & Disease Research Competitive Grant Proposals at Penn State University (2025), Results Driven Agriculture Research & Alberta Poultry Board (2024)
- Recipient twice of the Korean Government Scholarship Program for Overseas Study (short term in 2006, long term in 2010)
- Secured funding and hosted an international workshop on foody safety; invited 20 participants from 10 countries including members of the Association of Southeast Asian Nations in 2014
- Diplomate of American College of Veterinary Preventive Medicine (2021- present)
- Reviewer for several journals including Animal Bioscience, PlosOne, Journal of Animal Physiology and Animal Nutrition, Poultry Science, Preventive Veterinary Medicine, World's Poultry Science Journal

Awards and Honors:

- 2024, 2025: US Poultry Foundation, Industry Education Recruitment Funding
- 2021: Hy-Line International Genetics & Genomics Award, Certificate of Excellence, Poultry Science Association
- 2020-2022: International Doctoral Tuition Scholarships
- 2018: Art Fitzgerald Graduate Research Scholarship, Canada
- 2010-2012: Endeavour Postgraduate Award, Australia
- 2007: Minister's Award of Excellence, Ministry of Agriculture, Food and Rural Affairs, South Korea
- 2004: Commissioner's Award of Excellence, Animal and Plant Quarantine Agency, South Korea

IQBAL HAMZA

Professor, Molecular Genetics and Heme Transport

Education:

1989	B.S.	University of Bombay, Biochemistry and Life Sciences
1991	M.S.	University of Bombay, Biochemistry
1997	Ph.D.	SUNY at Buffalo School of Medicine, Biochemistry
2002	PostDoc	Washington University School of Medicine, Cell Biology
2010	Sabbatical	Dr. Paul Liu, National Human Genome Research Institute, NIH
2019	Sabbatical	Dr. David Bodine, National Human Genome Research Institute, NIH

Professional Experience:

1997-2002	Research Associate, Washington University School of Medicine, St. Louis
2002-2008	Assistant Professor, Department of Animal & Avian Sciences, University of Maryland
2008-2013	Associate Professor, Department of Animal & Avian Sciences, University of Maryland
2013-Present	Professor, Department of Animal & Avian Sciences, University of Maryland
2022-Present	Professor, Center for Blood Oxygen Transport and Hemostasis, Department of Pediatrics, University of Maryland School of Medicine (joint appointment)
2021, 2023	Visiting Professor, University of Torino, Italy

Teaching Responsibilities:

- Proposed, initiated, developed and taught ANSC327/627 Molecular and Quantitative Animal Genetics (2004-23)

Research Interest:

- To identify the molecular pathways of heme and iron metabolism in health and disease

Significant Accomplishments and Administrative Responsibilities:

- Total extra-mural competitive funding in the last 20+ years as PI: > $18 million
- Primary mentor to 7 Ph.D. students; 1 post-doctoral fellow; 1 research assistant professor
- Discovery of first heme trafficking pathways (*Nature 2008; Cell 2011; Cell Metab. 2013, 2014; Nature Cell Biology 2017; Nature 2022; Science 2026*)
- Founder and President: *Rakta Therapeutics, Inc.* a startup company that develops therapeutics targeted against heme transporters

Awards and Honors:

- 2024 Visiting Professor Scholarship, CAPES Print -Fiocruz, Brazil
- 2022: NIH Director's WALS Lecturer
- 2019: Chair, Gordon Research Conference, Cell Biology of Metals
- 2018: Erasmus+ International Credit Mobility Fellow, European Union (Lund University, Sweden)
- 2018: Chair, Gordon Research Conference, Chemistry and Biology of Tetrapyrroles.
- 2017: Fellow of the American Association for the Advancement of Science
- 2012-16: Standing Member, Integrative Nutrition and Metabolic Processes Study Section, NIH
- 2012: Fellow, Japan Society for the Promotion of Science
- 2011: Faculty Excellence Award, AGNR, UMCP
- 2011: Excellence in Research, 44th Annual Alumni Awards Celebration, AGNR, UMCP
- 2010: Kirwan Faculty Research and Scholarship Prize, UMCP
- 2006: Junior Faculty Excellence Award, AGNR, UMCP
- 2005: Outstanding Invention, UMCP
- 2002-05: NIH Research Career Development Award, NIDDK, K01
- 2001: Thirty Outstanding Alumni, Canada World Youth, Montreal, Canada
- 2000-02: NIH Post-Doctoral Fellowship, NHLBI, NRSA
- 1987: Duke of Edinburgh's Award Silver Standard for Outstanding Community Social Service

Editorial Board: *eLife; Blood (Red Cells & Iron)*

YOUNGGEON JIN

Assistant Professor, Gastrointestinal Health and Physiology

Education:

2009	D.V.M. & B.S.	College of Veterinary Medicine, Jeju National University, South Korea
2014	Ph.D.	Comparative Biomedical Sciences, College of Veterinary Medicine, NC State University

Professional Experience:

2009-2011	Post-DVM Researcher, Cancer Stem Cell Research Center and Laboratory of Neurosurgery, Samsung Biomedical Research Institute, South Korea
2011-2014	Graduate Research Assistant, Department of Clinical Sciences, NC State University
2014-2019	Postdoctoral Research Associate, Gastrointestinal Physiology Laboratory, NC State University
2019-Present	Assistant Professor, Department of Animal and Avian Sciences, University of Maryland

Teaching Responsibilities:

- Proposed, initiated, and developed ANSC445/645 Comparative Gut Physiology & Disease
- Initiated and developed ANSC401 Animal Growth and Development for Production Agriculture

Research Interest:

- Elucidate the critical mechanisms that contribute to gastrointestinal epithelial regeneration and development.

Significant Accomplishments:

- Authored or co-authored 27 refereed scientific publications and more than 60 abstracts presented at professional meetings
- Currently mentoring two doctoral students, one master's student, and five undergraduate students
- Guest editor, Special issue: "Role of Intestinal Epithelial Cells and Their Cellular Interactions", Biomedicine, 2023-present

Awards and Honors:

- 2026-2028: R21 (co-I), National Institutes of Health (NIH)
- 2025-2027: Discovery program (PI), Maryland Stem Cell Research Fund
- 2021-2023: LAUNCH program (PI), Maryland Stem Cell Research Fund
- 2023-2026: Grand Challenge Team Project Grant (co-PI), UMD
- 2020-2021, 2023-2024, 2026-2027: Maryland Agricultural Experiment Station (MAES) Competitive Grant Program (PI)
- 2019-2021: Innovate Biopharmaceuticals, Inc. (PI)
- 2017-2018: Pilot/Feasibility Grant (PI), Center for Gastrointestinal Biology and Disease
- 2015-2019: Large animal models core (Co-I), Center for Gastrointestinal Biology and Disease
- 2018: Certificate of Recognition, Digestive Disease Week 2018, For Your Scientific Accomplishment As An Early Career Investigator
- 2018: Notable Poster, Postdoctoral Research Symposium, NC State University
- 2017: Professional Development Award for Postdocs, Office of Postdoctoral Affairs, NC State University
- 2016: Postdoctoral Scholar of the Year Award, Department of Clinical Sciences of NC State University College of Veterinary Medicine
- 2016: 'Anticancer activity of TTAC-0001, a fully human anti-vascular endothelial growth factor receptor 2 (VEGFR-2/KDR) monoclonal antibody, is associated with inhibition of tumor angiogenesis' was selected for Open Select Biotechnology Collection
- 2014: CVM Graduate Student of the Month, NC State College of Veterinary Medicine

BYUNG-EUN KIM

Professor, Cellular and Molecular Nutrition

Education:

1993	B.S.	Kangwon National University in Korea
1996	M.S.	Kangwon National University in Korea
2004	Ph.D.	University of Missouri-Columbia

Professional Experience:

1995-1998	Researcher, Protein Engineering Laboratory, General Research Institute, Hyundai Pharmaceutical Industrial Company, Ltd., Korea
2000-2004	Graduate Research Assistant, Genetics Area Program, University of Missouri-Columbia
2005-2011	Postdoctoral Research Associate, Department of Pharmacology and Cancer Biology, Duke University School of Medicine
2011-2018	Assistant Professor, Department of Animal and Avian Sciences, University of Maryland
2011-Present	Affiliate Professor, Molecular and Cellular Biology Program, University of Maryland
2018-2025	Associate Professor, Department of Animal and Avian Sciences, University of Maryland
2025-Present	Professor, Animal and Avian Sciences, University of Maryland

Teaching Responsibilities:

- ANSC454(489O): Nutritional Aspects of Metabolic Disease (2013-present)
- ANSC630: Animal Metabolism (2023 and 2025)
- ANSC688O: Special Topics; Advanced Nutritional Pathophysiology (2013-present)

Research Interests:

- Regulation of trace element and micronutrient metabolism in health and disease
- Mechanisms whereby cardiac-specific copper deficiency induces cardiac hypertrophy
- Mechanisms of systemic copper homeostasis between organs
- Novel players in copper homeostasis
- New role for metals and metal transporters in systemic metabolism

Significant Accomplishments:

- Invited speaker at 30 national and international conferences and academic institutes
- Publications cited more than 5,300 times
- Authored or co-authored 27 refereed scientific publications, 1 review article, and more than 45 abstracts presented at professional meetings
- Served as review panel (Early Career Reviewer Program) for the Integrative Nutrition and Metabolic Processes (INMP) study section, 2012, and *ad hoc* reviewer for the Nutrition and Metabolism in Health and Disease (NMHD) study section, 2021 and 2025

Awards and Honors:

- 2015, 2020, 2015: Maryland Agricultural Experiment Station (MAES) Grant
- 2021: NIH Grant - The Role of Copper in the Regulation of Adipose Function
- 2017: NIH Grant - Systemic Copper Homeostasis
- 2012: University of Maryland nominee for Searle Scholars Program
- 2009: Postdoctoral Fellowship, American Heart Association
- 2008: Young Investigators Award, The Duke Cardiovascular Research Symposium, Duke University Medical Center
- 2006: RJR-Leon Golberg Memorial Postdoctoral Training Fellowship, Integrated Toxicology, and Environmental Health Program, Duke University
- 2004: First Place Winner, Cell Biology Poster Contest, Missouri Life Science Week, University of Missouri-Columbia

RICHARD KOHN

Professor, Animal Nutrition Management

Education:

1985	B.S.	Cornell University
1987	M.S.	University of New Hampshire
1993	Ph.D.	Michigan State University

Professional Experience:

1985-1987	Research Assistant, Department of Animal and Nutritional Sciences, University of New Hampshire
1989-1993	Research Assistant, Department of Animal Science, Michigan State University
1993-1996	Research Associate, School of Veterinary Medicine, University of Pennsylvania
1996-1997	Assistant Professor, Department of Animal Sciences, University of Maryland
1997-2001	Assistant Professor, Department of Animal and Avian Sciences, University of Maryland
2001-2006	Associate Professor, Department of Animal and Avian Sciences, University of Maryland
2006-Present	Professor, Department of Animal and Avian Sciences, University of Maryland

Teaching Responsibilities:

- ANSC 314: Comparative Animal Nutrition, Lecturer (2015-2017)
- ANSC 315: Animal Feeds and Feeding, Lecturer (2019-present)
- ANSC 371/2: Sustainable Agriculture and Environment Dominican Republic (2023-2024)
- ANSC 371/2: Sustainable Agriculture and Environment in Nicaragua, Leader (2022-2023)
- ANSC 617: Quantitative Techniques in Physiology and Nutrition, Lecturer (2001-2020, 5 times)
- ANSC 624: Seminar, Coordinator (2015-2025)
- ANSC 625: Developing Presentation Skills, Lecturer (2015-Present)
- ANSC 630: Animal Metabolism, Co-lecturer (2023, 2025)
- Current or past major advisor to 8 Ph.D. and 5 M.S. students, committee member for 49 students

Extension Responsibilities:

- Assist producers and consultants with reducing nutrient losses from animal production systems
- Public and government education on the impact of animal production on air and water

Research Interests:

- Mathematical modeling of farm nutrient flows and losses
- Environmental impact of animal management and feeding practices
- Protein and phosphorus digestion and utilization by dairy cattle
- Mathematical modeling in rumen physiology
- Biomass conversion to fuels using rumen microorganisms

Significant Accomplishments:

- Co-authored/edited 4 books, 12 book chapters, 58 refereed articles
- Presented >200 invited talks and abstracts of research
- 10 issued US patents

Awards and Honors:

- 2004: Outstanding Researcher, Maryland Agriculture Alumni
- 2002: Agway Young Scientist Award, American Dairy Science Association
- 2001: Junior Faculty Award, College of Agriculture and Natural Resources, University of Maryland
- 1999: Award for Excellence for Northeast Regional Project 132, Northeast Association of Agricultural Experiment Station Directors

LI MA

Professor, Statistical Genetics and Genomics

Education:

2002	B.S.	Fudan University
2010	M.S.	University of Minnesota
2010	Ph.D.	University of Minnesota

Professional Experience:

2010-2013	Postdoctoral Researcher, Department of Computational Biology and Biological Statistics, Cornell University
2013-2019	Assistant Professor, Department of Animal and Avian Sciences, University of Maryland
2014-Present	Visiting Scientist, Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, Maryland
2019-2024	Associate Professor, Department of Animal and Avian Sciences, University of Maryland
2024-Present	Professor, Department of Animal and Avian Sciences, University of Maryland

Teaching Responsibilities:

- BIOM 601: Biostatistics I
- BIOM 405: Computer Applications in Biometrics
- BIOM 688E Topics in Biometrics; Statistical Genomics (Jointly with Drs. Song and Salem)

Research Interests:

- Statistical Genetics, including GWAS and Genomic Selection
- Animal and Human Population Genetics
- Complex Traits and Diseases
- Dairy Cattle Genomics

On-going Research:

- Integration of functional genomics data with GWAS and genomic selection
- Sequenced-based genomic analyses in cattle
- Large-scale GWAS of complex traits
- Linkage and recombination study in cattle pedigree
- Powerful methods and fast tools for GWAS and genomic selection

Significant Accomplishments:

- 101 peer-reviewed journal articles with 5,383 citations (Google Scholar, as of 2/20/2026)
- 6 graduate students, 5 postdoctoral researchers, and 4 visiting scholars
- Extramurally funded research by USDA, NSF, and US-Israel BARD programs
- Senior Editorial Board of *BMC Genomics*, Editorial Board of *Journal of Dairy Science, and Associate Editor of Frontiers in Genetics*

Awards and Honors:

- 2025, 2021: Dean's Grantsmanship Award, College of Agriculture and Natural Resources, University of Maryland
- 2013: 3CPG travel award, Cornell Center for Comparative and Population Genomics, Cornell University

KRIS PELHAM MAYO

Lecturer and Pre-Veterinary Advisor

Education:

1991	B.A.	Modern Languages, The College of William and Mary
1996	D.V.M.	Mixed Animal Species Track, VA-MD College of Veterinary Medicine

Professional Experience:

1996-1999	Associate Veterinarian, private practice
1997-1999	Lecturer, J. Sargeant Reynolds Community College
1999-2000	Patent Examiner, U.S. Patent and Trademark Office
2000-2002	Associate Veterinarian, private practice
2004-2014	Veterinarian / Practice Owner / Horse Boarding Stable Owner and Manager
2005-2008	Adjunct Professor of Veterinary Technology, Community College of Baltimore County
2012-2023	High School/Middle School Laboratory Sciences Course Developer / Instructor
2016-Present	Veterinarian / Practice Owner
2023-Present	Lecturer, Department of Animal and Avian Sciences, University of Maryland

Teaching Responsibilities:

- ANSC 101: Principles of Animal Science (1 fall section, 1 spring section; 167 students enrolled in 2025)
- ANSC 103: Principles of Animal Science Lab (5 fall sections, 3 spring sections; 135 students enrolled in 2025)
- ANSC 210: Veterinary Medical Terminology (1 fall section, 1 spring section; 67 students enrolled in 2025)
- ANSC 250: Companion Animal Care and Management (1 spring section; 60 students enrolled in 2025)
- ANSC 455: Applied Animal Behavior (1 fall section; 43 students enrolled in 2025)

Professional Responsibilities:

- Pre-veterinary Academic Advisor
- Pre-veterinary Society Faculty Advisor
- Campus Farm Oversight Committee
- PCC Committee

Significant Accomplishments:

- Developed 9 new courses
- Extensively revised 4 existing courses
- Mentored and supervised 18 graduate teaching assistants and 88 undergraduate teaching assistants
- Authored 1 refereed scientific paper

Professional Interests:

- Pre-veterinary advising
- First-year university student success
- Faculty development
- Distance learning without being distant
- Integrating online learning tools in traditional classrooms
- Classical education model and flipped classroom education model
- Competency based education
- Multi-modal and multi-disciplinary education
- Increasing access to veterinary care
- Increasing exposure and access to veterinary education and careers
- Telehealth/Telemedicine in veterinary medicine
- Non-clinical career opportunities for veterinarians
- Epidemiology
- One Health
- Narcan/naloxone mobilization in the general population

TOM PORTER

Distinguished University Professor, Molecular and Cellular Endocrinology

Education:

1983	B.S.	Biology, University of Minnesota, Duluth
1988	Ph.D.	Animal Physiology, University of Minnesota

Professional Experience:

1988-1993	Postdoctoral Fellow, Department of Cell Biology & Anatomy, Medical University of South Carolina
1993-1997	Assistant Professor, Department of Poultry Science, Texas A&M University
1997-1999	Assistant Professor, Department of Animal and Avian Sciences, University of Maryland
1999-2004	Associate Professor, Department of Animal and Avian Sciences, University of Maryland
2004-2023	Professor, Department of Animal and Avian Sciences, University of Maryland
2007-2015	Chair, Department of Animal and Avian Sciences, University of Maryland
2016-2017	Interim Associate Dean and Associate Director, University of Maryland Extension
2023-Present	Distinguished University Professor, University of Maryland
2023-2024	Interim Department Chair, Department of Animal and Avian Sciences, University of Maryland

Teaching Responsibilities:

- ANSC401: Animal Growth and Development for Production Agriculture
- ANSC444: Domestic Animal Endocrinology
- ANSC452: Avian Physiology
- BISI 712: Responsible Conduct of Research

Research Interests:

- Regulation of anterior pituitary differentiation during embryonic development
- Neuroendocrine regulation of growth, metabolism, and body composition
- Mitigation of heat stress in broiler chickens
- Regulation of reproduction in turkey hens

Significant Accomplishments:

- Author of 118 refereed scientific papers, 23 book chapters or reviews, and 183 abstracts
- Publications cited more than 4,495 times with an h-index of 40 and an i10-index score of 104
- Author of 35,452 nucleotide sequence submissions to GenBank
- Recipient of more than $30M in funding from competitive federal grant support
- Recipient of continuous federal funding for 34 years and counting
- Research mentor to 9 postdoctoral fellows, 31 graduate students, and 52 undergraduate students

Awards and Honors:

- 2025: James H. Denton Distinguished Service Award from the Poultry Science Association
- 2024: Fellow of the American Association for the Advancement of Science
- 2023: Named Distinguished University Professor
- 2022-2023: President of the Poultry Science Association
- 2021-2026: Editor-in-Chief, *World's Poultry Science Journal*
- 2019: University of Minnesota Golden Alumni Award
- 2016: Fellow of the Poultry Science Association
- 2012: Fundamental Science Award from the Poultry Science Association
- 2010-2016: Editor-in-Chief, *Poultry Science*
- 2009: Dean Gordon Cairns Award for Distinguished Creative Work and Teaching in Agriculture
- 2007: College of Agriculture and Natural Resources Alumni Excellence in Instruction Award
- 2003: National Capital Area Chapter of Gamma Sigma Delta Research Award
- 2001: University of Maryland Alumni Association Excellence in Research Award
- 2000: College of Agriculture and Natural Resources Junior Faculty Excellence Award
- 1996: Poultry Science Association Research Award

EMILIA PRZYGRODZKA

Assistant Professor, Reproductive Biology

Education:

2009	B.S.	University of Warmia and Mazury, Biotechnology, Olsztyn, Poland
2016	Ph.D.	Institute of Animal Reproduction and Food Research, Polish Academy of Sciences, Animal Science, Olsztyn, Poland

Professional Experience:

2010	Technologist, Department of Local Physiological Regulations, Institute of Animal Reproduction and Food Research, Polish Academy of Sciences, Olsztyn, Poland
2012-2013	Assistant in the research project, Department of Hormonal Action Mechanism, Institute of Animal Reproduction and Food Research, Polish Academy of Sciences, Olsztyn, Poland
2015-2016	Technologist, Department of Hormonal Action Mechanism, Institute of Animal Reproduction and Food Research, Polish Academy of Sciences, Olsztyn, Poland
2016-2018	Assistant, Department of Hormonal Action Mechanism, Institute of Animal Reproduction and Food Research, Polish Academy of Sciences, Olsztyn, Poland
2018-2021	Post Doc Research Associate, Department of Obstetrics and Gynecology, University of Nebraska Medical Center (UNMC), Omaha, Nebraska, USA
2021-2023	Instructor, Department of Obstetrics and Gynecology, University of Nebraska Medical Center (UNMC), Omaha, Nebraska, USA
2024-Present	Assistant Professor, Department of Animal and Avian Sciences, University of Maryland, College Park, Maryland

Research Interests:

- Metabolic and Signaling pathways regulating the function of highly steroidogenic ovarian cells
- Role of metabolites as signaling molecules in the ovarian cells
- Molecular mechanisms triggered by conceptus signals in the corpus luteum during 'maternal recognition of pregnancy'

Significant Accomplishments:

- Reviewer for journals including *Reproductive Biology; Biology of Reproduction; Frontiers in Physiology; Animals; Life Science; International Journal of Molecular Sciences; The Journal of Steroid Biochemistry and Molecular Biology; Reproduction, Fertility, and Development; Molecular Metabolism; BBA-Molecular and Cell Biology of Lipids, etc.*
- Member of the Award Committee, Society for the Study of Reproduction
- Member of USDA Multistate Research Project, Contribution of Ovarian Function, Uterine Receptivity, and Embryo Quality to Pregnancy Success in Ruminants, NE2227

Awards and Honors:

- 2026: Invited speaker, Rutgers University, New Jersey
- 2025: Award from the journal of *Biology of Reproduction*
- 2024: NIH, Cellular, Molecular and Integrative Reproduction (CMIR) Study Section
- 2022: Invited Speaker, University of Lincoln, Lincoln, Nebraska, USA
- 2021: Invited Speaker, Annual Scientific Meeting of the Society for Reproductive Investigation, Boston, USA
- 2020: Award from the journal of *Biology of Reproduction*
- 2019: Invited Speaker, VA Medical Center, Omaha, Nebraska, USA
- 2018: Invited co-chair, Annual Meeting of the Society for the Study of Reproduction, Session: William Hansel Ovarian Biology Symposium: Mediators of Luteal Function, New Orleans, USA
- 2017: Fellowship, Livestock Biotechnology, Technical University of Munich, Freising, Germany

MOHAMED 'MOH' SALEM

Associate Professor, Aquaculture Genomics and Muscle Biology

Education:

1988	B.S.	Zagazig University
1995	M.S.	Zagazig University
2004	Ph.D.	West Virginia University

Professional Experience:

2005- 2007	Post-doc Research Fellow, Animal and Veterinary Sciences - WVU
2007- 2012	Research Assistant Professor, Animal and Nutritional Sciences - WVU
2012-2018	Assistant Professor, Biology Department, and the interdisciplinary Ph.D. programs in Molecular Bioscience and Computational science - MTSU
2018-2019	Associate Professor, Biology Department, and the interdisciplinary Ph.D. programs in Molecular Bioscience and Computational science - MTSU
2019-Present	Associate Professor, Department of Animal & Avian Sciences, University of Maryland

Teaching Responsibilities:

- ANSC 255: Introduction to Aquaculture
- ANSC 401: Animal Growth and Development for Production Agriculture

Research Interest:

- Aquaculture genomics and breeding
- Functional genomics, epigenomics, and gene regulation
- Genome annotation and bioinformatics
- Growth, muscle development, and product quality traits
- Host–microbiome interactions
- Fish stress, welfare, and environmental adaptation

Ongoing Projects:

- NIFA-AFRI Project - Genomics and metagenomics approaches for mitigating stress of rainbow trout in recirculation aquaculture systems
- NIFA-AFRI Project - Integrated genomics and metagenomics predictions and modulation of the gut microbiota muscle axis to improve fillet yield in rainbow trout
- USDA/AFRI Project- High-Quality Reference Assembly and Annotation of the Rainbow Trout Genome
- USDA/AFRI Project- Whole-Genome Analyses/Selection to Increase Muscle Yield and Reduce Fillet Downgrading In Rainbow Trout

Significant Accomplishments:

- Publication of >65 peer-reviewed journal articles with >3900 citations (i10-index = 50)
- Mentored 12 graduate students and 2 postdoctoral researcher
- Editor for BMC Genomics, Frontiers in Genetics, and Marine Biotechnology

ANDREW SCHIFFMACHER

Assistant Professor, Early Mammary Gland Development

Education:

1998	B.S.	Cornell University
2010	Ph.D.	University of Maryland

Professional Experience:

1998-2001	Research Assistant, Oregon National Primate Research Center, Beaverton, OR
2001-2004	Research Assistant, Department of Medicine, University at Buffalo, S.U.N.Y/ Veterans Affairs WNY Healthcare System, Buffalo, NY
2004-2010	Graduate Research Assistant, Department of Animal and Avian Sciences, University of Maryland
2010-2018	Postdoctoral Research Scholar, Department of Animal and Avian Sciences, University of Maryland
2018-2020	Staff Scientist, Neural Crest Development and Disease Unit, National Institute of Craniofacial and Dental Research, NIH, Bethesda, MD
2020-Present	Assistant Professor, Department of Animal and Avian Sciences, University of Maryland

Teaching Responsibilities:

- ANSC 435: Experimental Embryology
- ANSC 437: Animal Biotechnology
- ANSC 401: Animal Growth and Development
- GEMS 496, 497: Team FET:US Mentor

Research Interests:

- Developmental potential in early embryonic tissues
- Fetal reprogramming of the mammary gland
- Embryonic and fetal tissue specification and lineage segregation

Significant Accomplishments:

- Authored or co-authored 19 refereed scientific publications and presented 10 invited talks and 25 poster presentations at professional conferences
- Reviewer for several journals including Molecular and Cellular Biology, Molecular Reproduction and Development, and Reproduction, Fertility, and Development
- Graduate student committee member for 7 graduate students

Awards and Honors:

- 2026-2027: Awarded MAES Competitive Grants Program, “Transcriptional networks governing multipotency and differentiation during bovine mammary development”
- 2024: Gemstone Honors Program Sophomore/Junior Mentor of the Year
- 2023-2026: Awarded University of Maryland Grand Challenges (Single Investigator), “Fetal Mammary Stem Cell Programming and Hormone Dysfunction”
- 2023-2024: Awarded MAES Competitive Grants Program, “Unlocking the potential of bovine fetal mammary stem cells”
- 2017: Selected Co-Chair for Hilde Mangold Postdoctoral Symposium at the Society for Developmental Biology 76th Annual Meeting. Minneapolis, MN, USA
- Awarded NIH F32 Ruth L. Kirschstein National Research Service Award (F32DE022990) titled “Proteolysis of cadherins in cranial neural crest.”

HEEWON SEO

Assistant Professor, Reproductive and Developmental Biology

Education:

2005	B.S.	Yonsei University, Wonju, South Korea
2007	M.S.	Yonsei University, Wonju, South Korea
2012	Ph.D.	Yonsei University, Wonju, South Korea

Professional Experience:

2012–2013	Postdoctoral Research Associate, Department of Biological Resources and Technology, Yonsei University, Wonju, South Korea
2013–2018	Postdoctoral Research Associate, Department of Veterinary Integrative Biosciences, Texas A&M University, College Station, TX
2018–2023	Research Assistant Professor, Department of Veterinary Integrative Biosciences, Texas A&M University, College Station, TX
2024–Present	Assistant Professor, Department of Animal and Avian Sciences, University of Maryland, College Park, MD

Research Interest:

- Uterine and placental biology
- Implantation and placentation
- Biology of pregnancy in livestock species

Significant Accomplishments:

- 70 publications as a corresponding author, a first author and a co-author (h-index: 25)
- Research funding (over $3.3 million) including two funded USDA grants as a Principal Investigator (PI) and one funded USDA grant as a co-PI
- Invitation to orally present at 6 international meetings in Belgium, the USA, and Korea
- Editorial board member for Journal of Animal Reproduction and Biotechnology (2022-present)
- Ad Hoc reviewers for journals including Biology of Reproduction, Reproduction, the FASEB Journal, Frontiers in Endocrinology, Theriogenology

Awards and Honors:

- 2016: Trainee Research Finalist for the Platform Award, 49th Annual Meeting of the Society for the Study of Reproduction
- 2016: USDA-NIFA-AFRI Merit Award, 49th Annual Meeting of the Society for the Study of Reproduction

JIUZHOU 'JOHN' SONG

Professor, Epigenetics, Genetics, and Statistical Genomics

Education:

1986	M.S.	Northwest A&F University in China
1996	Ph.D.	China Agricultural University
1998	Postdoc	Hebrew University of Jerusalem
2001	Fellow	Indiana University

Professional Experience:

2001-2005	Biostatistician, Department of Biochemistry and Molecular Biology, Department of Infectious Disease and Microbiology, University of Calgary
2005-2011	Assistant Professor, Department of Animal and Avian Sciences, University of Maryland
2011-2016	Associate Professor, Department of Animal and Avian Sciences, University of Maryland
2012-Present	Director, Biometrics Program, University of Maryland
2013-Present	Special Scientist, Systems Biology Center, NHLBI, NIH
2016-Present	Professor, Department of Animal and Avian Sciences, University of Maryland
2017	AgriBio Centre for AgriBioscience, Applied Systems Biology. Melbourne, Victory. Australia

Teaching Responsibilities:

- BIOM 688E: Statistical Genomics
- BIOM 602: Experimental Design and Data Analysis

Research Interest:

- Epigenetics, genetics, statistical genomics, and artificial intelligence related to the representation, analysis, and interpretation of temporal and spatial information in animal science and health

Significant Accomplishments:

- Developed courses in Statistical Genomics, Experimental Design, and Data Analysis
- Authored or co-authored more than 236 refereed scientific publications, six book chapters, and 135 abstracts presented at professional meetings, with 8500 citations and a hi-index of 42
- Membership: AAAS, PSA, ASAS, ISAG, and ASHG

Awards and Honors:

- 2020-2022: Senior Expert in Oxford Global Key Opinion Leaders Advisory Board
- 2003: The Excellence Prize of the Conference of CAMIS and SCMAI
- 1998: Excellence Scholar, Ministry of Foreign Affairs, Israel
- 1997: Golda Meir Fellowship Award, Ministry of Education, Israel
- 1994: First Prize, Journal of Cattle Science, Research Article

NISHANTH SUNNY

Associate Professor, Nutritional Biochemistry and Metabolism

Education:

2001	B.V.Sc & A.H.	College of Veterinary and Animal Sciences, Kerala, India
2005	M.S.	University of Maryland
2008	Ph.D.	University of Maryland

Professional Experience:

2002-2005	Graduate Research Assistant, University of Maryland
2005-2007	Graduate Teaching Assistant, University of Maryland
2008-2010	Postdoctoral Researcher, Advanced Imaging Research Center, University of Texas Southwestern Medical Center at Dallas
2010-2012	Assistant Instructor, Advanced Imaging Research Center, University of Texas Southwestern Medical Center at Dallas
2012-2017	Research Assistant Professor, Department of Medicine, Division of Endocrinology, Diabetes and Metabolism, University of Florida, Gainesville
2017-2023	Assistant Professor, Department of Animal and Avian Sciences, University of Maryland
2023-Present	Associate Professor, Department of Animal and Avian Sciences, University of Maryland

Research Interest:

- Profiling of metabolic pathways and mitochondrial function during health and disease using stable isotopes coupled with mass spectrometry and utilizing model systems including embryonic-to-neonatal transition period in chicken, diet induced mice models of obesity and *in vitro* cell culture.

Significant Accomplishments:

- Authored or co-authored 38-refereed scientific publications and 40 abstracts presented at professional meetings
- Principal investigator on a USDA-NIFA award - Macronutrient regulation of the metabolic switch in newly hatched chicken
- Has mentored four post-doctoral scholars, five graduate students and sixteen undergraduate students at the University of Maryland
- Reviewer for several journals including Aging Cell, American Journal of Pathology, American Journal of Physiology Endocrinology and Metabolism, Gastroenterology, Gut, Journal of Nutrition, Molecular Metabolism, Nature Communications, PLOS ONE and Scientific Reports

Awards and Honors:

- 2021: Dean's Grantsmanship award, College of Agriculture and Natural Resources, University of Maryland
- 2016: Excellence in Teaching Award, Dept. of Medicine, University of Florida
- 2011: Young Investigator Award, American Diabetes Association
- 2007: Jacob K. Goldhaber Travel Grant, Graduate School, University of Maryland, College Park
- 2007: Travel grant, Energy and macronutrient metabolism research interest section, American Society for Nutrition
- 2007: Distinguished Teaching Assistant, University of Maryland, College Park
- 2005: Poster presentation award, 3rd Mid-Atlantic nutrition conference, Timonium, MD
- 2004: Bioscience research and technology review day, Poster Award. University of Maryland, College Park
- 2002: Junior Research Fellowship, College of Veterinary and Animal Sciences, Kerala, India

LISA TANEYHILL

Professor, Developmental Biology

Education:

1995	B.S.	Western Maryland College (McDaniel College)
2000	Ph.D.	Princeton University

Professional Experience:

2002-2006	Postdoctoral Scholar, Division of Biology, California Institute of Technology
2006-2007	Senior Research Fellow, Division of Biology, California Institute of Technology
2007-2015	Assistant Professor, Department of Animal and Avian Sciences, University of Maryland
2007-Present	Faculty, Neuroscience and Cognitive Science Program, University of Maryland
2007-Present	Faculty, Biological Sciences Graduate Program, University of Maryland
2010-Present	Affiliate Faculty, Department of Cell Biology and Molecular Genetics, University of Maryland
2015-2019	Associate Professor, Department of Animal and Avian Sciences, University of Maryland
2019-Present	Professor, Department of Animal and Avian Sciences, University of Maryland
2023-2024	Assistant Chair, Department of Animal and Avian Sciences, University of Maryland
2025-Preset	Associate Provost for Academic Affairs, University of Maryland

Teaching Responsibilities:

- ANSC497/688G Animal Biotechnology Recombinant DNA laboratory (2009-2025)
- Proposed, initiated and developed ANSC498T/688G Organismal Development

Research Interests:

- To elucidate the molecular mechanisms underlying the formation and function of neural crest cells and placode cells during development and disease.

Significant Accomplishments and Administrative Responsibilities:

- Author of 41 refereed scientific papers, 12 book chapters or reviews, and 85 abstracts
- Publications cited 2,998 times
- Recipient of over $7,650,000 in total costs through competitive research grants
- Current major advisor to 2 Ph.D. students and 2 undergraduate students

Awards and Honors:

- 2024-2025: Big10 Academic Alliance Academic Leadership Program
- 2023 & 2025: Vice-Chair (2023) and Chair (2025), Gordon Research Conference on Neural Crest and Cranial Placodes
- 2023: AGNR Diversity, Equity, Inclusion and Respect Faculty Standard of Excellence Award
- 2023: Fellow, American Association for Anatomy
- 2021-2023: AGNR ADVANCE Professor
- 2020-2023: University of Maryland University Research Council Chair
- 2020-2021: University of Maryland ADVANCE Leadership Fellows Program
- 2019-2021: University of Maryland Chapter, Phi Beta Kappa Society, Vice-President
- 2017-21, 2021-24: American Association for Anatomy Program Committee (2017-21), Board of Directors (2021-24)
- 2016-19, 2024-26, 2026-28: Secretary (2016-19), Vice-President (2024-26), and President-elect (2026-28), Society for Craniofacial Genetics and Developmental Biology
- 2015-2016: National Academy of Science Committee Member: Gene Drives Research in Non-Human Organisms: Recommendations of Responsible Conduct
- 2012: McDaniel College Alumni Professional Achievement Award
- 2012: AGNR Junior Faculty Excellence Award
- 2011: AGNR Outstanding Faculty Educator
- 2007: Elsevier Scholars Foundation Award for Women in Science
- 2006-2011: NIH Pathway to Independence Award for New Investigators (K99/R00)

ADELE TURZILLO

Professor and Department Chair, Animal and Avian Sciences

Education:

1984	B.A.	Cornell University
1992	Ph.D.	Cornell University

Professional Experience:

1992-1998	Postdoctoral Fellow, Animal Reproduction and Biotechnology Lab, Colorado State Univ.
2004-2008	Physiologist, FDA Center for Veterinary Medicine
2008-2013	National Program Leader, Division of Animal Systems, National Institute of Food and Agriculture (NIFA)
2013-2019	Director, Division of Animal Systems, USDA NIFA
2020-2024	Department Head, Department of Animal Science, Penn State Univ.
2024-Present	Professor and Chair, Department of Animal and Avian Sciences, Univ. of Maryland

Scholarly Interests:

- Ovarian follicular development in cattle
- Synthesis and secretion of pituitary gonadotropins
- Communication of scientific information

Significant Accomplishments:

- Co-chair, USDA National Animal Health Laboratory Network Executive Committee 2013-2019
- Co-leader, USDA National Stakeholder Workshops on Animal Health & Animal Production 2016
- In-country team member, USDA-U.S. Agency for International Development (USAID) assessment of the livestock sector in Nepal 2012
- Editor and contributing author, FDA Risk Assessment on Animal Cloning 2008
- Subject Matter Expert, World Trade Organization Dispute DS320: EC-Hormones dispute pertaining to the safety of U.S. beef 2004-2008

Awards and Honors:

- 2018: Individual Award, USDA National Institute of Food and Agriculture
- 2016: Abraham Lincoln Honor Award, USDA
- 2012: Secretary's Honor Award for Excellence, USDA
- 2006: Outstanding New Reviewer Award, FDA Center for Veterinary Medicine
- 2004: Outstanding Investigator Award, University of Arizona
- 1994: New Investigator Award, Society for the Study of Reproduction

ZHENGGUO XIAO

Professor, Immunology

Education:

1988	D.V.M.	Nanjing Agricultural University, China
1991	M.S.	Nanjing Agricultural University, China
2004	Ph.D.	University of Minnesota

Professional Experience:

1988-1991	Research Assistant, Nanjing Agricultural University, China
1991-1999	Research Scientist &Veterinarian, Nanjing Animal and Plant Quarantine Bureau, China
2000-2004	Research Assistant, University of Minnesota
2004-2008	Postdoctoral fellow, Department of Medicine, Medical School, University of Minnesota, Minneapolis, MN
2008-2014	Assistant Professor, Department of Animal & Avian Sciences, University of Maryland
2014-2020	Associate Professor, Department of Animal & Avian Sciences, University of Maryland
2020-Present	Professor, Department of Animal & Avian Sciences, University of Maryland

Teaching Responsibilities:

- ANSC460/688I: Comparative Vertebrate Immunology

Research Interests:

- CD8+ T cell-derived exosomes and their functions
- Intraepithelial T lymphocytes in the gut
- Molecular mechanisms for functional CD8+ T responses
- Activation of bovine T cells
- Mucosal immune response to parasite infection in cattle

Significant Accomplishments:

- 2021: Ad Hoc Reviewer: Swiss National Science Foundation
- 2020: Ad Hoc Reviewer: Wellcome trust/DBT India Alliance Fellowship
- 2014: Academic advisor to 60 undergraduate students in ANSC
- 2014: Ad Hoc Reviewer: Qatar National Research Fund
- 2013: Editorial board member for eight peer reviewed journals
- 2010: Major professor for 10 graduate students
- 2009: Member on 42 graduate student thesis committees
- 2009-2013: Lead guest editor for a special issue on *Cytotoxic T Lymphocytes and Vaccine Development*, Journal of Biomedicine and Biotechnology
- 2004: Ad Hoc Reviewer–National Pork Board and NRI/NC229 PRRS research proposals
- Authored or co-authored 42 refereed scientific publications, co-editor of 1 book
- Working as a veterinarian in Nanjing Animal and Plant Quarantine Bureau for 8 years. The incomplete list of animals I had worked with includes most of domestic animals, tiger, sharks, seals, snakes, shrimp, fish

Staff and Research Specialists

Name	Title
Exempt Staff	
Angela Black, DVM, Ph.D.	Animal Care Coordinator
Karly Bowe	Assistant Farm Manager
Megan Calloway	Campus Farm Manager
Jessica Karunaratne	Research Assistant
Adriana Kempen	Coordinator, Laboratory Courses and Equipment
Michael Mobley	Manager of Computer Services
Ashley Montalvan	Academic Program Coordinator
Victoria Pearlman	Assistant Director of Undergraduate Program
Jennifer Reynolds	Coordinator (Equine-Poultry Extension Activities)
Racheal Slattery	Coordinator (Dairy-Beef Extension Activities)
Jonathan Stephanoff	Webmaster / Multimedia Specialist
Paul Vaughn	Director of Administrative Services
Pablo Villafranco	Senior Business Manage
Nonexempt Staff	
Jose Austin	Lab Animal Technician Assistant
Clare Capotosto	Program Management Specialist
Peter Chamberlain	Program Administrative Specialist
Daniel Ding	Ag Worker II
Justine Gange	Lab Animal Technician
Sheryl Grey	Business Services Specialist
Mariana Guillen	Lab Animal Technician
Research Assistants and Associates	
Chiranjibi Chhotarya, Ph.D.	Post-Doctoral Associate
Joe Cain, Ph.D.	Post-Doctoral Associate
Razib Das, Ph.D.	Post-Doctoral Associate
Boonyarit Kamkrathok, Ph.D.	Faculty Assistant
Zubair Khalid, Ph.D.	Post-Doctoral Associate
Carrie Leonard, Ph.D.	Assistant Research Professor
Lei Li	Faculty Specialist
Qunhao Niu, Ph.D.	Post-Doctoral Associate
Panpradub “Nok” Sinpru, Ph.D.	Faculty Specialist
Nichola Thompson	Faculty Specialist
Liu Yang, Ph.D.	Post-Doctoral Associate

Graduate Students

Name	Advisor/Supervisor	Degree Program
Usman Abubakar	Zhengguo Xiao	Ph.D.
Hammed Ayansola	Younggeon Jin	Ph.D.
Taiwo Bello	Emilia Przygrodzka	Ph.D.
Bishal Bhattachan	Sunoh Che	Ph.D.
Indira Bhattacharya	Iqbal Hamza	Ph.D.
Arianna Bond	Tom Porter	Ph.D.
Jiarui Cai	Li Ma	Ph.D.
Jasmin Celedon	Nishanth Sunny	M.S.
Jiecheng Chen	Younggeon Jin	M.S.
Tamseel Fatima	Byung-Eun Kim	Ph.D.
Ray Gao	John Song	Ph.D
Sandeepan Ghosh	Iqbal Hamza	Ph.D.
Jyothsna Girish	Andrew Broadbent	Ph.D.
Christopher Kim	Mohamed Salem	M.S.
Jason Na	Sunoh Che	M.S.
Sonika Neupane	Heewon Seo	M.S.
Melissa Perry (BISI)	Iqbal Hamza	Ph.D.
Anna Phan (BISI)	Debabrata Biswas	Ph.D.
Thomas Podles	Andrew Schiffmacher	M.S.
Pratibha Poudel	Byung-Eun Kim	Ph.D.
Guglielmo Raymo	Mohamed Salem	Ph.D.
Andrew Rock	Iqbal Hamza	Ph.D.
Caitlin Ryan	Nishanth Sunny	Ph.D.
Johena Sanyal (BISI)	Lisa Taneyhill	Ph.D.
Ricardo Sierra-Arroyo (BISI)	Tom Porter	Ph.D.
Juliana Sand	Emilia Przygrodska	M.S.
Kanchan Thapa	Debabrata Biswas	Ph.D.

Degree Awarded in 2025-2026

Ridwan Ahmed	Mohamed Salem	Ph.D.
Oladipupo Ridwan Bello	Li Ma	Ph.D.
Parama Bhattacharjee	Nishanth Sunny	Ph.D.
Andrew Brodrick	Andrew Broadbent	Ph.D.
Hannah Burchard	Fabiana Cardoso	M.S.
Akanksha Hada	Zhengguo Xiao	Ph.D.
Caroline Halmi	Lisa Taneyhill	Ph.D.
Paige Meisner	Tom Porter	M.S
Michaela Riedel	Tom Porter	M.S.
Niraj Suresh	Fabiana Cardoso	M.S.
Anand Tiwari	Richard Kohn	Ph.D.
Xuedi Zhang	Iqbal Hamza	Ph.D.

Graduating Seniors: Animal Sciences Majors

Bachelor of Science - Fall 2025

Katelyn Louise Amoss
Emma Kemper Boyd
Leah Danielle Booker
Jenna Lauren Feinberg
Athena Nicole Kalargyros
Lluviza Elena Kuiper Vargas
Amanda Rachel Loewenthal
Dayanara Alexa Machuca
Stephanie Caroll Mejia
Aryannah Nasser
Jason Yoonchae Na
Rachel Anna Palatinsky
Xenia Elizabeth Rivas
Ella Prizer Roth
Patricia Carolina Santos
Emmaline Lee Sundvall
Alexis Nattapa Urbanz
Jordan Alexander Weinstein-Long
Jada Ashanti Willis
Arianna Yae Jin Yi

Bachelor of Science - Spring 2026

Linsey Carol Anderson
Morgan Jade Aronsky
Zachary Babasa
Mikaili Olyvia Barreras
Mary Barsoum
Esther Chaya Baum
Sarah Maya Blackman
Riley Morgan Bjerkness
Giselle Arahi Blanco
Raquel Leigh Bowman
Kendal Jane Burzynski
Gabriela Jeannette Carcamo Valladares
William Basil Diguiseppe
Gabrielle Ronae Dorsey
Emily Grace Duenas
Jacqueline Isabel Espinoza
Allison Flaherty
Madelynn Huari Gilmore
Theodore J Glister
Lauren Alianny Gomez
Lian Pearl Goodman
Hadiya Dhakira Grier
Emma Jane Gross
Kathryn Emily Grow
Ellie Rose Guzman
Ethan Neil Harris
Raven Noel Herron
Romi Faith Hodor
Hannah Faith Hopkins
Irene Hyunyoung Ki
Ava Kneale
Batsheva Lerner
Lisa Lian
Elizabeth Adelita Munoz
Kalei Anne Murray
Miku Nagao
Diem-Thu Qui Nguyen
Michelle Andy Ortez
Sarah Elizabeth Pearl
Mara Juliet Pizzano
Hailey Marie Poole
Isabella Jane Richardson
Elizabeth Ruth Ridenour
Gabrielle Nicole Riess
Xenia Elizabeth Rivas
Summer Lauren Roach
Lilly Anne Rodman
Amber Mishele Sadiq
Anna Paige Senatore
Gabriele Amelia Smith-Hicks
Tyler Alan Soderstrom
Samari Symone Stephens
Emily Elizabeth Todd
Faith Comen Trivett
Lauren Unger
Julianne Grace Vengroski
Gabriella Marie Warner
Maggie McNeal Weisman
Ella Gaye Wise
Raphael Zukowski

Publications

Articles in Refereed Journals - 2025

Phan, A., Mijar, S., Harvey, C., and **Biswas, D.** 2025. Staphylococcus aureus in Foodborne Diseases and Alternative Intervention Strategies to Overcome Antibiotic Resistance by Using Natural Antimicrobials. Microorganisms 2025, 13, 1732. doi.org/10.3390/microorganisms13081732

Tung, C., Thapa, K., Phan, A., and **Biswas, D.** 2025. Limitation of the lytic effect of bacteriophages on Salmonella and other enteric bacterial pathogens and approaches to overcome. International Journal of Microbiology, Article ID 5936070 https://doi.org/10.1155/ijm/5936070.

Phan, A., Thapa, K., Hashmi, M., Mahapatra, A., Ho, G., Tholan, G. and **Biswas, D.** 2025. Prophylactic efficacy of probiotics and their metabolites against Staphylococcus epidermidis. BMC Microbiology 25: 621 https://doi.org/10.1186/s12866-025-04382-w

Goodwyn, B., Millner, P., Punchihewage, A., Schwarz, M., Hashem, F., Bowers, J., **Biswas, D.** and Parveen, S. 2025. Integrated crop-livestock farming systems influence the incidence of Salmonella, Listeria monocytogenes, Shiga toxin-producing Escherichia coli, and indicator bacteria on fresh produce. Spectrum Microbiology. 10.1128/spectrum.00862-25.

Tung, C., Thapa, K., Phan, A., Hashmi, M., Mahapatra, A., Bleich, K. and **Biswas, D.** 2025. Antibacterial activity of a fused endolysin ENDO-1252/KL9P against multiple serovars of Salmonella enterica. Microbial Biotechnology, 2025; 18:e70237. https://doi.org/10.1111/1751-7915.70237

Cardoso F. F, Garcia L, Thompson J. S, de Jesus M. N, Smith A. H, Rehberger T. G, Cardoso F. C. Effects of feeding direct-fed Bacillus subtilis and Clostridium beijerinckii on health, performance, and blood biomarkers during the transition period and early lactation in Holstein cows. Journal of Dairy Sci. 2025. doi:10.3168/jds.2025-27417.

Che, S., Susta, L., Sanpinit, P., Malila, Y. and Barbut, S., (2025). Gaping Conditions of the Pectoralis Minor (tenders) in Commercial Broilers: Prevalence, Histology, and Gene Expression. Poultry Science, 104976.

Greene, E., **Che, S.,** Soglia, F., Iwasaki, T., Watanabe, T., Kawasaki., T., Susta., L., Petracci, M., Scanes, C., Dridi, S., (2025) Breast muscle myopathies: twists and turns in modern broilers, Avian Pathology, 1–57

Gordon, L., Leacy, A., Pham, P.H., Tuling, J., **Che, S.,** El-Khouri, A., Caswell, J.L., Lillie, B.N. and Susta, L., (2025). Pathogenesis of Aquatic Bird Bornavirus 1 in Turkeys of Different Age. npj Viruses, 3(1):14

Che, S., Al-Tobasei, R., Ahmed, R., Raymo, G., Ali, A., Salem, M., Genetic and histopathological characterization of spaghetti meat in broiler chickens, Poultry Science Association Meeting, NC, USA, 2025

Che, S., Goeringer, P., Ghanem, M., Rhodes, J., Perdue, M., Moyle, J. Assessing evolving challenges and educational needs in commercial and backyard poultry management, Poultry Science Association Meeting, NC, USA, 2025

Mitchell, R., Moyle, J. **Che. S.** Leveraging AI-driven sentiment analysis and natural language processing to inform extension efforts in the poultry industry, Poultry Science Association Meeting, NC, USA, 2025

Lee JK, He Y, Flores SR, Woloshun RR, Wang X, Shine JS, Ebea-Ugwuanyi PO, Sriram S, Fraga M, Zhu S, Yu Y, **Hamza I,** Collins JF. Development of rat and mouse models of heme-iron absorption. JCI Insight. 2025 Jun 9;10(11):e184742. doi: 10.1172/jci.insight.184742. eCollection 2025 Jun 9.

Ayansola, H., **Jin, Y.** (2025) An Optimized Sequential Isolation of Crypts and Mesenchymal Stromal Cells from Porcine Intestinal Tissue. joVE. 2025 December. DOI:10.3791/69429

Kim, J., Madan, J.P., Laumas, S., Krishnan, B.R., **Jin Y.** (2025) Larazotide Acetate Protects the Intestinal Mucosal Barrier from Anoxia/Reoxygenation Injury via Various Cellular Mechanisms. Biomedicines. 2025 October. DOI:10.3390/biomedicines13102483

Holt, B. M., Stine, J. M., Beardslee, L. A., Ayansola, H., **Jin, Y**., Pasricha, P. J., Ghodssi, R. (2025), An Ingestible Bioimpedance Sensing Device for Wireless Monitoring of Epithelial Barrier, Microsystems and Nanoengineering, 11;24.

Lee YS, Kim HS, Nguyen PL, Lee J, Moon C, Cho KO, **Kim BE**, Ahn J, Osborne TF, Duysak T, Kim JS, Jung CH, Jeon TI. Copper deficiency disrupts OXPHOS and mitochondrial dynamics through MTCH2-dependent copper trafficking in skeletal muscle. *bioRxiv*. 2025 Nov; 19. Doi: 10.1101/2025.11.19.688750.

J Cai†, L Yang†, Y Gao, GE Liu, Y Da, **L Ma** (2025) Selection Signature Analysis of Whole-Genome Sequences to Identify Genome Differences Between Selected and Unselected Holstein Cattle. Animals 15 (15), 2247

Y Gao, GE Liu, **L Ma**, L Fang, C Li, and RL Baldwin (2025) Transcriptomic profiling of gastrointestinal tracts in dairy cattle during lactation reveals molecular adaptations for milk synthesis. Journal of Advanced Research 71, 67-80

Z Xu, Q Lin, X Cai, Z Zhong, J Teng, B Li, H Zeng, Y Gao, Z Cai, X Wang, **L Ma** (2025) Integrating large-scale meta-GWAS and PigGTEx resources to decipher the genetic basis of 232 complex traits in pigs. National Science Review, nwaf048

Y Gao, L Yang, K Kuhn, W Li, G Zanton, M Bowman, P Zhao, Y Zhou, **L Ma** (2025) Long read and preliminary pangenome analyses reveal breed-specific structural variations and novel sequences in Holstein and Jersey cattle. Journal of Advanced Research 79, 137-150

Y Gao, GE Liu, **L Ma**, C Li, RL Baldwin (2025) A resource of longitudinal RNA-seq data of Holstein cow rumen, duodenum, and colon epithelial cells during the lactation cycle, BMC Genomic Data 26 (1), 9

L Fang, J Teng, Q Lin, Z Bai, S Liu, D Guan, B Li, Y Gao, **L Ma** (2025) The Farm Animal Genotype–Tissue Expression (FarmGTEx) Project. Nature Genetics, 1-11. https://doi.org/10.1038/s41588-025-02121-5

Klug ST, Ellestad LE, **Porter TE** (2025) Pituitary-targeted knockout of glucocorticoid receptors disrupts growth hormone expression during embryonic development. Endocrinology 166: bqaf119 doi.org/10.1210/endocr/bqaf11

Kamkrathok B, Beckford RC, Klug S, Diehl K, Farley L, **Porter TE** (2025) Effect of early-life thermal conditioning on mRNA expression in tissues under heat stress and nonheat stress conditions in broiler chickens. Poult Sci doi.org/10.1016/j.psj.2025.106244

Ali, A†., Ali, Y. †, Raymo, G. †, Dalei, A†., & **Salem, M.** Molecular signatures and machine learning driven stress biomarkers for rainbow trout aquaculture and climate adaptation. Sci Rep 2025 https://doi.org/10.1038/s41598-025-30120-3

Ali A†, Gao G, Al-Tobasei R, Youngblood RC, Waldbieser GC, Scheffler BE, Palti Y, **Salem M**: Chromosome level genome assembly and annotation of the Swanson rainbow trout homozygous line. Sci Data 2025, 12(1):345. https://doi.org/10.1038/s41597-025-04693-7

Sah N, Stenhouse C, Halloran KM, Moses RM, Newton MG, **Seo H**, Cain JW, Johnson GA, Wu G, Bazer FW. Effect of gestational age and fetal sex on metabolism of creatine by uteri, placentae, and fetuses of pigs. Biol Reprod. 2025; 112(4):728-742.

Lopez AN, Olivarez MA, Stenhouse C, Moses RM, Newton MG, Sah N, **Seo H**, Cain J, Lefevre C, Ross A, Ryan P, Wiegert JG, Wu G, Johnson GA, Bazer FW. Effects of dietary supplementation of creatine on fetal development in gilts at d 60 and d 90 of gestation. J Anim Sci Biotechnol. 2025; 16(1):31.

Stenhouse C, Halloran KM, Hoskins EC, Moses RM, Newton MG, Sah N, Wolpo YE, Tyree MF, **Seo H**, Johnson GA, Wu G, Bazer FW. Characterization of the expression of XPR1 in ovine utero-placental tissues. Reproduction. 2025; 169(6):e250072.

Cain JW, Erikson DW, **Seo H**, Ross A, Burghardt RC, Bazer FW, Johnson GA. SPARC expression in the mouse decidua, placenta, and fetus: correlations with SPP1 expression. Placenta 2025; 168:125-134

Liu X, Mi S, Dari G, Chen S, **Song J**, MacHugh DE, Yu Y. Functional validation to explore the protective role of miR-223 in Staphylococcus aureus-induced bovine mastitis. J Anim Sci Biotechnol. 2025 Mar 4;16(1):34. doi: 10.1186/s40104-025-01152-6. PMID: 40033327; PMCID: PMC11877765.

Liu G, Peng Y, Li Z, Zhu X, Sun H, Chen G, Zuo Q, Niu Y, **Song J**, Han W, et al. An Inducible CYP19A1 Excision Model for Sexual Differentiation in Chicken (Gallus gallus) via the CRSPIR/Cas9 System. Veterinary Sciences. 2025; 12(4):296. https://doi.org/10.3390/vetsci12040296

Liu X, Wu J, Peng Y, Qian H, Lv X, Li F, Jin K, Niu Y, **Song J**, Han W, et al. Chicken Primordial Germ Cells Do Not Proliferate in Insulin-Lacking Media. International Journal of Molecular Sciences. 2025; 26(7):3122. https://doi.org/10.3390/ijms26073122

Ding Y, Dunn J, Zhang H, Zhao K, **Song J**. Comparative transcriptomic analysis of chicken immune organs affected by Marek's disease virus infection at latency phases. Front Physiol. 2025 Apr 2;16:1520826. doi: 10.3389/fphys.2025.1520826. PMID: 40241721; PMCID: PMC12000659.

Sun C, **Song J**, Ali MA, Sun H, Niu Y, Zuo Q, Han W, Li B, Jin K. Molecular Mechanism of HINTW (HINT Gene in W-Chromosome)-Mediated UBE2I (Ubiquitin Conjugating Enzyme E2 I) Interaction in Female Differentiation of Chicken Embryos. Genes (Basel). 2025 Mar 22;16(4):366. doi: 10.3390/genes16040366. PMID: 40282326; PMCID: PMC12026566.

Liu G, Peng Y, Li Z, Zhu X, Sun H, Chen G, Zuo Q, Niu Y, **Song J**, Han W, Wei W, Li B, Jin K. An Inducible CYP19A1 Excision Model for Sexual Differentiation in Chicken (Gallus gallus) via the CRISPR/Cas9 System. Vet Sci. 2025 Mar 22;12(4):296. doi: 10.3390/vetsci12040296. PMID: 40284798; PMCID: PMC12031565.

Liu X, Wu J, Peng Y, Liu G, Jin K, Niu Y, **Song J**, Han W, Chen G, Li B, Zuo Q. Functional Equivalence of Insulin and IGF-1 in the In Vitro Culture of Chicken Primordial Germ Cells. Genes (Basel). 2025 Apr 24;16(5):481. doi: 10.3390/genes16050481. PMID: 40428303; PMCID: PMC12110881

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Bhattacharjee P, Fadlaoui A, Ryan CE, Carlson CB, Zhang D, **Sunny NE**. (2025) Induction of Fructose Mediated De Novo Lipogenesis Co-exists with the Upregulation of Mitochondrial Oxidative Function in Mice Liver. J Nutr. S0022-3166(25)00276-7. doi: 10.1016/j.tjnut.2025.04.030. Online ahead of print. PMID: 40334788.

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Leonard CE, McIntosh AT, Sanyal J, and **Taneyhill LA**. The transcriptional landscape of the developing trigeminal ganglion. Dev Biol. 2025. doi: 10.1016/j.ydbio.2024.12.013.

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Hada, A. & **Xiao, Z**. Ligands for Intestinal Intraepithelial T Lymphocytes in Health and Disease. Pathogens 14 (2025)

Hada, A. & **Xiao, Z**. T Cell Responses to Influenza Infections in Cattle. Viruses 2025, 17, 1116.

Chapters in Books - 2025

Broadbent, A A veterinary virapalooza: a summary of the 2024 American Society for Virology (ASV) Veterinary/ Zoonotic Virology Satellite Symposium and online H5N1 panel discussion. Journal of Virology, 2025, Jun 17;99(6):e0049925. doi:10.11.28/jvi.00499-25. *UMD affiliation

Refereed Abstracts - 2025

Yuan, X, Belot A, Samuel TK, Xue X, Hall C, Pek R, Dutt S, Korolnek T, Spence J, Shah Y, and **Hamza I.** Functional adaption of human HRG1 as an intestinal heme transporter. International BioIron Society Meeting, Montreal, Canada, May 25-29, 2025.

Belot A, Rock A, Bodine D and **Hamza I.** Fine-tuning of hemoglobinization through heme import by erythrocytic HRG1. International BioIron Society Meeting, Montreal, Canada, May 25-29, 2025. (invited speaker)

Zhang X, Pandey V, Bodine D, Wohlschlegel J, **Hamza I.** In Vivo Proteomics Identifies the Heme Transporter HRG1 Interactome. Gordon Research Conference/Seminar. Cell Biology of Metals, University of Southern Maine, Aug 2-3, 2025. (invited Speaker).

Belot A, **Hamza I.** A cell-nonautonomous heme acquisition pathway enables erythroid hemoglobinization. Red Cell Club and East-West Iron Club, Baltimore, Oct 27-29, 2025 (invited speaker).

Bhattacharya I, **Hamza I.** Mechanisms of hemozoin formation in mammals. Red Cell Club and East-West Iron Club, Baltimore, Oct 27-29, 2025 (invited speaker).

Zhang X, **Hamza I.** In vivo proteomics identifies the heme transporter HRG1 interactome. Red Cell Club and East-West Iron Club, Baltimore, Oct 27-29, 2025 (invited speaker).

Perry M, **Hamza I.** Heme Homeostasis at the Leishmania-Host Interface. Red Cell Club and East West Iron Club, Baltimore, Oct 27-29, 2025 (invited speaker).

Kohn, R. A. and A. Tiwari. 2025. How is media consensus on greenhouse gas emissions from animal agriculture evolving? J. Dairy Science Supplement 108: 170.

Tiwari, A. and **R. A. Kohn**. 2025. A quick method to measure non-carbon dioxide gas from a mixture of fermentation gases. J. Dairy Science Supplement 108: 339.

Craig, H., A. Tiwari, **R. Kohn**, J. E. Rico, and B. Lamp. 2025. In vitro and in situ evaluations of black soldier fly larvae as a methane-mitigating protein substitute in dairy cattle diets. J. Dairy Science Supplement 108: 349.

Tiwari, A. and **R. Kohn**. 2025. Evaluation of red algae sources on rumen gas production in vitro. J. Dairy Science Supplement 108: 417.

Liu K-L, **Porter TE** (2025) Characterization of glucocorticoid effects on gene expression in chicken embryonic cortico-somatotrophs by single-cell RNA sequencing. Program 32nd Plant and Animal Genome Conference.

Yang L, Fusco E, He Y, Chen P, **Porter TE**, Song J (2025) Long-read Transcriptome Analysis of Amphoteric ESCs and PGCs in Chicken . Program 32nd Plant and Animal Genome Conference.

Meisner P,. Berger M, Ferreira C, Hanlon C, **Porter TE**, Diehl K (2025) Lipid biomarkers associated with egg storage and early embryonic mortality in broiler breeder chickens. Program 2025 Annual Meeting of the Poultry Science Association.

Bond A, Long J, Garrett W, Shannon A, Flack B, Harford I, **Porter TE**, Diehl K (2025) Sperm mobility phenotype impact on broiler breeder sperm cell and seminal plasma proteome. Program 2025 Annual Meeting of the Poultry Science Association.

Sinpru P, Diehl K, Ellestad LE, **Porter TE** (2025) The effect of genetic selection on gene expression in the developing neuroendocrine system of broiler chickens. Program 2025 Annual Meeting of the Poultry Science Association.

Sierra Arroyo RG, **Porter TE**, Diehl K (2025) In vitro transcriptomic response of pituitary cells from low and high turkey egg producers to thyroid hormone and gonadotropin releasing hormone. Program 2025 Annual Meeting of the Poultry Science Association.

Kamkrathok B, Klug S, Beckford RC, **Porter TE** (2025) Effect of early-life thermal conditioning on mRNA expression in tissues during heat stress in broiler chickens. Program 2025 Annual Meeting of the Poultry Science Association.

Riedel MA, Bhattacharjee P, Sunny NE, **Porter TE** (2025) Effects of delayed feeding and semi-purified diets on anterior pituitary mRNA expression in broiler chicks. Program 2025 Annual Meeting of the Poultry Science Association.

Whittle R, Forga A, Graham D, **Porter TE**, Weimer S (2025) Thermal conditioning: No behavioral strategy shift under chronic heat stress. 2025 Annual Meeting of the Poultry Science Association.

Bhattacharjee P, Riedel MA, **Porter TE**, Sunny NE (2025) Macronutrient specific initiation of metabolic switch in newly hatched chickens. 2025 Annual Meeting of the Poultry Science Association.

Porter TE (2025) Mechanisms regulating induction of pituitary growth hormone production during chicken embryonic development. Poultry Science Association Pacific Rim Scientific Conference

Przygrodzka E, Haine S, Do L, Weisman M, Glasper C, Murphy E. Protein Kinase A (PKA) Mediated Chromatin Accessibility and Transcriptomic Alterations in Granulosa Cells. SSR 2025 Annual Meeting, July, 2025, Washington, D.C.

Haine S, Glasper C, Do L, Weismann M, Murphy E, **Przygrodzka E**. Protein kinase A (PKA) stimulated glucose metabolism is essential for granulosa cell function. ANSC Annual Symposium, May 2025, College Park, MD.

Cain JW, Wu G, Bazer FW, Johnson GA and **Seo H**. Trophectoderm of elongating conceptuses use reverse TCA cycle flux to supply biosynthetic precursors within a physiologically low oxygen intrauterine environment in pigs. Annual Meeting of the Society for the Study of Reproduction, 2025.

Yang, L. Porter, T. **Song, J.** Epigenetic Profile of Chicken Embryonic Stem Cells
Chicken ESC and PGC. Plant and Animal Genome Conference PAG 31 January 11-15,
2025

Yang, L. Porter, T. **Song, J**. Epigenetic Atlas and Long-read transcriptome analysis of sex-specific ESCs and PGCs in Chickens. ISAG 2025, Daejeon, Korea, 2025. OP115

Mitra, A. Zhang, H. Dunn, J. **Song, J**. Temporal Profiling of the Bursa Transcriptome Reveals Systemic Differences Induced by MDV Infection in Inbred Chicken Lines with Varying MD-resistance. 2025 Poultry Science Association Pacific Rim Scientific Conference, Macau, China. October 12-16.

Ryan CE, Bhattacharjee P, Mishra I, **Sunny NE** (2025) Adaptations in Tricarboxylic Acid Cycle and Branched-Chain Amino Acid Degradation in Embryonic and Neonatal Chicken Muscle. American Physiology Summit 2025, Baltimore, MD.

Bhattacharjee P, Riedel M, Porter T, **Sunny NE** (2025). Macronutrient specific initiation of the metabolic switch in newly hatched chickens. 2025 PSA Annual Meeting, Raleigh, NC.

Ryan CE, Carlson C, Bhattacharjee P, **Sunny NE** (2025). In ovo supplementation of branched-chain amino acids and hepatic mitochondrial function in developing chicken embryos. 2025 PSA Annual Meeting, Raleigh, NC.

Refereed Posters - 2025

Che, S., Al-Tobasei, R., Ahmed, R., Raymo, G., Ali, A., Salem, M., Genetic and histopathological characterization of spaghetti meat in broiler chickens, Poultry Science Association Meeting, NC, USA, 2025

Che, S., Goeringer, P., Ghanem, M., Rhodes, J., Perdue, M., Moyle, J. Assessing evolving challenges and educational needs in commercial and backyard poultry management, Poultry Science Association Meeting, NC, USA, 2025

Mitchell, R., Moyle, J. **Che. S**. Leveraging AI-driven sentiment analysis and natural language processing to inform extension efforts in the poultry industry, Poultry Science Association Meeting, NC, USA, 2025

Girma, B., Chen, J. ,Kim, J., Ayansola, H., Phan, R., Muthyala, S., **Jin, Y** . Reprogramming Intestinal Regeneration: E-cadherin as a Novel Target for Mucosal Healing in IBD.(2025), GI Epithelium: Plasticity and Pathways to Disease. FASEB.

Kim, J., Miko, C., Gruskin, Z., Chen, J., Ayansola, H., **Jin, Y**. "Exploring E-Cadherin as a Therapeutic Target for Enhancing Mucosal Healing through Intestinal Stem Cell Regeneration", American Physiology Summit 2025, Baltimore, MD.

Ayansola, H., Kim, J., **Jin Y.** "Transcriptomic profiling of intestinal mesenchymal stromal cells reveals age-dependent gene expression changes during postnatal development in pre-weaned piglets" American Physiology Summit 2025, Baltimore, MD.

Chen, J., Kim, J., Muthyala, S., Phan, R., Ayansola, H., **Jin, Y.** "Role of E-Cadherin in Intestinal Stem Cells during Epithelial Repair Following Colitis Damage" American Physiology Summit 2025, Baltimore, MD.

Ayansola, H., **Jin Y.** "The dual roles of immunomodulation and epithelial regeneration in MSCs primed by injured colonoids: a novel priming method for enhancing mucosal healing in IBD" American Physiology Sumit 2025, Baltimore, MD.

Liu Y., Fatima T., **Kim BE.** Insights into the mechanism of liver iron mobilization for peripheral tissue development. Combined Red Cell Club and the East-West Iron Club Meeting, SMC Campus Center, University of Maryland, Baltimore, October 27-29, 2025

Przygrodzka E, Haine S, Do L, Weisman M, Glasper C, Murphy E. Protein Kinase A (PKA) Mediated Chromatin Accessibility and Transcriptomic Alterations in Granulosa Cells. SSR 2025 Annual Meeting, July, 2025, Washington, D.C.

Haine S, Glasper C, Do L, Weismann M, Murphy E, **Przygrodzka E.** Protein kinase A (PKA) stimulated glucose metabolism is essential for granulosa cell function. ANSC Annual Symposium, May 2025, College Park, MD.

Contracts, Gifts, and Grants

Funded Projects - 2025

Name	Title of Project	Funding Source	Amount
Biswas, D. Broadbent, A.	Control major infectious disease of poultry grown in backyard/integrated farms and improve product safety (2024-2027)	USDA-NIFA	$650,000
Broadbent, A. Coughlan, L.	Development of vaccines against emerging avian influenza viruses for use in humans and poultry: A one-health approach to prevent zoonotic virus spillover events and support pandemic preparedness (2022-2024)	UMD-MPower	$250,000
Broadbent, A.	Evaluating the causes and consequences of infectious bursal disease virus (IBDV) antigenic drift and reassortment in the USA (2023-2026)	USDA NIFA AFRI	$627,000
Broadbent, A. Jin, Y. Schull, M.	Modeling the evolution of avian influenza viruses in the pre-pandemic period using chicken and duck intestinal organoids and air-liquid interface cultures (2023-2026)	UMD-GC	$548,066
Broadbent, A.	2024 American Society for Virology (ASV) Veterinary Virology Satellite Symposium (2024-2025)	USDA NIFA AFRI	$24,625
Broadbent, A.	Defining the sequence diversity and transcriptomic signatures of infectious bursal disease virus (IBDV) strains isolated from the Delmarva (DMV) region (2024-2025)	MAES	$30,000
Manicassamy, B. Broadbent, A.	Investigation of host glycan requirements for the transmission of influenza viruses at the human-animal interface (2024-2029)	NIH	$354,783
Burk, A.	Greener Pastures: Practical solutions for sustainable horse farm management (2024)	MD Horse Industry Board	$850
Cardoso, F.	Evaluating the efficacy of inoculant application in short-stature and conventional corn silage on fermentation quality, nutritional value, and dairy cow performance (2025-2026)	Lallemand Animal Nutrition	$49,095
Cardoso, F.	Enhancing Farm Sustainability: How Can Management Strategies Reduce the Negative Impacts of Clostridium and Mycotoxins Contamination on the TMR? (2024-2026)	Northeast SARE Partnership Program	$28,245
Cardoso, F.	Dietary strategies to protect waterbodies and enhance sustainability practices on Nitrogen use by dairy farmers (2023-2025)	NASDA	$95,420

Cardoso, F.	Exploring Agrifood & Natural Resource Systems in Brazil	International Programs in Agriculture and Natural Resources (IPAN)	$3,200
Cardoso, F.	Hologenomics, Epigenetics and Beef Quality	Jorgensen Foundation	$5,000
Cardoso, F.	A New Feed Strategy to Improve Forage Quality: Effect of Short Stature Whole Plant Corn Silage on Animal Performance and Farm Profitability (2024-2025)	MAES	$26,046
Che, S.	Industry Education Recruitment Funding (2025-2026)	US POULTRY Foundation	$7,000
Che, S.	Evaluation of a Nutri-P–Supplemented Broiler Diets (2025-2026)	AgFS	$2,000
Che, S.	Mitigating broiler breast myopathies: investigating dietary and processing interventions to improve meat quality and industry sustainability (2025-2026)	MAES	$30,000
Che, S.	Industry Education Recruitment Funding	US POULTRY Foundation	$5,650
Che, S.	Investigating the association between pH and chicken meat quality	Allen Harim Foods	$1,400
Hamza, I.	Heme trafficking and recycling in iron metabolism (2020-2025)	NIDDK	$1,933,733
Hamza, I.	Dissecting the molecular pathways for mammalian hemozoin formation in iron homeostasis	SFI-PD-	$72,000
Hamza, I.	Inter-organ signaling in heme metabolism and organismal Homeostasis (2022-2026)	NIDDK	$1,985,959
Yasuda, M. Hamza, I.	Mechanisms of Intercellular Heme Homeostasis in Liver (2023-2027)	NIDDK	$662,567
Reddi, A. Hamza, I.	Lifespan regulation by inter-organellar heme signaling (2023-2028)	NIA	$965,625
Collins, J. Hamza, I.	Mechanisms of Intestinal Heme-iron Absorption in Rat Models of Iron Deficiency and Iron Overload (2024-2029)	NIDDK	$1,738,125
Jin, Y.	Fine tuning of MSC priming for mucosal healing in IBD: Dual targeting intestinal stem cell regeneration and immunomodulation (2025-2027)	Maryland Stem Cell Research Fund	$350,000

Jin, Y.	Modeling the evolution of avian influenza viruses (2023-2026)	Grand Challenge Grant Team Project	$548,006
Kim, BE	The Role of Iron in Adipocyte Signaling and Homeostasis (2025-2026)	MAES	$30,000
Kim, BE	The Role of Copper and CTR1 in the Regulation of Adipose Function (2021-2025)	NIDDK/NIH	$996,480
Ma, L. Toghiani, S.	Large-scale genomic and functional genomic investigation to improve cattle fertility (2024-2028)	USDA- NIFA	$630,000
Jiang, J. Ma, L.	A unified mixed-model method for integrating functional annotations into genome-to-phenome analysis (2023-2025)	USDA-NIFA	$18,099
Liu, H.C. Porter, T.	Engaging Multicultural Scholars in Feed-the-Future Careers in the Animal Sciences (2020-2025)	USDA-NIFA Higher Education Multicultural Scholars Program	$200,000
Venkitanarayana, K. Porter, T.	Systems-based integrated program for enhancing the sustainability of antibiotic-restricted poultry production (2020-2025)	USDA Sustainable Agriculture Systems	$399,999
Brady, K. Porter, T.	Regulation of reproduction in turkey hens by thyroid hormones (2023-2026)	USDA-NIFA-Agriculture and Food Research Initiative	$650,000
Porter, T.	Regulation of Growth Hormone Production in Broiler Chicken Embryos (2023-2026)	USDA-NIFA-Agriculture and Food Research Initiative	$650,000
Porter, T. Song, J.	Single-Cell Chromatin Status and Fates of Cell Lineages in Chicken Embryonic Stem Cell Differentiation (2024-2028)	USDA-NIFA-Agriculture and Food Research Initiative	$650,000
Porter, T. Sunny, N.	Macronutrient regulation of the metabolic switch in newly hatched chicken (2025-2028)	USDA-NIFA-Agriculture and Food Research Initiative	$650,000
Davis, J. Przygrodzka, E.	Metabolic and Mitochondrial Signals During Ovulation (2023-2027)	USDA-NIFA	$1,750,000
Salem, M.	Whole-Genome Analyses/Selection to Increase Muscle Yield and Reduce Fillet Downgrading in Rainbow Trout (2021-2025)	USDA-AFRI	$500,000

Salem, M.	High-quality Reference Assembly and Annotation of the Rainbow Trout Genome (2020-2025)	USDA-AFRI	$500,000
Salem, M.	Functional Annotation of Wild and Hatchery-Produced Hybrid Rainbow Trout Genomes to Advance Salmonid Pan-Genomics and Community Genomic Resources (2025-2027)	USDA/ NRSP8	$20,000
Salem, M.	Integrated Genomics and Metagenomics Predictions and Modulation of The Gut Microbiota–Muscle Axis To Improve Fillet Yield In Rainbow Trout (2023-2026)	USDA-AFRI	$650,000
Salem, M.	Using HDAC inhibitors to improve swine growth (2024-2025)	USDA-AFRI	$500,000
Schiffmacher, A.	Fetal Mammary Stem Cell Programming and Hormone Dysfunction (2023-2026)	UMD Grand Challenges Grants Program	$75,000
Johnson, G.A. Seo, H. Bazer, F.W.	Metabolic adaptation of conceptuses to a hypoxic uterine environment (2022-2027)	USDA-NIFA-AFRI	$575,000
Seo, H. Johnson, G.A. Pohler, K.G Cai, J. Burghardt, R.C.	Early Placental Development in Cattle (2024-2028)	USDA-NIFA-AFRI	$650,000
Song, J. He, Y.	An integrated transcriptomic and epigenetic atlas of chicken embryonic stem cells (2023-2027)	USDA-NIFA	$650,000
Song, J. Porter, T. Chen, P.	Single-Cell Chromatin Status and Fates of Cell Lineages in Chicken Embryonic Stem Cell Differentiation (2024-2028)	USDA-NIFA	$650,000
Sunny, N.	Regulation of Mitochondrial Metabolism and Lipogenesis in Embryonic to Post-hatch Chicken		
Sunny, N.	Regulation of Mitochondrial Metabolism and Lipogenesis in Embryonic to Post-hatch Chicken (2012-2025)	USDA-NIFA-AFRI	$500,000
Sunny, N.	Impact of Branched Chain Amino Acid Degradation on Hepatic Lipid Metabolism (2024-2026)	MAES	$29,832
Sunny, N.	Macronutrient regulation of the metabolic switch in newly hatched chicken	AFRI/NIFA	$650,000
Taneyhill, L.	Coordinated regulation of EMTs by cadherin proteolytic products (2020-2025)	NSF	$1,200,000
Taneyhill, L.	Elucidating craniofacial deficits in Familial Dysautonomia (2024-2025)	UMD New Directions Award	$50,000
Taneyhill, L.	Trigeminal nerve-target tissue interactions during craniofacial development (2024-2026)	NIH	$275,000

Taneyhill, L.	The role of N-cadherin in trigeminal axon outgrowth	American Association for Anatomy	$25,000
Xiao, Z.	CD4+ IELs in the gut of Grass-fed cattle (2025)	Jorgensen Foundation	$5,000
Xiao, Z.	CD4+ iIELs in the Gut of Cattle	MAES	$30,000
Upadhyaya, A. Xiao, Z.	Investigating the Role of Active Chromatin Dynamics in T Cell Activation and Differentiation (2024-2028)	NSF	$200,000

Acknowledgments

Members of the Annual Symposium Committee:

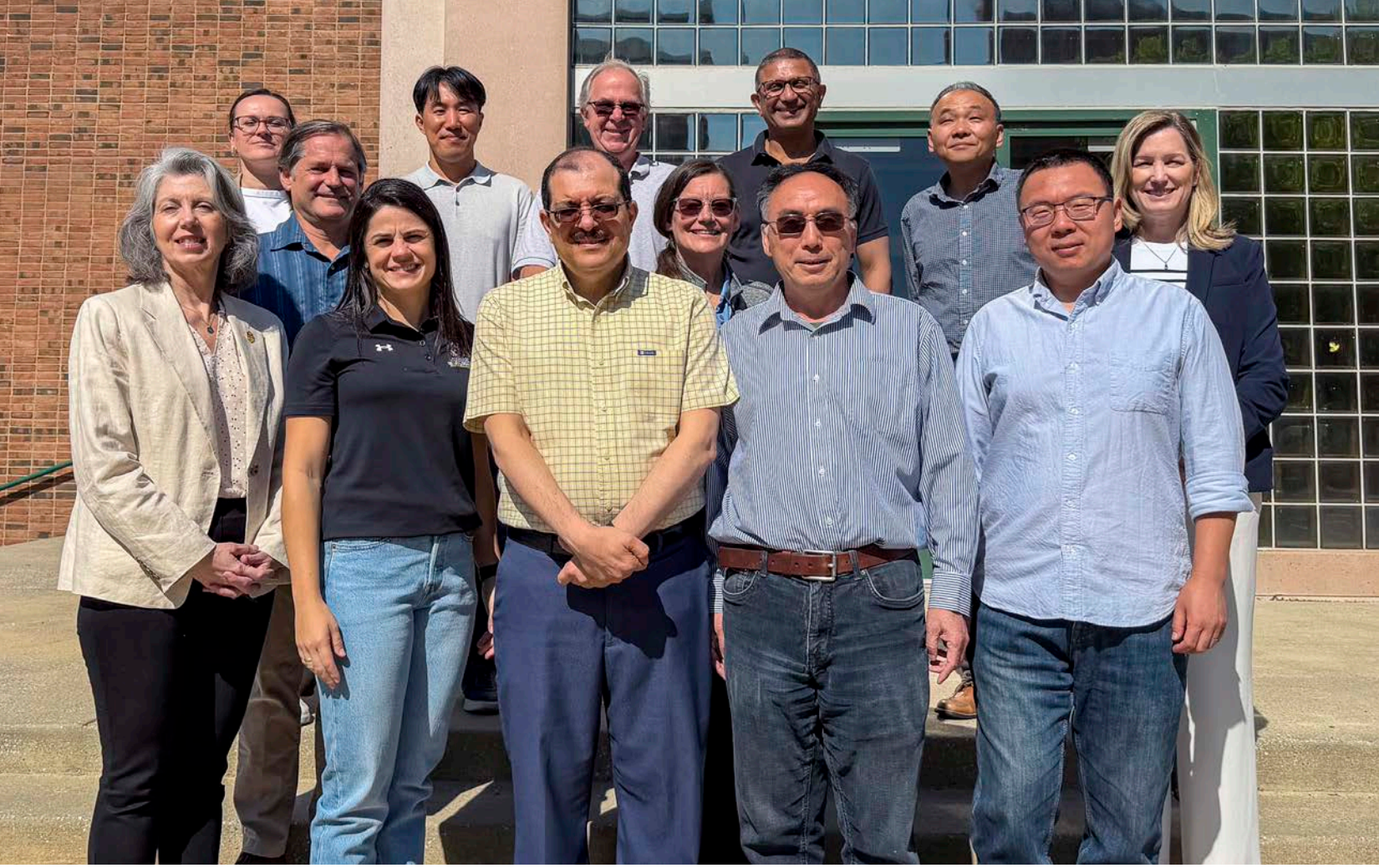
Sunoh Che, Chair
Heewon Seo, Co-chair
Bishal Bhattachan
Adriana Kempen
Michael Mobley
Ashley Montalvan
Jonathan Stephanoff

The Annual Symposium Committee gratefully thanks the Social Events Committee for organizing the food and refreshments for today's Symposium:

Peter Chamberlain
Paul Vaughan
Ashley Montalvan
Andy Schiffmacher
Heewon Seo
Pablo Villafranco
Zhengguo Xiao

Special thanks are extended to the individuals who served as judges of our poster and oral presentations:

Mostafa Ghanem, UMD Vet Med
Kristen Diehl, USDA
Ryan Blaustein, UMD NFSC
Yuanyuan (Rose) Rose Li, UMD NFSC
Joe Cain, UMD ANSC
Zubair Khalid, UMD ANSC



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