**APPENDIX D**

**SAES-422**

**Format for Multistate Research Activity**

**Accomplishments Report**

**Project/Activity Number: NRSP8**

**Project/Activity Title: Building Applied Genomic Capacity for Animal Industries**

**Period Covered: 10/2023-9/2024 (“Year 1”)**

**Date of This Report: 9/25/2024**

**Annual Meeting Date(s): 1/14/2024**

**Participants:** The annual meeting in January 2024 marked a significant transition from the “old” NRSP8 to the “new” NRSP8. Despite the retention of the number designator, there are significant differences in aims and organization between the multistate programs. The NRSP8 leadership team met as a group to discuss the transition plan from the organization by species groups to organization by aims (see below for details). The leadership meting was attended by 19 individuals (below).

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Later that afternoon, the general business meeting was held, and was attended by approximately 80 individuals representing many academic institutions, industry, and the USDA.

**Brief summary of minutes of annual meeting:** The meeting opened with a legacy perspective on the “old” NRSP8 provided by Noelle Cockett, including the accomplishments of the community over the past two decades. Plans for future funding to continue the scientific efforts of the community, including a pending application for a RCN project, were discussed along with some challenges to be faced in the transition. Comments were given by Steve Lommel on behalf of the NRSP review committee emphasizing the need to push forward to deliverables rather than technology. Brief final reports were provided by the species coordinators from the “old” NRSP8. Angelica Van Goor provided a USDA update including upcoming calls for funding and opportunities for conference grants. The new Aim Coordinators were introduced to the group and provided their visions for activities for the coming year. The group moved, seconded, and unanimously approved a return to PAG in January 2025 for the next annual meeting. The meeting was then adjourned.

**Accomplishments:** With the sunsetting of the “old” NRSP8, the National Animal Genome Research Program, in 2023, the agricultural genetics community recognized the need to maintain an umbrella multistate program that would support our collective efforts at developing shared resources and educational tools. A writing committee, spearheaded by Fiona McCarthy (University of Arizona) and Stephanie McKay (University of Missouri) crafted a new proposal focused on capacity development that was widely supported by the genomics community and industry stakeholders. This proposal was approved in late 2023 and the designation NRSP8 was kept in an effort to reflect the continuity of community efforts and engagement. The “new” NRSP8, Building Applied Genomic Capacity for Animal Industries. has three aims:

AIM 1: Extending genomics capacity to a broader range of Animal Science stakeholders.

AIM 2: Supporting capacity to integrate genomic and biological data.

AIM 3: Education, training, and outreach to develop a data-savvy workforce.

**Milestones and Activities:** The focus of the first few months of the new NRSP8 has been organization under the new framework and setting the community up for successful achievement of proposed milestones. These include:

*1. Creation of an External Advisory Board.* A key component of NRSP8’s proposed activities is the engagement of stakeholders representing diverse facets of animal agriculture. Stakeholders will be engaged in multiple aspects of this project, including key decision-making processes. An External Advisory Board (EAB) of industry stakeholders will help ensure that project activities are focused on industry needs. The EAB will meet with NRSP8 leadership at least annually. Nine individuals representing extension, commodity industry groups, and the technology sector have been recruited to the EAB. A virtual meeting in planned for Fall 2024 with an in-person meeting in January 2025 at the annual meeting.

*2. Development of stakeholder surveys.* There are many potential stakeholders that have an interest in the activities of the NRSP8 community. Two stakeholder surveys are currently in development, one focused on educators and one focused on extension specialists. The results of these surveys will be presented at the next annual meeting.

*3. Support for students and early career investigators to engage with genomics research.* Travel support to meetings is a key component for engaging students and early career investigators. A call has been made for applications for travel awards to the 2025 annual meeting. Ten awards will be given.

*4. Development of workshops and other training opportunities.* Initial outreach activities have been undertaken by the NRSP8 leadership team with presentations and booths at various conferences not typically focused on genetics (e.g., ASAS). In addition to this, and to species-focused activities that will occur at PAG in 2025 in parallel to the NRSP8 annual meeting, a workshop is planned for Summer 2025. The target audience is scientists, educators, and extension agents who are interested in harnessing genetics/genomics tools to further their research, teaching, and extension goals. Specific topics will be guided by the results of the stakeholder surveys. Online instructional materials will also be constructed.

**Outputs:** A key deliverable for NRSP8 is accessibility of the tools and resources developed by the community. The animalgenome.org website and AnGenMap listserv have been important tools historically leveraged by the NRSP8 community. The website is in the initial stages of a major overhaul to make it an attractive and user-friendly portal for both geneticists and the general public. The AnGenMap listserv is still being used to aid in communication of initiatives, and a NRSP8 bulletin board has been established to provide a central location for both academic and industry members to post workshop announcements, training opportunities, internships, etc.

**Impacts:** Currently, a major focus is retention of previous members and recruitment of new members to the multistate group, with particular interest in involving extension officers and industry stakeholders. The stakeholder surveys will be used to guide future actions by the NRSP8 community to maximize impacts on the broader agricultural industry.

**Indicators:** The “new” NRSP8 application was accompanied by letters of support from more than 20 industry stakeholder groups, indicating broad buy-in for the efforts of the community to extend genomics capacity to a broader range of Animal Science stakeholders. Industry leaders approached about EAB membership were also enthusiastic about participation. Continued indicators of success will include membership in NRSP8, completion of stakeholder surveys, and attendance at NRSP8-sponsored meetings and workshops.

**Publications**

Durward-Akhurst SA, Marlowe JL, Schaefer RJ, Springer K, Grantham B, Carey WK, Bellone RR, Mickelson JR, **McCue ME**. Predicted genetic burden and frequency of phenotype-associated variants in the horse. Sci Rep. 2024 Apr 10;14(1):8396. doi: 10.1038/s41598-024-57872-8.

Clark BL, Norton EM, Bamford NJ, Randhawa IAS, Kemp KL, **McCue ME**, Bertin FR, Stewart AJ.

Epidemiological investigation of insulin dysregulation in Shetland and Welsh ponies in Australia. Equine Vet J. 2024 Mar;56(2):281-290. doi: 10.1111/evj.14044. Epub 2024 Jan 3.

**Da Y**, Prakapenka D, Liang Z. Large-Sample Genomic Data Mining for Quantitative Traits in U.S. Holstein Cows. J Data Mining Genomics Proteomics. 2024;15(2):340. Epub 2024 May 13.

Prakapenka D, Liang Z, Zaabza HB, VanRaden PM, Van Tassell CP, **Da Y**. Large-Sample Genome-Wide Association Study of Resistance to Retained Placenta in U.S. Holstein Cows. Int J Mol Sci. 2024 May 20;25(10):5551. doi: 10.3390/ijms25105551.

Prakapenka D, Liang Z, Zaabza HB, VanRaden PM, Van Tassell CP, **Da Y**. A Million-Cow Validation of a Chromosome 14 Region Interacting with All Chromosomes for Fat Percentage in U.S. Holstein Cows. Int J Mol Sci. 2024 Jan 4;25(1):674. doi: 10.3390/ijms25010674.

Liang Z, Prakapenka D, **Da Y**. Comparison of the Accuracy of Epistasis and Haplotype Models for Genomic Prediction of Seven Human Phenotypes. Biomolecules. 2023 Oct 3;13(10):1478. doi: 10.3390/biom13101478.

House LC, Hasan A, Asnayanti A, Alrubaye AAK, Pummill J, **Rhoads D**. Phylogenomic Analyses of Three Distinct Lineages Uniting Staphylococcus cohnii and Staphylococcus urealyticus from Diverse Hosts. Microorganisms. 2024 Jul 29;12(8):1549. doi: 10.3390/microorganisms12081549.

Yamashita T, **Rhoads DD**, Pummill J. A robust genome assembly with transcriptomic data from the striped bark scorpion, Centruroides vittatus. G3 (Bethesda). 2024 Aug 7;14(8):jkae120. doi: 10.1093/g3journal/jkae120.

**Rhoads DD**, Pummill J, Alrubaye AAK. Molecular Genomic Analyses of Enterococcus cecorum from Sepsis Outbreaks in Broilers. Microorganisms. 2024 Jan 25;12(2):250. doi: 10.3390/microorganisms12020250.

Botchway PK, Amuzu-Aweh EN, Naazie A, Aning GK, Otsyina HR, Saelao P, Wang Y, Zhou H, **Dekkers JCM**, **Lamont SJ**, Gallardo RA, Kelly TR, Bunn D, Kayang BB. Genotypic and phenotypic characterisation of three local chicken ecotypes of Ghana based on principal component analysis and body measurements. PLoS One. 2024 Aug 7;19(8):e0308420. doi: 10.1371/journal.pone.0308420. eCollection 2024.

Yu H, Fernando RL, **Dekkers JCM**. Use of the linear regression method to evaluate population accuracy of predictions from non-linear models. Front Genet. 2024 May 31;15:1380643. doi: 10.3389/fgene.2024.1380643. eCollection 2024.

Kanlisi RA, Amuzu-Aweh EN, Naazie A, Otsyina HR, Kelly TR, Gallardo RA, **Lamont SJ**, Zhou H, **Dekkers J**, Kayang BB. Genetic architecture of body weight, carcass, and internal organs traits of Ghanaian local chickens. Front Genet. 2024 Mar 13;15:1297034. doi: 10.3389/fgene.2024.1297034. eCollection 2024.

Wang Y, Saelao P, Chanthavixay G, Gallardo RA, Wolc A, Fulton JE, **Dekkers JM**, **Lamont SJ**, Kelly TR, Zhou H. Genomic Regions and Candidate Genes Affecting Response to Heat Stress with Newcastle Virus Infection in Commercial Layer Chicks Using Chicken 600K Single Nucleotide Polymorphism Array. Int J Mol Sci. 2024 Feb 24;25(5):2640. doi: 10.3390/ijms25052640.

Teng J, Gao Y, Yin H, Bai Z, Liu S, Zeng H; PigGTEx Consortium; Bai L, Cai Z, Zhao B, Li X, Xu Z, Lin Q, Pan Z, Yang W, Yu X, Guan D, Hou Y, Keel BN, Rohrer GA, Lindholm-Perry AK, Oliver WT, Ballester M, Crespo-Piazuelo D, Quintanilla R, Canela-Xandri O, Rawlik K, Xia C, Yao Y, Zhao Q, Yao W, Yang L, Li H, Zhang H, Liao W, Chen T, Karlskov-Mortensen P, Fredholm M, Amills M, Clop A, Giuffra E, Wu J, Cai X, Diao S, Pan X, Wei C, Li J, Cheng H, Wang S, Su G, Sahana G, Lund MS, **Dekkers JCM**, Kramer L, **Tuggle CK**, Corbett R, Groenen MAM, Madsen O, Gòdia M, Rocha D, Charles M, Li CJ, Pausch H, Hu X, Frantz L, Luo Y, Lin L, Zhou Z, Zhang Z, Chen Z, Cui L, Xiang R, Shen X, Li P, Huang R, Tang G, Li M, Zhao Y, Yi G, Tang Z, **Jiang J**, Zhao F, Yuan X, Liu X, Chen Y, Xu X, Zhao S, Zhao P, Haley C, Zhou H, Wang Q, Pan Y, Ding X, **Ma L**, Li J, Navarro P, Zhang Q, Li B, Tenesa A, Li K, Liu GE, Zhang Z, Fang L. A compendium of genetic regulatory effects across pig tissues. Nat Genet. 2024 Jan;56(1):112-123. doi: 10.1038/s41588-023-01585-7. Epub 2024 Jan 4.

**Tuggle CK**, Clarke JL, **Murdoch BM**, Lyons E, Scott NM, Beneš B, Campbell JD, Chung H, Daigle CL, Das Choudhury S, **Dekkers JCM**, Dórea JRR, Ertl DS, Feldman M, Fragomeni BO, Fulton JE, Guadagno CR, **Hagen DE**, **Hess AS**, Kramer LM, Lawrence-Dill CJ, Lipka AE, Lübberstedt T, **McCarthy FM**, **McKay SD**, Murray SC, **Riggs PK**, **Rowan TN**, Sheehan MJ, **Steibel JP**, Thompson AM, Thornton KJ, Van Tassell CP, Schnable PS. Current challenges and future of agricultural genomes to phenomes in the USA. Genome Biol. 2024 Jan 3;25(1):8. doi: 10.1186/s13059-023-03155-w.

Lim KS, Cheng J, **Tuggle C**, Dyck M, Canada P, Fortin F, Harding J, Plastow G, **Dekkers J**. Genetic analysis of the blood transcriptome of young healthy pigs to improve disease resilience. Genet Sel Evol. 2023 Dec 12;55(1):90. doi: 10.1186/s12711-023-00860-9.

Zhao T, Wang F, Mott R, **Dekkers J**, Cheng H. Using encrypted genotypes and phenotypes for collaborative genomic analyses to maintain data confidentiality. Genetics. 2024 Mar 6;226(3):iyad210. doi: 10.1093/genetics/iyad210.

Munguía Vásquez MF, Gill CA, **Riggs PK**, Herring AD, Sanders JO, Riley DG. Genetic evaluation of crossbred Bos indicus cow temperament at parturition. J Anim Sci. 2024 Jan 3;102:skae022. doi: 10.1093/jas/skae022.

**Kalbfleisch TS**, **McKay SD**, **Murdoch BM**, Adelson DL, Almansa-Villa D, Becker G, Beckett LM, Benítez-Galeano MJ, Biase F, Casey T, Chuong E, Clark E, Clarke S, **Cockett N**, Couldrey C, Davis BW, Elsik CG, Faraut T, Gao Y, Genet C, Grady P, Green J, Green R, Guan D, **Hagen D**, Hartley GA, Heaton M, Hoyt SJ, **Huang W**, Jarvis E, Kalleberg J, Khatib H, Koepfi KP, **Koltes J**, Koren S, Kuehn C, Leeb T, Leonard A, Liu GE, Low WY, McConnell H, McRae K, Miga K, Mousel M, **Neibergs H**, Olagunju T, Pennell M, Petry B, Pewsner M, Phillippy AM, Pickett BD, Pineda P, Potapova T, Rachagani S, Rhie A, Rijnkels M, Robic A, Rodriguez Osorio N, Safonova Y, Schettini G, **Schnabel RD**, Sirpu Natesh N, Stegemiller M, Storer J, Stothard P, Stull C, Tosser-Klopp G, Traglia GM, **Tuggle CK**, Van Tassell CP, Watson C, Weikard R, Wimmers K, Xie S, Yang L, Smith TPL, O'Neill RJ, Rosen BD. The Ruminant Telomere-to-Telomere (RT2T) Consortium. Nat Genet. 2024 Aug;56(8):1566-1573. doi: 10.1038/s41588-024-01835-2. Epub 2024 Aug 5.

Goldkamp AK, **Hagen DE**. Implications of tRNA abundance on translation elongation across bovine tissues. Front Genet. 2023 Dec 19;14:1308048. doi: 10.3389/fgene.2023.1308048. eCollection 2023.

Goldkamp AK, Lahuis CH, **Hagen DE**, **Taxis TM**. Influence of Maternal BLV Infection on miRNA and tRF Expression in Calves. Pathogens. 2023 Nov 3;12(11):1312. doi: 10.3390/pathogens12111312.

Zhong C, Li X, Guan D; ChickenGTEx Consortium; Zhang B, Wang X, Qu L, **Zhou H**, Fang L, Sun C, Yang N. Age-dependent genetic architectures of chicken body weight explored by multidimensional GWAS and molQTL analyses. J Genet Genomics. 2024 Sep 19:S1673-8527(24)00240-6. doi: 10.1016/j.jgg.2024.09.003. Online ahead of print.

Yang L, Yin H, Bai L, Yao W, Tao T, Zhao Q, Gao Y, Teng J, Xu Z, Lin Q, Diao S, Pan Z, Guan D, Li B, **Zhou H**, Zhou Z, Zhao F, Wang Q, Pan Y, Zhang Z, Li K, Fang L, Liu GE. Mapping and functional characterization of structural variation in 1060 pig genomes. Genome Biol. 2024 May 7;25(1):116. doi: 10.1186/s13059-024-03253-3.

Degalez F, Charles M, Foissac S, **Zhou H**, Guan D, Fang L, Klopp C, Allain C, Lagoutte L, Lecerf F, Acloque H, Giuffra E, Pitel F, Lagarrigue S. Enriched atlas of lncRNA and protein-coding genes for the GRCg7b chicken assembly and its functional annotation across 47 tissues. Sci Rep. 2024 Mar 19;14(1):6588. doi: 10.1038/s41598-024-56705-y.

Lozada-Soto EA, **Maltecca C**, **Jiang J**, Cole JB, VanRaden PM, Tiezzi F. Effect of germplasm exchange strategies on genetic gain, homozygosity, and genetic diversity in dairy stud populations: A simulation study. J Dairy Sci. 2024 Aug 29:S0022-0302(24)01085-3. doi: 10.3168/jds.2024-24992. Online ahead of print.

**Jiang J**. MPH: fast REML for large-scale genome partitioning of quantitative genetic variation. Bioinformatics. 2024 May 2;40(5):btae298. doi: 10.1093/bioinformatics/btae298.

Zhuo Y, Du H, Diao C, Li W, Zhou L, Jiang L, **Jiang J**, Liu J. MAGE: metafounders-assisted genomic estimation of breeding value, a novel additive-dominance single-step model in crossbreeding systems. Bioinformatics. 2024 Feb 1;40(2):btae044. doi: 10.1093/bioinformatics/btae044.

Lozada-Soto EA, Parker Gaddis KL, Tiezzi F, **Jiang J**, **Ma L**, Toghiani S, VanRaden PM, Maltecca C. Inbreeding depression for producer-recorded udder, metabolic, and reproductive diseases in US dairy cattle. J Dairy Sci. 2024 May;107(5):3032-3046. doi: 10.3168/jds.2023-23909. Epub 2023 Dec 4.

Gao Y, Marceau A, Iqbal V, Torres-Vázquez JA, Neupane M, **Jiang J**, Liu GE, **Ma L**. Genome-wide association analysis of heifer livability and early first calving in Holstein cattle. BMC Genomics. 2023 Oct 21;24(1):628. doi: 10.1186/s12864-023-09736-0.

Han Y, Tu W, Zhang Y, Huang J, Meng X, Wu Q, Li S, Liu B, Michal JJ, **Jiang Z**, Tan Y, Zhou X, Wang H. Comprehensive analysis of single-nucleotide variants and alternative polyadenylation between inbred and outbred pigs. Int J Biol Macromol. 2024 Oct;278(Pt 2):134416. doi: 10.1016/j.ijbiomac.2024.134416. Epub 2024 Aug 3.

Beiki H, **Murdoch BM**, Park CA, Kern C, Kontechy D, Becker G, Rincon G, Jiang H, Zhou H, Thorne J, **Koltes JE**, Michal JJ, Davenport K, Rijnkels M, Ross PJ, Hu R, Corum S, **McKay S**, Smith TPL, **Liu W**, Ma W, Zhang X, Xu X, Han X, **Jiang Z**, Hu ZL, **Reecy JM**. Enhanced bovine genome annotation through integration of transcriptomics and epi-transcriptomics datasets facilitates genomic biology. Gigascience. 2024 Jan 2;13:giae019. doi: 10.1093/gigascience/giae019.

de Jong TV, Pan Y, Rastas P, Munro D, Tutaj M, Akil H, Benner C, Chen D, Chitre AS, Chow W, Colonna V, Dalgard CL, Demos WM, Doris PA, Garrison E, Geurts AM, Gunturkun HM, Guryev V, Hourlier T, Howe K, Huang J, **Kalbfleisch T**, Kim P, Li L, Mahaffey S, Martin FJ, Mohammadi P, Ozel AB, Polesskaya O, Pravenec M, Prins P, Sebat J, Smith JR, Solberg Woods LC, Tabakoff B, Tracey A, Uliano-Silva M, Villani F, Wang H, Sharp BM, Telese F, **Jiang Z**, Saba L, Wang X, Murphy TD, Palmer AA, Kwitek AE, Dwinell MR, Williams RW, Li JZ, Chen H. A revamped rat reference genome improves the discovery of genetic diversity in laboratory rats. Cell Genom. 2024 Apr 10;4(4):100527. doi: 10.1016/j.xgen.2024.100527. Epub 2024 Mar 26.

Carrion SA, Michal JJ, **Jiang Z**. Alternative Transcripts Diversify Genome Function for Phenome Relevance to Health and Diseases. Genes (Basel). 2023 Nov 8;14(11):2051. doi: 10.3390/genes14112051.

Xiang G, He X, Giardine BM, Isaac KJ, Taylor DJ, McCoy RC, Jansen C, Keller CA, Wixom AQ, Cockburn A, Miller A, Qi Q, **He Y**, Li Y, Lichtenberg J, Heuston EF, Anderson SM, Luan J, Vermunt MW, Yue F, Sauria MEG, Schatz MC, Taylor J, Göttgens B, Hughes JR, Higgs DR, Weiss MJ, Cheng Y, Blobel GA, Bodine DM, Zhang Y, Li Q, Mahony S, Hardison RC. Interspecies regulatory landscapes and elements revealed by novel joint systematic integration of human and mouse blood cell epigenomes. Genome Res. 2024 Aug 20;34(7):1089-1105. doi: 10.1101/gr.277950.123.

**He Y**, Taylor RL Jr, Bai H, **Ashwell CM**, Zhao K, Li Y, Sun G, Zhang H, **Song J**. Transgenerational epigenetic inheritance and immunity in chickens that vary in Marek's disease resistance. Poult Sci. 2023 Dec;102(12):103036. doi: 10.1016/j.psj.2023.103036. Epub 2023 Aug 26.

Xu C, Hutchins ED, Eckalbar W, Pendarvis K, Benson DM, Lake DF, **McCarthy FM**, Kusumi K. Comparative proteomic analysis of tail regeneration in the green anole lizard, Anolis carolinensis. Nat Sci (Weinh). 2024 Jan;4(1):e20210421. doi: 10.1002/ntls.20210421. Epub 2023 Aug 17.

Sparling BA, Ng TT, Carlo-Allende A, **McCarthy FM**, Taylor RL Jr, **Drechsler Y**. Immunoglobulin-like receptors in chickens: identification, functional characterization, and renaming to cluster homolog of immunoglobulin-like receptors. Poult Sci. 2024 Feb;103(2):103292. doi: 10.1016/j.psj.2023.103292. Epub 2023 Nov 17.

Wang J, Hua G, Chen J, Cui K, Yang Z, Han D, Yang X, Dong X, Ma Y, Cai G, Zhang Y, Li J, Tai Y, Da L, Li X, **Ma L**, Ma Q, Li R, Liu J, Darwish HYA, Wu K, Rong W, **Liu W**, Zhao Y, Deng X. Epigenetic mechanism of Gtl2-miRNAs causes the primitive sheep characteristics found in purebred Merino sheep. Cell Biosci. 2023 Oct 13;13(1):190. doi: 10.1186/s13578-023-01142-z.

Al-Mamun HA, Danilevicz MF, Marsh JI, **Gondro C**, Edwards D. Exploring genomic feature selection: A comparative analysis of GWAS and machine learning algorithms in a large-scale soybean dataset. Plant Genome. 2024 Sep 10:e20503. doi: 10.1002/tpg2.20503. Online ahead of print.

Nawaz MY, Savegnago RP, Lim D, Lee SH, Gondro C. Signatures of selection in Angus and Hanwoo beef cattle using imputed whole genome sequence data. Front Genet. 2024 Aug 2;15:1368710. doi: 10.3389/fgene.2024.1368710. eCollection 2024.

Niciura SCM, Cardoso TF, Ibelli AMG, Okino CH, Andrade BG, Benavides MV, Chagas ACS, Esteves SN, Minho AP, Regitano LCA, **Gondro C.** Multi-omics data elucidate parasite-host-microbiota interactions and resistance to Haemonchus contortus in sheep. Parasit Vectors. 2024 Mar 1;17(1):102. doi: 10.1186/s13071-024-06205-9.

Cuyabano BCD, Boichard D, **Gondro C**. Expected values for the accuracy of predicted breeding values accounting for genetic differences between reference and target populations. Genet Sel Evol. 2024 Feb 29;56(1):15. doi: 10.1186/s12711-024-00876-9.

**Tammen I**, Mather M, Leeb T, Nicholas FW. Online Mendelian Inheritance in Animals (OMIA): a genetic resource for vertebrate animals. Mamm Genome. 2024 Aug 14. doi: 10.1007/s00335-024-10059-y. Online ahead of print.

**Tammen I**, **Bailey E**, Mather M, Nicholas FW. Equus in Online Mendelian Inheritance in Animals (OMIA). Animals (Basel). 2024 Jul 15;14(14):2069. doi: 10.3390/ani14142069.

Mullen KR, **Tammen I**, Matentzoglu NA, Mather M, Mungall CJ, Haendel MA, Nicholas FW, Toro S; Vertebrate Breed Ontology Consortium. The Vertebrate Breed Ontology: Towards Effective Breed Data Standardization. ArXiv [Preprint]. 2024 Jun 3:arXiv:2406.02623v1.

Johns LT, Smythe MP, Dewberry LS, Staiger EA, Allen K, **Brooks SA**. Digital video analysis reveals gait parameters that predict performance in the jumping test phase of three-day eventing. J Equine Vet Sci. 2024 Oct;141:105166. doi: 10.1016/j.jevs.2024.105166. Epub 2024 Aug 17.

McFadden A, Vierra M, Robilliard H, Martin K, **Brooks SA**, Everts RE, Lafayette C. Population Analysis Identifies 15 Multi-Variant Dominant White Haplotypes in Horses. Animals (Basel). 2024 Feb 5;14(3):517. doi: 10.3390/ani14030517.

McFadden A, Vierra M, Martin K, **Brooks SA**, Everts RE, Lafayette C. Spotting the Pattern: A Review on White Coat Color in the Domestic Horse. Animals (Basel). 2024 Jan 30;14(3):451. doi: 10.3390/ani14030451.

Wang J, Hu Y, Xiang L, Morota G, **Brooks SA**, Wickens CL, Miller-Cushon EK, Yu H. Technical note: ShinyAnimalCV: open-source cloud-based web application for object detection, segmentation, and three-dimensional visualization of animals using computer vision. J Anim Sci. 2024 Jan 3;102:skad416. doi: 10.1093/jas/skad416.

Alhaddad H, Powell BB, Pinto LD, Sutter N, **Brooks SA**, Alhajeri BH. Geometric morphometrics of face profile across horse breeds and within Arabian horses. J Equine Vet Sci. 2024 Jan;132:104980. doi: 10.1016/j.jevs.2023.104980. Epub 2023 Dec 8.

Gossett CL, Guyer D, Hein J, **Brooks SA**. Digital Phenotyping Reveals Phenotype Diversity and Epistasis among White Spotting Alleles in the American Paint Horse. Genes (Basel). 2023 Oct 27;14(11):2011. doi: 10.3390/genes14112011.

Walker LR, Vu HL, Montooth KL, Ciobanu DC. Functional and evolutionary analysis of host Synaptogyrin-2 in porcine circovirus type 2 susceptibility. PLoS Genet. 2023 Nov 27;19(11):e1011029. doi: 10.1371/journal.pgen.1011029. eCollection 2023 Nov.

Han JH, Lee HJ, **Kim TH**. Characterization of transcriptional enhancers in the chicken genome using CRISPR-mediated activation. Front Genome Ed. 2023 Oct 25;5:1269115. doi: 10.3389/fgeed.2023.1269115. eCollection 2023.

Fanalli SL, Gomes JD, de Novais FJ, Gervásio IC, Fukumasu H, Moreira GCM, Coutinho LL, **Koltes J**, Amaral AJ, Cesar ASM. Key co-expressed genes correlated with blood serum parameters of pigs fed with different fatty acid profile diets. Front Genet. 2024 Jul 3;15:1394971. doi: 10.3389/fgene.2024.1394971. eCollection 2024.

Yilmaz Adkinson A, Abouhawwash M, VandeHaar MJ, Parker Gaddis KL, Burchard J, Peñagaricano F, White HM, Weigel KA, Baldwin R, Santos JEP, **Koltes JE**, Tempelman RJ. Assessing different cross-validation schemes for predicting novel traits using sensor data: An application to dry matter intake and residual feed intake using milk spectral data. J Dairy Sci. 2024 Oct;107(10):8084-8099. doi: 10.3168/jds.2024-24701. Epub 2024 Jun 13.

Toghiani S, VanRaden PM, VandeHaar MJ, Baldwin RL, Weigel KA, White HM, Peñagaricano F, **Koltes JE**, Santos JEP, Parker Gaddis KL, Tempelman RJ. Dry matter intake in US Holstein cows: Exploring the genomic and phenotypic impact of milk components and body weight composite. J Dairy Sci. 2024 Sep;107(9):7009-7021. doi: 10.3168/jds.2023-24296. Epub 2024 May 15.

The genetic architecture of complete blood counts in lactating Holstein dairy cows.

Siberski-Cooper CJ, Mayes MS, Gorden PJ, Kramer L, Bhatia V, Koltes JE.

Front Genet. 2024 Mar 27;15:1360295. doi: 10.3389/fgene.2024.1360295. eCollection 2024.

Durbin HJ, Yampara-Iquise H, **Rowan TN**, **Schnabel RD**, **Koltes JE**, Powell JG, Decker JE. Genomic loci involved in sensing environmental cues and metabolism affect seasonal coat shedding in Bos taurus and Bos indicus cattle. G3 (Bethesda). 2024 Feb 7;14(2):jkad279. doi: 10.1093/g3journal/jkad279.

Cavani L, Parker Gaddis KL, Baldwin RL, Santos JEP, **Koltes JE**, Tempelman RJ, VandeHaar MJ, White HM, Peñagaricano F, Weigel KA. Consistency of dry matter intake in Holstein cows: Heritability estimates and associations with feed efficiency. J Dairy Sci. 2024 Feb;107(2):1054-1067. doi: 10.3168/jds.2023-23774. Epub 2023 Sep 26.

Houlahan K, Schenkel FS, Miglior F, Jamrozik J, Stephansen RB, González-Recio O, Charfeddine N, Segelke D, Butty AM, Stratz P, VandeHaar MJ, Tempelman RJ, Weigel K, White H, Peñagaricano F, **Koltes JE**, Santos JEP, Baldwin RL 6th, Baes CF. Estimation of genetic parameters for feed efficiency traits using random regression models in dairy cattle. J Dairy Sci. 2024 Mar;107(3):1523-1534. doi: 10.3168/jds.2022-23124. Epub 2023 Sep 9.

van Staaveren N, Rojas de Oliveira H, Houlahan K, Chud TCS, Oliveira GA Jr, Hailemariam D, Kistemaker G, Miglior F, Plastow G, Schenkel FS, Cerri R, Sirard MA, Stothard P, Pryce J, Butty A, Stratz P, Abdalla EAE, Segelke D, Stamer E, Thaller G, Lassen J, Manzanilla-Pech CIV, Stephansen RB, Charfeddine N, García-Rodríguez A, González-Recio O, López-Paredes J, Baldwin R, Burchard J, Parker Gaddis KL, **Koltes JE**, Peñagaricano F, Santos JEP, Tempelman RJ, VandeHaar M, Weigel K, White H, Baes CF. The Resilient Dairy Genome Project-A general overview of methods and objectives related to feed efficiency and methane emissions. J Dairy Sci. 2024 Mar;107(3):1510-1522. doi: 10.3168/jds.2022-22951. Epub 2023 Sep 9.

Stephansen RB, Martin P, Manzanilla-Pech CIV, Gredler-Grandl B, Sahana G, Madsen P, Weigel K, Tempelman RJ, Peñagaricano F, Parker Gaddis KL, White HM, Santos JEP, **Koltes JE**, Schenkel F, Hailemariam D, Plastow G, Abdalla E, VandeHaar M, Veerkamp RF, Baes C, Lassen J. Novel genetic parameters for genetic residual feed intake in dairy cattle using time series data from multiple parities and countries in North America and Europe. J Dairy Sci. 2023 Dec;106(12):9078-9094. doi: 10.3168/jds.2023-23330. Epub 2023 Sep 9.

Ambalavanan A, Chang L, Choi J, Zhang Y, Stickley SA, Fang ZY, Miliku K, Robertson B, Yonemitsu C, Turvey SE, Mandhane PJ, Simons E, Moraes TJ, Anand SS, Paré G, Williams JE, **Murdoch BM**, Otoo GE, Mbugua S, Kamau-Mbuthia EW, Kamundia EW, Gindola DK, Rodriguez JM, Pareja RG, Sellen DW, Moore SE, Prentice AM, Foster JA, Kvist LJ, **Neibergs HL**, McGuire MA, McGuire MK, Meehan CL, Sears MR, Subbarao P, Azad MB, Bode L, Duan Q. Human milk oligosaccharides are associated with maternal genetics and respiratory health of human milk-fed children. Nat Commun. 2024 Sep 4;15(1):7735. doi: 10.1038/s41467-024-51743-6.

Becker GM, Thorne JW, Burke JM, Lewis RM, Notter DR, Morgan JLM, Schauer CS, Stewart WC, Redden RR, **Murdoch BM**. Genetic diversity of United States Rambouillet, Katahdin and Dorper sheep. Genet Sel Evol. 2024 Jul 30;56(1):56. doi: 10.1186/s12711-024-00905-7.

Shira KA, Thornton KJ, **Murdoch BM**, Becker GM, Chibisa GE, Murdoch GK. Expression and secretion of SPARC, FGF-21 and DCN in bovine muscle cells: Effects of age and differentiation. PLoS One. 2024 Jul 3;19(7):e0299975. doi: 10.1371/journal.pone.0299975. eCollection 2024.

Kelson VC, Kiser JN, Davenport KM, Suarez EM, **Murdoch BM**, **Neibergs HL**. Identifying Regions of the Genome Associated with Conception Rate to the First Service in Holstein Heifers Bred by Artificial Insemination and as Embryo Transfer Recipients. Genes (Basel). 2024 Jun 11;15(6):765. doi: 10.3390/genes15060765.

Smitchger JA, Taylor JB, Mousel MR, Schaub D, Thorne JW, Becker GM, **Murdoch BM**. Genome-wide associations with longevity and reproductive traits in U.S. rangeland ewes. Front Genet. 2024 May 27;15:1398123. doi: 10.3389/fgene.2024.1398123. eCollection 2024.

Smith T, Olagunju T, Rosen B, **Neibergs H**, Becker G, Davenport K, Elsik C, Hadfield T, Koren S, Kuhn K, Rhie A, Shira K, Skibiel A, Stegemiller M, Thorne J, Villamediana P, **Cockett N**, **Murdoch B**. The first complete T2T Assemblies of Cattle and Sheep Y-Chromosomes uncover remarkable divergence in structure and gene content. Res Sq [Preprint]. 2024 Apr 3:rs.3.rs-4033388. doi: 10.21203/rs.3.rs-4033388/v1.

Thorne JW, Redden R, Bowdridge SA, Becker GM, Khilji SF, Xie S, Bentley KL, **Murdoch BM**. Reducing fecal egg count through selective breeding alters dorper lamb response to Haemonchus contortus in an artificial challenge trial. Vet Parasitol. 2024 Jun;328:110177. doi: 10.1016/j.vetpar.2024.110177. Epub 2024 Apr 3.

Shira KA, **Murdoch BM**, Thornton KJ, Reichhardt CC, Becker GM, Chibisa GE, Murdoch GK. Myokines Produced by Cultured Bovine Satellite Cells Harvested from 3- and 11-Month-Old Angus Steers. Animals (Basel). 2024 Feb 24;14(5):709. doi: 10.3390/ani14050709.

Nilson SM, Burke JM, **Murdoch BM**, Morgan JLM, Lewis RM. Pedigree diversity and implications for genetic selection of Katahdin sheep. J Anim Breed Genet. 2024 May;141(3):304-316. doi: 10.1111/jbg.12842. Epub 2023 Dec 18.

Xie S, Isaacs K, Becker G, **Murdoch BM**. A computational framework for improving genetic variants identification from 5,061 sheep sequencing data. J Anim Sci Biotechnol. 2023 Oct 2;14(1):127. doi: 10.1186/s40104-023-00923-3.

Cinar MU, Oliveira RD, Hadfield TS, Lichtenwalner A, Brzozowski RJ, Settlemire CT, Schoenian SG, Parker C, **Neibergs HL**, **Cockett NE**, White SN. Genome-wide association with footrot in hair and wool sheep. Front Genet. 2024 Jan 15;14:1297444. doi: 10.3389/fgene.2023.1297444. eCollection 2023.

Bowden CF, Kiser JN, Miller RS, Buckley AC, Boggiatto PM, Giglio RM, Brown VR, Garrick D, **Neibergs HL**, Piaggio AJ, Speidel SE, Smyser TJ. Genomic regions associated with pseudorabies virus infection status in naturally infected feral swine (Sus scrofa). Front Genet. 2023 Nov 23;14:1292671. doi: 10.3389/fgene.2023.1292671. eCollection 2023.

Richman J, **Phelps M**. Activin Signaling Pathway Specialization During Embryonic and Skeletal muscle Development in Rainbow Trout (Oncorhynchus mykiss). Mar Biotechnol (NY). 2024 Aug;26(4):766-775. doi: 10.1007/s10126-024-10345-5. Epub 2024 Jul 25.

Richman JA, Davis LR, **Phelps MP**. Gene Function is a Driver of Activin Signaling Pathway Evolution Following Whole-Genome Duplication in Rainbow Trout (Oncorhynchus mykiss). Genome Biol Evol. 2024 May 2;16(5):evae096. doi: 10.1093/gbe/evae096.

Rate of body weight gain during early gestation in F0 beef heifers has effects that extend multigenerationally to the F2 fetuses.

Baumgaertner F, Ramírez-Zamudio GD, Menezes ACB, Jurgens IM, Hirchert MR, Hurlbert JL, Bochantin KA, Diniz WJS, Reynolds LP, Ward AK, Borowicz PP, Underdahl SR, Kirsch JD, Dorsam ST, Sedivec KK, Swanson KC, Caton JS, Dahlen CR.

J Anim Sci. 2024 Sep 26:skae295. doi: 10.1093/jas/skae295. Online ahead of print.

Banerjee P, **Diniz WJS**. Advancing Dairy and Beef Genetics Through Genomic Technologies. Vet Clin North Am Food Anim Pract. 2024 Aug 23:S0749-0720(24)00033-1. doi: 10.1016/j.cvfa.2024.05.009. Online ahead of print.

Anas M, Ward AK, McCarthy KL, Borowicz PP, Reynolds LP, Caton JS, Dahlen CR, **Diniz WJS**. lncRNA-gene network analysis reveals the effects of early maternal nutrition on mineral homeostasis and energy metabolism in the fetal liver transcriptome of beef heifers. J Nutr Biochem. 2024 Oct;132:109691. doi: 10.1016/j.jnutbio.2024.109691. Epub 2024 Jun 13.

Dávila Ruiz BJ, Dahlen CR, McCarthy KL, Caton JS, Hurlbert JL, Baumgaertner F, B Menezes AC, **Diniz WJS**, Underdahl SR, Kirsch JD, Sedivec KK, Bochantin KA, Borowicz PP, Canovas S, Reynolds LP. Influence of Maternal Supplementation with Vitamins, Minerals, and (or) Protein/Energy on Placental Development and Angiogenic Factors in Beef Heifers during Pregnancy. Vet Sci. 2024 Mar 2;11(3):111. doi: 10.3390/vetsci11030111.

**Diniz WJS**, Afonso J, Kertz NC, Dyce PW, Banerjee P. Mapping Expression Quantitative Trait Loci Targeting Candidate Genes for Pregnancy in Beef Cows. Biomolecules. 2024 Jan 26;14(2):150. doi: 10.3390/biom14020150.

Kertz NC, Banerjee P, Dyce PW, **Diniz WJS**. Harnessing Genomics and Transcriptomics Approaches to Improve Female Fertility in Beef Cattle-A Review. Animals (Basel). 2023 Oct 21;13(20):3284. doi: 10.3390/ani13203284.

Malheiros JM, Correia BSB, Ceribeli C, Bruscadin JJ, **Diniz WJS**, Banerjee P, da Silva Vieira D, Cardoso TF, Andrade BGN, Petrini J, Cardoso DR, Colnago LA, Bogusz Junior S, Mourão GB, Coutinho LL, Palhares JCP, de Medeiros SR, Berndt A, de Almeida Regitano LC. Ruminal and feces metabolites associated with feed efficiency, water intake and methane emission in Nelore bulls.

Sci Rep. 2023 Oct 21;13(1):18001. doi: 10.1038/s41598-023-45330-w.

Reynolds LP, Dahlen CR, Ward AK, Crouse MS, Borowicz PP, Davila-Ruiz BJ, Kanjanaruch C, Bochantin KA, McLean KJ, McCarthy KL, Menezes ACB, **Diniz WJS**, Cushman RA, Caton JS. Role of the placenta in developmental programming: Observations from models using large animals. Anim Reprod Sci. 2023 Oct;257:107322. doi: 10.1016/j.anireprosci.2023.107322. Epub 2023 Aug 30.

Banerjee P, **Diniz WJS**, Dyce PW. Dataset for miRNA expression analysis in the peripheral white blood cells of beef heifers at weaning. Data Brief. 2023 Aug 22;50:109515. doi: 10.1016/j.dib.2023.109515. eCollection 2023 Oct.

Jara TC, Park K, Vahmani P, **Van Eenennaam AL**, Smith LR, Denicol AC. Stem cell-based strategies and challenges for production of cultivated meat. Nat Food. 2023 Oct;4(10):841-853. doi: 10.1038/s43016-023-00857-z. Epub 2023 Oct 16.

Mienaltowski MJ, Callahan M, De La Torre U, **Maga EA**. Comparing microbiotas of foals and their mares' milk in the first two weeks after birth. BMC Vet Res. 2024 Jan 8;20(1):17. doi: 10.1186/s12917-023-03864-1.

Novo LC, Poindexter MB, Rezende FM, Santos JEP, Nelson CD, Hernandez LL, **Kirkpatrick BW**, Peñagaricano F. Identification of genetic variants and individual genes associated with postpartum hypocalcemia in Holstein cows. Sci Rep. 2023 Dec 11;13(1):21900. doi: 10.1038/s41598-023-49496-1.

Hunt HL, **Kirkpatrick BW**. Degree of leukochimerism with calf age in Angus-crossbred twin sets. Anim Genet. 2023 Oct;54(5):619-622. doi: 10.1111/age.13349. Epub 2023 Aug 9.

Yang Z, Zhao T, **Cheng H**, Yang J. Microbiome-enabled genomic selection improves prediction accuracy for nitrogen-related traits in maize. G3 (Bethesda). 2024 Mar 6;14(3):jkad286. doi: 10.1093/g3journal/jkad286.

Zhao T, **Cheng H**. Interpreting single-step genomic evaluation as a neural network of three layers: pedigree, genotypes, and phenotypes. Genet Sel Evol. 2023 Oct 3;55(1):68. doi: 10.1186/s12711-023-00838-7.

Li J, **Miller LC**, Sang Y. Current Status of Vaccines for Porcine Reproductive and Respiratory Syndrome: Interferon Response, Immunological Overview, and Future Prospects. Vaccines (Basel). 2024 Jun 1;12(6):606. doi: 10.3390/vaccines12060606.

Davila KMS, Nelli RK, Mora-Díaz JC, Sang Y, **Miller LC**, Giménez-Lirola LG. Transcriptome Analysis in Air-Liquid Interface Porcine Respiratory Epithelial Cell Cultures Reveals That the Betacoronavirus Porcine Encephalomyelitis Hemagglutinating Virus Induces a Robust Interferon Response to Infection. Viruses. 2024 Jun 11;16(6):939. doi: 10.3390/v16060939.

Nicholson TL, Waack U, Fleming DS, Chen Q, **Miller LC**, Merkel TJ, Stibitz S. The contribution of BvgR, RisA, and RisS to global gene regulation, intracellular cyclic-di-GMP levels, motility, and biofilm formation in Bordetella bronchiseptica. Front Microbiol. 2024 Mar 7;15:1305097. doi: 10.3389/fmicb.2024.1305097. eCollection 2024.

Hu Y, Wu X, Tian Y, Jiang D, Ren J, Li Z, Ding X, Zhang Q, Yoo D, **Miller LC**, Lee C, Cong X, Li J, Du Y, Qi J. GTPase activity of porcine Mx1 plays a dominant role in inhibiting the N-Nsp9 interaction and thus inhibiting PRRSV replication. J Virol. 2024 Apr 16;98(4):e0184423. doi: 10.1128/jvi.01844-23. Epub 2024 Mar 4.

Sarlo Davila KM, Nelli RK, Phadke KS, Ruden RM, Sang Y, Bellaire BH, Gimenez-Lirola LG, **Miller LC**. How do deer respiratory epithelial cells weather the initial storm of SARS-CoV-2 WA1/2020 strain? Microbiol Spectr. 2024 Feb 6;12(2):e0252423. doi: 10.1128/spectrum.02524-23. Epub 2024 Jan 8.

**Posbergh CJ**, Miles AM, Pettifor NL, Thonney ML.Short Communication: Artificially reared ewes cannot be distinguished from natural reared ewes based on observed maternal behavior or lamb weaning weights. J Anim Sci. 2024 Sep 21:skae283. doi: 10.1093/jas/skae283. Online ahead of print.

Kvamme K, Marques RS, Alves Cruz V, Limede Cintra A, Ogg MA, McCoski SR, **Posbergh CJ**, Bradbery AN, Mercadante VRG, Mackey SJ, Pickett AT, Cooke RF. Multiple administrations of bovine-appeasing substance during a 42-d preconditioning program followed by feedlot receiving and its effects on physiologic, health, and performance responses of feeder cattle. J Anim Sci. 2024 Jan 3;102:skae151. doi: 10.1093/jas/skae151.

Mulim HA, Pedrosa VB, Pinto LFB, Tiezzi F, **Maltecca C**, Schenkel FS, Brito LF. Detection and evaluation of parameters influencing the identification of heterozygous-enriched regions in Holstein cattle based on SNP chip or whole-genome sequence data. BMC Genomics. 2024 Jul 26;25(1):726. doi: 10.1186/s12864-024-10642-2.

Tiezzi F, Schwab C, Shull C, **Maltecca C**. Multiple-trait genomic prediction for swine meat quality traits using gut microbiome features as a correlated trait. J Anim Breed Genet. 2024 Jul 10. doi: 10.1111/jbg.12887. Online ahead of print.

Wen H, Johnson JS, Gloria LS, Araujo AC, Maskal JM, Hartman SO, de Carvalho FE, Rocha AO, Huang Y, Tiezzi F, **Maltecca C**, Schinckel AP, Brito LF. Genetic parameters for novel climatic resilience indicators derived from automatically-recorded vaginal temperature in lactating sows under heat stress conditions. Genet Sel Evol. 2024 Jun 10;56(1):44. doi: 10.1186/s12711-024-00908-4.

Fabbri MC, Tiezzi F, Crovetti A, **Maltecca C**, Bozzi R. Investigation of cosmopolitan and local Italian beef cattle breeds uncover common patterns of heterozygosity. Animal. 2024 May;18(5):101142. doi: 10.1016/j.animal.2024.101142. Epub 2024 Mar 25.

Mancin E, **Maltecca C**, Huang YJ, Mantovani R, Tiezzi F. A first characterization of the microbiota-resilience link in swine. Microbiome. 2024 Mar 15;12(1):53. doi: 10.1186/s40168-024-01771-7.

Déru V, Tiezzi F, Carillier-Jacquin C, Blanchet B, Cauquil L, Zemb O, Bouquet A, **Maltecca C**, Gilbert H. The potential of microbiota information to better predict efficiency traits in growing pigs fed a conventional and a high-fiber diet. Genet Sel Evol. 2024 Jan 19;56(1):8. doi: 10.1186/s12711-023-00865-4.

Wen H, Johnson JS, Freitas PHF, Maskal JM, Gloria LS, Araujo AC, Pedrosa VB, Tiezzi F, **Maltecca C**, Huang Y, Schinckel AP, Brito LF. Longitudinal genomic analyses of automatically-recorded vaginal temperature in lactating sows under heat stress conditions based on random regression models. Genet Sel Evol. 2023 Dec 21;55(1):95. doi: 10.1186/s12711-023-00868-1.

Lozada-Soto EA, Parker Gaddis KL, Tiezzi F, Jiang J, **Ma L**, Toghiani S, VanRaden PM, **Maltecca C**. Inbreeding depression for producer-recorded udder, metabolic, and reproductive diseases in US dairy cattle. J Dairy Sci. 2024 May;107(5):3032-3046. doi: 10.3168/jds.2023-23909. Epub 2023 Dec 4.

Kuthyar S, Diaz J, Avalos-Villatoro F, **Maltecca C**, Tiezzi F, Dunn RR, Reese AT. Domestication shapes the pig gut microbiome and immune traits from the scale of lineage to population. J Evol Biol. 2023 Dec;36(12):1695-1711. doi: 10.1111/jeb.14227. Epub 2023 Oct 26.

Déru V, Tiezzi F, VanRaden PM, Lozada-Soto EA, Toghiani S, **Maltecca C**. Imputation accuracy from low- to medium-density SNP chips for US crossbred dairy cattle. J Dairy Sci. 2024 Jan;107(1):398-411. doi: 10.3168/jds.2023-23250. Epub 2023 Aug 23.

Bordini M, Wang Z, Soglia F, Petracci M, **Schmidt CJ**, **Abasht B**. RNA-sequencing revisited data shed new light on wooden breast myopathy. Poult Sci. 2024 Aug;103(8):103902. doi: 10.1016/j.psj.2024.103902. Epub 2024 May 25.

Velleman SG, Coy CS, **Abasht B**. Research Note: Chicken breast muscle satellite cell function: effect of expression of CNN1 and PHRF1. Poult Sci. 2024 Jul;103(7):103781. doi: 10.1016/j.psj.2024.103781. Epub 2024 Apr 20.

Wang Z, Khondowe P, Brannick E, **Abasht B**. Spatial transcriptomics reveals alterations in perivascular macrophage lipid metabolism in the onset of Wooden Breast myopathy in broiler chickens. Sci Rep. 2024 Feb 11;14(1):3450. doi: 10.1038/s41598-024-53904-5.

Fulton JE, McCarron AM, Lund AR, Drobik-Czwarno W, Mullen A, Wolc A, Szadkowska J, **Schmidt CJ**, Taylor RL Jr. The RHCE gene encodes the chicken blood system I. Genet Sel Evol. 2024 Jun 19;56(1):47. doi: 10.1186/s12711-024-00911-9.

Swaggerty CL, Siegel PB, Honaker CF, Kogut MH, Anderson RC, **Ashwell CM**, Taylor RL Jr. Selection for high and low antibody responses to sheep red blood cells influences cytokine and chemokine expression in chicken peripheral blood leukocytes and splenic tissue. Poult Sci. 2024 Sep;103(9):103972. doi: 10.1016/j.psj.2024.103972. Epub 2024 Jun 11.

Nolin SJ, Siegel PB, **Ashwell CM**. Differences in the microbiome of the small intestine of Leghorn lines divergently selected for antibody titer to sheep erythrocytes suggest roles for commensals in host humoral response. Front Physiol. 2024 Jan 8;14:1304051. doi: 10.3389/fphys.2023.1304051. eCollection 2023.

Maiorano AM, Ablondi M, Qiao Y, **Steibel JP**, Bernal Rubio YL. Editorial: Increasing sustainability in livestock production systems through high-throughput phenotyping approaches. Front Genet. 2024 Apr 5;15:1403133. doi: 10.3389/fgene.2024.1403133. eCollection 2024.

Fedorka CE, El-Sheikh-Ali H, Scoggin KE, **Coleman S**, Humphrey EA, Troutt L, Troedsson MHT. The Effect of Seminal Plasma on the Equine Endometrial Transcriptome. Reprod Domest Anim. 2024 Sep;59(9):e14711. doi: 10.1111/rda.14711.

Moss CD, Wilson AL, Reed KJ, Jennings KJ, Kunz IGZ, Landolt GA, Metcalf J, Engle TE, **Coleman SJ**. Gene Expression Analysis before and after the Pelvic Flexure in the Epithelium of the Equine Hindgut. Animals (Basel). 2024 Aug 8;14(16):2303. doi: 10.3390/ani14162303.

Kalleberg J, Rissman J, **Schnabel RD**. Overcoming Limitations to Deep Learning in Domesticated Animals with TrioTrain. bioRxiv [Preprint]. 2024 Apr 20:2024.04.15.589602. doi: 10.1101/2024.04.15.589602.

**Rowan TN**, **Schnabel RD**, Decker JE. Uncovering the architecture of selection in two Bos taurus cattle breeds. Evol Appl. 2024 Feb 22;17(2):e13666. doi: 10.1111/eva.13666. eCollection 2024 Feb.

Quan J, Yang M, Wang X, Cai G, Ding R, Zhuang Z, Zhou S, Tan S, Ruan D, Wu J, Zheng E, Zhang Z, Liu L, Meng F, Wu J, Xu C, Qiu Y, Wang S, Lin M, Li S, Ye Y, Zhou F, Lin D, Li X, Deng S, Zhang Y, Yao Z, Gao X, Yang Y, Liu Y, Zhan Y, Liu Z, Zhang J, Ma F, Yang J, Chen Q, Yang J, Ye J, Dong L, Gu T, Huang S, Xu Z, Li Z, Yang J, **Huang W**, Wu Z. Multi-omic characterization of allele-specific regulatory variation in hybrid pigs. Nat Commun. 2024 Jul 3;15(1):5587. doi: 10.1038/s41467-024-49923-5.

Ma Y, Cao X, Sumayya, Lu Y, Han W, **Lamont SJ**, Sun H. Identification and Functional Analysis of Novel Long Intergenic RNA in Chicken Macrophages Infected with Avian Pathogenic Escherichia coli. Microorganisms. 2024 Aug 6;12(8):1594. doi: 10.3390/microorganisms12081594.

Sun HY, Ma YY, Cao XQ, Li H, Han W, Qu LJ, **Lamont SJ**. PTEN regulated by gga-miR-20a-5p is involved in chicken macrophages inflammatory response to APEC infection via autophagy. Poult Sci. 2024 Aug 5;103(11):104170. doi: 10.1016/j.psj.2024.104170. Online ahead of print.

Cao X, Ge J, Ma Y, Li H, Han W, **Lamont SJ**, Sun H. MiR-20a-5p Targeting the TGFBR2 Gene Regulates Inflammatory Response of Chicken Macrophages Infected with Avian Pathogenic E. coli. Animals (Basel). 2024 Aug 5;14(15):2277. doi: 10.3390/ani14152277.

Wang L, Xie T, Zhou X, Yang G, Guo Z, Huang Y, **Lamont SJ**, Lan X. LncIRF1 promotes chicken resistance to ALV-J infection. 3 Biotech. 2023 Nov;13(11):367. doi: 10.1007/s13205-023-03773-y. Epub 2023 Oct 14.

Yang P, Corbett R, Daharsh L, Uribe JH, Byrne KA, Loving CL, **Tuggle C**. Definition of regulatory elements and transcription factors controlling porcine immune cell gene expression at single cell resolution using single nucleus ATAC-seq. Genomics. 2024 Sep 24:110944. doi: 10.1016/j.ygeno.2024.110944. Online ahead of print.

Widmer KM, Rahic-Seggerman F, Forster A, Ahrens-Kress A, Sauer M, Mooyottu S, Vinithakumari A, Dunkerson-Kurzhumov A, Sponseller B, Kiupel M, Schmitz-Esser S, **Tuggle CK**. EFFECT OF GENOTYPE AND AGE ON A DEFINED MICROBIOTA IN GNOTOBIOTIC SCID PIGLETS. bioRxiv [Preprint]. 2024 Sep 7:2024.09.03.611011. doi: 10.1101/2024.09.03.611011.

Samuel BER, Diaz FE, Maina TW, Corbett RJ, **Tuggle CK**, McGill JL. Evidence of innate training in bovine γδ T cells following subcutaneous BCG administration. Front Immunol. 2024 Jul 18;15:1423843. doi: 10.3389/fimmu.2024.1423843. eCollection 2024.

Pluta A, Jaworski JP, Droscha C, VanderWeele S, **Taxis TM**, Valas S, Brnić D, Jungić A, Ruano MJ, Sánchez A, Murakami K, Nakamura K, Puentes R, De Brun M, Ruiz V, Gómez MEL, Lendez P, Dolcini G, Camargos MF, Fonseca A, Barua S, Wang C, Giza A, Kuźmak J. Inter-laboratory comparison of eleven quantitative or digital PCR assays for detection of proviral bovine leukemia virus in blood samples. BMC Vet Res. 2024 Aug 26;20(1):381. doi: 10.1186/s12917-024-04228-z.

Pluta A, **Taxis TM**, van der Meer F, Shrestha S, Qualley D, Coussens P, Rola-Łuszczak M, Ryło A, Sakhawat A, Mamanova S, Kuźmak J. An immunoinformatics study reveals a new BoLA-DR-restricted CD4+ T cell epitopes on the Gag protein of bovine leukemia virus. Sci Rep. 2023 Dec 15;13(1):22356. doi: 10.1038/s41598-023-48899-4.

Kravitz A, Liao M, Morota G, Tyler R, **Cockrum R**, Manohar BM, Ronald BSM, Collins MT, Sriranganathan N. Retrospective Single Nucleotide Polymorphism Analysis of Host Resistance and Susceptibility to Ovine Johne's Disease Using Restored FFPE DNA. Int J Mol Sci. 2024 Jul 15;25(14):7748. doi: 10.3390/ijms25147748.

Morales AG, **Cockrum RR**, Teixeira IAMA, Ferreira G, Hanigan MD. Graduate Student Literature Review: System, plant, and animal factors controlling dietary pasture inclusion and their impact on ration formulation for dairy cows. J Dairy Sci. 2024 Feb;107(2):870-882. doi: 10.3168/jds.2023-23810. Epub 2023 Sep 26.

Rajab SAS, Andersen LK, Kenter LW, Berlinsky DL, Borski RJ, McGinty AS, **Ashwell CM**, Ferket PR, Daniels HV, **Reading BJ**. Combinatorial metabolomic and transcriptomic analysis of muscle growth in hybrid striped bass (female white bass Morone chrysops x male striped bass M. saxatilis). BMC Genomics. 2024 Jun 10;25(1):580. doi: 10.1186/s12864-024-10325-y.

**Bailey E**. Ancient DNA reveals an early adoption of horse culture by Native Americans. Trends Genet. 2023 Nov;39(11):808-809. doi: 10.1016/j.tig.2023.06.010. Epub 2023 Jul 7.

**Mueller ML**, **Courter JT**, Spare R. Innovating Beef Cattle Veterinary Practices: Leveraging Genetic and Genomic Tools. Vet Clin North Am Food Anim Pract. 2024 Aug 23:S0749-0720(24)00028-8. doi: 10.1016/j.cvfa.2024.05.004. Online ahead of print.

Clark BL, **Norton EM**, Bamford NJ, Randhawa IA, Kemp KL, **McCue ME**, Bertin F-R, Stewart AJ. Epidemiological investigation of insulin dysregulation in Shetland and Welsh ponies in Australia. Equine Vet J. 2024 Mar;56(2):281-290. doi: 10.1111/evj.14044. Epub 2024 Jan 3.

Ram Das A, Pillai N, **Nanduri B**, Rothrock MJ Jr, Ramkumar M. Exploring Pathogen Presence Prediction in Pastured Poultry Farms through Transformer-Based Models and Attention Mechanism Explainability. Microorganisms. 2024 Jun 23;12(7):1274. doi: 10.3390/microorganisms12071274.

Lee JH, Ayoola MB, Shack LA, Swiatlo E, **Nanduri B**. Characterization of an Arginine Decarboxylase from Streptococcus pneumoniae by Ultrahigh-Performance Liquid Chromatography-Tandem Mass Spectrometry. Biomolecules. 2024 Apr 10;14(4):463. doi: 10.3390/biom14040463.

Ayoola MB, Shack LA, Phanstiel O 4th, **Nanduri B**. Impact of Difluoromethylornithine and AMXT 1501 on Gene Expression and Capsule Regulation in Streptococcus pneumoniae. Biomolecules. 2024 Feb 2;14(2):178. doi: 10.3390/biom14020178.

Ayoola MB, Das AR, Krishnan BS, Smith DR, **Nanduri B**, Ramkumar M. Predicting Salmonella MIC and Deciphering Genomic Determinants of Antibiotic Resistance and Susceptibility. Microorganisms. 2024 Jan 10;12(1):134. doi: 10.3390/microorganisms12010134.

Ayoola MB, Pillai N, **Nanduri B**, Rothrock MJ Jr, Ramkumar M. Predicting foodborne pathogens and probiotics taxa within poultry-related microbiomes using a machine learning approach. Anim Microbiome. 2023 Nov 15;5(1):57. doi: 10.1186/s42523-023-00260-w.

Kosonsiriluk S, **Reed KM**, Noll SL, Wileman BW, Studniski MM, Boukherroub KS. Prolonged repeated inseminations trigger a local immune response and accelerate aging of the uterovaginal junction in turkey hens. Front Physiol. 2023 Nov 22;14:1275922. doi: 10.3389/fphys.2023.1275922. eCollection 2023.

**Reed KM**, Mendoza KM, Kono T, Powell AA, Strasburg GM, Velleman SG. Expression of miRNAs in turkey muscle satellite cells and differential response to thermal challenge. Front Physiol. 2023 Nov 23;14:1293264. doi: 10.3389/fphys.2023.1293264. eCollection 2023.

Inupala S, Uzzaman MR, Pande P, Jagana S, **Worku M**. Effect of a garlic drench on Galectin gene expression in ovine whole blood. Anim Biotechnol. 2024 Nov;35(1):2344208. doi: 10.1080/10495398.2024.2344208. Epub 2024 May 13.

Ekwemalor K, Asiamah E, Adjei-Fremah S, Eluka-Okoludoh E, Mulakala B, Osei B, **Worku M**. Diverse pathogen-associated molecular patterns affect transcription of genes in the toll-like receptor signaling pathway in goat blood. Anim Biotechnol. 2023 Dec;34(8):3729-3738. doi: 10.1080/10495398.2023.2214189. Epub 2023 May 25.

Role of PI3K/AKT signaling pathway involved in self-renewing and maintaining biological properties of chicken primordial germ cells.

Liu X, Ye L, Ding Y, Gong W, Qian H, Jin K, Niu Y, Zuo Q, **Song J**, Han W, Chen G, Li B.

Poult Sci. 2024 Aug 8;103(11):104140. doi: 10.1016/j.psj.2024.104140. Online ahead of print.

Identification of Two Potential Gene Insertion Sites for Gene Editing on the Chicken Z/W Chromosomes.

Wu G, Liang Y, Chen C, Chen G, Zuo Q, Niu Y, **Song J**, Han W, Jin K, Li B.

Genes (Basel). 2024 Jul 22;15(7):962. doi: 10.3390/genes15070962.

**Rowan TN**. Genetics and Genomics 101. Vet Clin North Am Food Anim Pract. 2024 Aug 23:S0749-0720(24)00025-2. doi: 10.1016/j.cvfa.2024.05.001. Online ahead of print.

Myer PR, Blair S, Mason KM, Shepherd EA, Downey BC, McLean KJ, **Rowan TN**, Eckelkamp EA, Schrick FN, Zambito Ivey JL. Promoting public engagement in interdisciplinary biological systems education by leveraging American sports-inspired bracket contests on social media and web. J Microbiol Biol Educ. 2024 Aug 29;25(2):e0007824. doi: 10.1128/jmbe.00078-24. Epub 2024 Jul 16.

Walt HK, Jordan HR, Meyer F, **Hoffmann FG**. Detection of Known and Novel Virus Sequences in the Black Solider Fly and Expression of Host Antiviral Pathways. Viruses. 2024 Jul 30;16(8):1219. doi: 10.3390/v16081219.

Walt HK, Bronzato-Badial A, Maedo SE, Hinton JA, King JG, Pietri JE, **Hoffmann FG**. Under the radar: Transcriptomic responses of bed bugs to an entomopathogen, environmental bacteria, and a human pathogen. J Invertebr Pathol. 2024 Sep;206:108182. doi: 10.1016/j.jip.2024.108182. Epub 2024 Aug 22.

Langleib M, Calvelo J, Costábile A, Castillo E, Tort JF, **Hoffmann FG**, Protasio AV, Koziol U, Iriarte A. Evolutionary analysis of species-specific duplications in flatworm genomes. Mol Phylogenet Evol. 2024 Oct;199:108141. doi: 10.1016/j.ympev.2024.108141. Epub 2024 Jul 2.

Walt HK, Ahn SJ, **Hoffmann FG**. Horizontally transferred glycoside hydrolase 26 may aid hemipteran insects in plant tissue digestion. Mol Phylogenet Evol. 2024 Sep;198:108134. doi: 10.1016/j.ympev.2024.108134. Epub 2024 Jun 18.

Walt HK, King JG, Towles TB, Ahn SJ, **Hoffmann FG**. Comparative Genomics and the Salivary Transcriptome of the Redbanded Stink Bug Shed Light on Its High Damage Potential to Soybean. Genome Biol Evol. 2024 Jul 3;16(7):evae121. doi: 10.1093/gbe/evae121.

Walt HK, King JG, Sheele JM, Meyer F, Pietri JE, **Hoffmann FG**. Do bed bugs transmit human viruses, or do humans spread bed bugs and their viruses? A worldwide survey of the bed bug RNA virosphere. Virus Res. 2024 May;343:199349. doi: 10.1016/j.virusres.2024.199349. Epub 2024 Mar 7.

Pluta A, Rola-Łuszczak M, **Hoffmann FG**, Donnik I, Petropavlovskiy M, Kuźmak J. Genetic Variability of Bovine Leukemia Virus: Evidence of Dual Infection, Recombination and Quasi-Species. Pathogens. 2024 Feb 15;13(2):178. doi: 10.3390/pathogens13020178.

Pennance T, Calvelo J, Tennessen JA, Burd R, Cayton J, Bollmann SR, Blouin MS, Spaan JM, **Hoffmann FG**, Ogara G, Rawago F, Andiego K, Mulonga B, Odhiambo M, Loker ES, Laidemitt MR, Lu L, Iriarte A, Odiere MR, Steinauer ML. The genome and transcriptome of the snail Biomphalaria sudanica s.l.: immune gene diversification and highly polymorphic genomic regions in an important African vector of Schistosoma mansoni. BMC Genomics. 2024 Feb 19;25(1):192. doi: 10.1186/s12864-024-10103-w.

Pennance T, Calvelo J, Tennessen JA, Burd R, Cayton J, Bollmann SR, Blouin MS, Spaan JM, **Hoffmann FG**, Ogara G, Rawago F, Andiego K, Mulonga B, Odhiambo M, Loker ES, Laidemitt MR, Lu L, Iriarte A, Odiere M, Steinauer ML. The genome and transcriptome of the snail Biomphalaria sudanica s.l.: Immune gene diversification and highly polymorphic genomic regions in an important African vector of Schistosoma mansoni. bioRxiv [Preprint]. 2023 Nov 2:2023.11.01.565203. doi: 10.1101/2023.11.01.565203.

Munguía Vásquez MF, **Gill CA**, Riggs PK, Herring AD, Sanders JO, Riley DG. Genetic evaluation of crossbred Bos indicus cow temperament at parturition. J Anim Sci. 2024 Jan 3;102:skae022. doi: 10.1093/jas/skae022.

Boschiero C, Neupane M, Yang L, Schroeder SG, Tuo W, **Ma L**, Baldwin RL 6th, Van Tassell CP, Liu GE. A Pilot Detection and Associate Study of Gene Presence-Absence Variation in Holstein Cattle. Animals (Basel). 2024 Jun 28;14(13):1921. doi: 10.3390/ani14131921.

Ng M, **Ma L**, Shi J, Jeffery WR. Natural reversal of cavefish heart asymmetry is controlled by Sonic Hedgehog effects on the left-right organizer. Development. 2024 Jul 15;151(14):dev202611. doi: 10.1242/dev.202611. Epub 2024 Jul 18.

Gao Y, Liu GE, **Ma L**, Fang L, Li CJ, Baldwin RL 6th. Transcriptomic profiling of gastrointestinal tracts in dairy cattle during lactation reveals molecular adaptations for milk synthesis. J Adv Res. 2024 Jun 24:S2090-1232(24)00257-1. doi: 10.1016/j.jare.2024.06.020. Online ahead of print.

Wilson CS, **Petersen JL**, Brito LF, Freking BA, Nilson SM, Taylor JB, Murphy TW, Lewis RM. Assessment of genetic diversity and population structure of U.S. Polypay sheep from breed origins to future genomic selection. Front Genet. 2024 Aug 5;15:1436990. doi: 10.3389/fgene.2024.1436990. eCollection 2024.

Hess MK, Mersha A, Ference SS, Nafziger SR, Keane JA, Fuller AM, Kurz SG, Sutton CM, Spangler ML, **Petersen JL**, Cupp AS. Puberty classifications in beef heifers are moderately to highly heritable and associated with candidate genes related to cyclicity and timing of puberty. Front Genet. 2024 Jun 13;15:1405456. doi: 10.3389/fgene.2024.1405456. eCollection 2024.

Beer HN, Lacey TA, Gibbs RL, Most MS, Hicks ZM, Grijalva PC, Marks-Nelson ES, Schmidt TB, **Petersen JL**, Yates DT. Daily Eicosapentaenoic Acid Infusion in IUGR Fetal Lambs Reduced Systemic Inflammation, Increased Muscle ADRβ2 Content, and Improved Myoblast Function and Muscle Growth. Metabolites. 2024 Jun 18;14(6):340. doi: 10.3390/metabo14060340.

Batt MC, Venzor LG, Gardner K, Reith RR, Roberts KA, Herrera NJ, Fuller AM, Sullivan GA, Mulliniks JT, Spangler ML, Valberg SJ, Steffen DJ, **Petersen JL**. An autosomal recessive variant in PYGM causes myophosphorylase deficiency in Red Angus composite cattle. BMC Genomics. 2024 Apr 27;25(1):417. doi: 10.1186/s12864-024-10330-1.

Heath H, Peng S, Szmatola T, Ryan S, Bellone R, **Kalbfleisch T**, **Petersen J**, Finno C. A Comprehensive Allele Specific Expression Resource for the Equine Transcriptome.

Res Sq [Preprint]. 2024 Apr 4:rs.3.rs-4182812. doi: 10.21203/rs.3.rs-4182812/v1.

Gibbs RL, Wilson JA, Swanson RM, Beard JK, Hicks ZM, Beer HN, Marks-Nelson ES, Schmidt TB, **Petersen JL**, Yates DT. Daily Injection of the β2 Adrenergic Agonist Clenbuterol Improved Muscle Glucose Metabolism, Glucose-Stimulated Insulin Secretion, and Hyperlipidemia in Juvenile Lambs Following Heat-Stress-Induced Intrauterine Growth Restriction. Metabolites. 2024 Mar 7;14(3):156. doi: 10.3390/metabo14030156.

Reith RR, Batt MC, Fuller AM, Meekins JM, Diehl KA, Zhou Y, Bedwell PS, Ward JA, Sanders SK, **Petersen JL**, Steffen DJ. A recessive CLN3 variant is responsible for delayed-onset retinal degeneration in Hereford cattle. J Vet Diagn Invest. 2024 May;36(3):438-446. doi: 10.1177/10406387241239918. Epub 2024 Mar 22.

Reith RR, Beever JE, Paschal JC, Banta J, Porter BF, Steffen DJ, Hairgrove TB, **Petersen JL**. A de novo mutation in CACNA1A is associated with autosomal dominant bovine familial convulsions and ataxia in Angus cattle. Anim Genet. 2024 Jun;55(3):344-351. doi: 10.1111/age.13409. Epub 2024 Mar 1.

Palomino Lago E, Baird A, Blott SC, McPhail RE, Ross AC, **Durward-Akhurst SA**, Guest DJ. A Functional Single-Nucleotide Polymorphism Upstream of the Collagen Type III Gene Is Associated with Catastrophic Fracture Risk in Thoroughbred Horses. Animals (Basel). 2023 Dec 28;14(1):116. doi: 10.3390/ani14010116.

**Rojas de Oliveira H**, Chud TCS, Oliveira GA Jr, Hermisdorff IC, Narayana SG, Rochus CM, Butty AM, Malchiodi F, Stothard P, Miglior F, Baes CF, Schenkel FS. Genome-wide association analyses reveal copy number variant regions associated with reproduction and disease traits in Canadian Holstein cattle. J Dairy Sci. 2024 Sep;107(9):7052-7063. doi: 10.3168/jds.2023-24295. Epub 2024 May 23.

**Rojas de Oliveira H**, Campos GS, Lazaro SF, Jamrozik J, Schinckel A, Brito LF. Phenotypic and genomic modeling of lactation curves: A longitudinal perspective. JDS Commun. 2024 Feb 1;5(3):241-246. doi: 10.3168/jdsc.2023-0460. eCollection 2024 May.

Maskal JM, Pedrosa VB, **Rojas de Oliveira H**, Brito LF. A comprehensive meta-analysis of genetic parameters for resilience and productivity indicator traits in Holstein cattle. J Dairy Sci. 2024 May;107(5):3062-3079. doi: 10.3168/jds.2023-23668. Epub 2023 Dec 4.

Sousa LPB Junior, Pinto LFB, Cruz VAR, Oliveira GA Jr, **Rojas de Oliveira H**, Chud TS, Pedrosa VB, Miglior F, Schenkel FS, Brito LF. Genome-wide association and functional genomic analyses for various hoof health traits in North American Holstein cattle. J Dairy Sci. 2024 Apr;107(4):2207-2230. doi: 10.3168/jds.2023-23806. Epub 2023 Nov 7.