Darren Hagen

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Research Interests:

The research conducted in my laboratory aims to understand biological mechanisms of gene expression and regulation using computational biology and bioinformatics tools. We are interested in understanding the role of non-coding RNAsin transcriptional regulation and post-transcriptional control of translation and especially interested in expression and epigenetic modification of tRNAs. tRNA abundance differs among tissues and life stages, having direct effects on translational efficiency and MRNA stability. We use cell culture and tissue derived from evolutionarily close livestock species. Livestock are among the best phenotype and genotype species and can offer great insight into evolution and conservation of gene regulation mechanisms. A long term goal of this line of research is to identify novel mechanisms of molecular regulation and epigenetic control of gene expression at specific times and tissues during development.

Education:
2012: Postdoc, Computational Biology/Bioinformatics, Georgetown University, DC
2007: Genetics Ph.D., Texas A&M University, TX
2001: Biology B.S., Angelo State University, TX

Academic Appointments:
2017-Present: Assistant Professor, Oklahoma State University, OK
2012-2017: Research Assistant Professor, University of Missouri, MS
2008-2012: Assistant Lecturer, Georgetown University, DC
2007-2012: Postdoctoral Fellow, Georgetown University, DC
2005-2007: Adjunct Lecturer, Blinn College, TX

Awards and Honors:
2020: Co-Chair, NRSP-8: National Animal Genome Research Program, Cattle and Swine Workshop
2012: International Society for Animal Genetics, Member
2007: American Association for the Advancement of Science, Member

Research Support:

- 1/1/2021-12/31/2022: USDA-NIFA-AFRI, “Ribosome-bound Transcriptomics Linking Gene Expression to Translation”, Role: PI

- 1/1/2021-12/31/2022: USDA-NIFA-AFRI, “The Role Of Glucose Metabolism In The Regulation Of Feed Intake And Nutrient Utilization Efficiency Of Beef Cattle”, Role: CoPI
- 1/1/2021-12/31/2022: USDA-NIFA-AFRI, “Growth performance, nutrients utilization and gut microbiota of pigs fed with low protein diets supplemented with isoleucine and valine”, Role: CoPI
- 7/1/2020-6/30/2022: USDA-NIFA-AFRI, “Influence Of Prenatal Stress On Immune Function, Behavior, And Welfare Of The Progeny”, Role: CoPI
- 1/1/2020-12/31/2022: USGA-TERP, “Expression profiling of host plants and Ophiosphaerella spp. during infection and colonization of diseased and asymptomatic hosts”, Role: CoPI
- 1/1/2018-12/31/2023: USDA-NIFA-AFRI, “Use of a Bovine Overgrowth Syndrome to Characterize the Molecular Etiology of BWS”, Role: CoPI

Selected Publications:

1. Li Y, Hagen DE, Ji T, et al. Altered microRNA expression profiles in large offspring syndrome and Beckwith-Wiedemann syndrome. Epigenetics. 2019;14(9):850-876. doi:10.1080/15592294.2019.1615357
2. Chen Z., Hagen, DE., Ji, T., Elsik, CG., Rivera, RM. Global misregulation of genes largely uncoupled to DNA methylome epimutations characterizes a congenital overgrowth syndrome. 2017. Scientific Reports. Oct 4;7(1):12667. PMID: 28978943
3. Chen Z, Hagen DE, Wang J, Elsik CG, Ji T, Siqueira LG, Hansen PJ, Rivera RM. Global assessment of imprinted gene expression in the bovine conceptus by next generation sequencing. Epigenetics. 2016 Jul 2;11(7):501-16. PMID:28379294
4. Chen, Z., Hagen, DE., Elsik, CG., Ji, T., Moon, LE., Morris, CJ., and , Rivera, RM. Characterization of global loss-of-imprinting in fetal overgrowth syndrome induced by assisted reproduction. Proc Natl Acad Sci U S A. 2015 Apr 14;112(15):4618-23. doi: 10.1073/pnas.1422088112. Epub 2015 Mar 30. PMID: 25825726