

Annual Report for  
 NC1170 Advanced Technologies for the Genetic Improvement of Poultry.  
 Period: January 1, 2012 thru December 31, 2013  
 Program Leader: Douglas Rhoads  
 Program Secretary: David Froman

This report consists of:

1. Status of NC1170 renewal
2. Summary of the annual NC1170 business meeting
3. Summary of significant achievements for 2012
4. Summary of impact statements
5. Publications for 2012
6. Leveraging and Funding

**1. Status of NC1170 Renewal**

The project renewal for NC1170 was assembled and produced by the writing committee (Mary Delaney- chair, Kent Reed, Eric Wong and Douglas Rhoads). The draft was circulated to the project members and then submitted at the end of November 2012. That renewal draft is available on NIMSS.

**2. Summary of the annual NC1170 business Meeting**

Convened 11:15 AM, January 13, 2013, Town and Country Resort and Convention Center

Chair: Douglas Rhoads

Secretary: David Froman

Project Participants	*-indicates present at business meeting	
Station	Station Leader	Other Station Scientist(s)
Beckmann Research Institute at the City of Hope	Miller, Marcia*	
Iowa State University	Lamont, Susan J.*	Dekkers, Jack
Michigan State University	Dodgson, Jerry*	Brown, C. Titus*
Mississippi State University	Edelmann, Mariola J	
North Carolina State University	Ashwell, Christopher*	Petitte, James
Oregon State University	Froman, David*	
Purdue University	Muir, William*	
University of Arizona	McCarthy, Fiona*	Burgess, Shane
University of Arkansas	Kuenzel, Wayne*	Rhoads, Douglas*; Kong, Byung-Whi
University of California Davis	Zhou, Huaijun*	
University of California Davis	Delany, Mary E.	
University of Delaware	Abasht, Behnam*	
University of Georgia	Aggrey, Samuel*	
University of Maryland	Porter, Tom E*	Song, Jiuzhou*
University of Minnesota	Reed, Kent*	
University of Wisconsin	Rosa, Guilherme*	

USDA-ARS-Avian Disease and Oncology Lab	Cheng, Hans*	Zhang, Huanmin*
Virginia Tech	Wong, Eric A.*	

1. Administrative Advisor: Mo Saif
  - a. Shared that he will be retiring from USDA the end of January, and that Sue Lamont will become the new Administrative Advisor.
  - b. Indicated the project has been very productive and meeting the goals of the multistate projects as envisioned.
  - c. The group extended their best wishes and thanked him for his support and guidance over these many years.
  - d. Annual report for the project is due in one month.
  - e. The project renewal has been posted and is up for final approval in March.
2. Poultry Coordinator Dodgson Report
  - a. Plans for this year are to continue work to improve reference assembly and more microchromosome sequence in assembly
  - b. Wants to make feedback on assembly errors more democratic
  - c. Researchers can contact Wes Warren directly with problems and suggested resolutions, including wet lab experiments. Washington University is equipped.
  - d. Washington University has dedicated annotators
  - e. Cobb Vantress contributed \$150,000 to Washington University to support fixing known gaps in the assembly
  - f. Will be some PacBio sequencing contributions and other new technologies to see if they advance the problem sequences
  - g. Money is a problem on several fronts for finishing and improving the genome
  - h. Dave Burt mentioned some work at Roslin for sorting microchromosomes and that they may have some data to contribute. Problems they face are with interfacing with ENSEMBL and access to a single contact person.
  - i. The coordinator's report is on the website as pdf, with photos.
  - j. Any suggestions on use of coordinator funds are welcome.
3. NRSP8 coordinator: Tom Porter
  - a. Renewal is in process this year, with resubmission planned this summer.
  - b. Very important that annual reports include impact statements. USDA relies heavily on these impact statements.
  - c. Mo Saif agreed with the importance and will be sending email to the group reinforcing.
  - d. Dodgson and Cheng indicated that a NIFA person is using these for 1 page documents that go to congressional staffers and others to inform about NIFA activities. Very critical for funding.
4. Other business
  - a. Motion to have next NC1170 meeting with Plant and Animal Genome workshop for January 2014, seconded, and passed unanimously.
  - b. Hans Cheng asked for feedback on PAG format:
    - i. WiFi better but still not the best.

- ii. New system for submission of presentations good but why is deadline so early. Need to allow submission closer to actual meeting.
- iii. There are some inadequacies with the system for rearranging workshop schedule after the deadline. Cumbersome and caused some technical problems.
- iv. Some objections to speakers emails being given/sold to vendors. Result is lots of spam. Is this a breach of privacy?
- c. Mo Saif said he is editor of Avian Diseases and would welcome manuscripts.
- d. Tom Porter said he is editor of Poultry Science and he wants the manuscripts, too.
- e. Sue Lamont:
  - i. Group should thank Mo Saif: Group complied
  - ii. Group should thank Doug and Carl: Group complied.
- f. Doug Rhoads: reminder that the Conference grant to Carl and Doug will be available next year so look for the announcement. Did not spend half the money this year so there will be extra next year for speakers and travel awards.

### **3. Summary of significant achievements for 2012**

The NC1170 group, in conjunction with NRSP8, hosted a 1.5 day long (January 12 and 13, 2013) workshop on Poultry Genetics as part of the Plant and Animal Genome meeting in San Diego, CA. Presentations included 5 invited speakers, 16 NC1170 members, and 3 guests. Invited speakers were from the United Kingdom, Canada, and the USA. Eight students received travel awards and gave brief 2 minute lightning talks as well. Travel awardees were from the USA, Pakistan, Iran, Brazil, and China. The schedule of talks is presented below. Attendance was variable for the different sessions, but during Saturday AM there were roughly 85-90 people in attendance. The number may have gone closer to 100 for Saturday PM.

Invited Speakers who were funded by the Conference Grant to Schmidt and Rhoads were:

- Kaiser, Peter                      Roslin Institute, United Kingdom
- Nicholas, Frank                  University of Sydney, Australia
- Lyons, Eric                         University of Arizona
- Magor, Katharine                University of Alberta, Canada
- Sharif, Shayan                    University of Guelph, Canada

Summary of Accomplishments for each Objective

#### **Objective 1: Create and share data and technology to enhance the development and application of genomics and systems biology in poultry.**

- Further defined the genes on chicken chromosome16 regarding MHC functions.
- Developed a BAC- based integrated physical, genetic, and comparative map was developed for the turkey genome. The map was compared to the chicken map to identify important chromosomal rearrangements
- Used next generation sequence data for chicken cell lines for a new reference chicken genome assembly.
- Used proteomics to identify new chicken deubiquitinases to annotate these enzymes

and quantify their activity during Salmonella infection.

- Analyzed changes in gene expression of DNA methyltransferases in chicken embryonic tissues
- Used Next Generation Sequencing to Identify Genetic Adaptations Associated with Traits and disease (Animal Well-being, Disease Resistance, Domestication)
- Analyzed the literature for both chicken and turkey to develop a ranked list of prioritized genes for manual curation. These ranked gene lists will also be made publicly available via AgBase for community comment and feedback.
- Developed guidelines for standardized gene nomenclature for chicken genes to assign nomenclature to (1) MHC genes; (2) genes highly expressed in egg white, yolk and eggshell; (3) histone; and (4) myosin genes. This nomenclature is being shared with NCBI and Ensembl.
- Continued development of a tissue specific compendium of gene expression using RNA and proteome data for chicken gene products. This information is distributed through Chickspress.
- Used global genome sequencing for genetically selected chicken lines to identify regions affecting cancer progression, ascites, muscle quality, and vitiligo.
- Contributed RNAseq data for the chicken testis to Roslin Institute for a new chicken transcriptome assembly, to improve annotation of the genome
- Analyzed sites of MDV integration using temporal profiles of immune cells and tumors.
- Mapped and characterize additional class III MHC genes including the MHC-B of the Greater Prairie Chicken and Ocellated turkey.
- Measured MHC haplotype diversity within turkeys with a survey of haplotype variation in both commercial and wild turkeys using SNPs
- Quantified gene expression for the turkey MHC in different immune system tissues
- Collaborated on assembly of turkey genome build 5.0.
- Parallel Monte Carlo Markov Chain (MCMC) algorithms were applied to a dataset of 50K SNP genotypes to compute complex Bayesian models, which leads to a dramatic speedup in computing and can be used to optimize model parameters in complex Bayesian models.
- Bayesian Networks (BN) were used to capture several genetic markers associated as clusters, implying that markers are inter-related in a complicated manner. Further, the BN detected conditionally dependent markers. The results confirm that LD relationships are of a multivariate nature and that  $r^2$  gives an incomplete description and understanding of LD.
- An ensemble-based approach using different software was developed for imputation of moderate-density genotypes for genomic selection. The approach can solve imputation inconsistencies among different imputation methods, hence leading to a more reliable system for imputing genotypes.
- Maintained 39 chicken lines with special genetic characteristics for tumor or viral susceptibility that also differ for immunological and physiological traits.

**Objective 2: Facilitate the creation and sharing of poultry research populations and the collection and analysis of relevant new phenotypes including those produced by gene**

**transfer.**

- Maintained 13 unique chicken research lines [including highly inbred; MHC- congenic; closed populations; and advanced intercross lines (AIL)] that serve as resources for identifying genes and QTL of economic importance. Genetic material (chicks, fertile eggs, blood, tissues, DNA or RNA) has been shared with cooperating investigators to expand studies on the chicken genome.
- Developed methods for the first documented cases of germline transmission of cultured female primordial germ cells (PGCs)
- Participated in an NSF funded Research Coordination Network (RCN) to develop methods for phenotype-genotype analysis. Developed a chicken anatomy ontology for the adult chicken. The anatomy ontology will be used in project such as Chickspress, GEISHA, eChickAtlas and to curate chicken phenotype data.

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**Objective 3: Elucidate genetic mechanisms that underlie economic traits and develop new methods to apply that knowledge to poultry breeding practices.**

- Analyzed changes in gene expression for host responses to Marek's disease virus infection in susceptible and resistant spleens of chickens.
- Initiated a major research project to elucidate the genomics of heat resistance in poultry.
- Analyzed miRNA transcriptome in Marek's disease virus-induced lymphomas to identify differentially expressed miRNAs.
- Determined the genetic parameters for feed consumption, feed conversion ratio and residual feed intake in laying hens.
- Identified genomic regions affecting body weight and hen house production using genomic prediction methods in broiler chickens
- Used GWAS to map the chicken L alloantigen system to chromosome 4
- Employed GWMAS (Genome Wide Marker Assisted Selection) to address social and ethical concerns while at the same time demonstrating the power and limitations of GWMAS in a multi-generational selection experiment.
- Continued analysis of the genetic determinants contributing to low sperm mobility and reduced male fertility in roosters. Established primordial germ cell lines from high and low mobility research lines.
- Confirmed three chromosomal regions for linkage disequilibrium with ascites in three commercial line and three experimental lines. Candidate genes in these regions have been identified and are under investigation for sequence polymorphisms
- Identified a second vasotocin receptor, VT4R, that plays a role in the stress response of birds. Identified cell types in the brain expressing VT4R and analyzed changes in expression associated with stress.
- Used fine-mapping of chicken genomic aberrations to identify copy number variants associated with *Campylobacter jejuni* colonization
- Identified differentially expressed microRNAs associated with avian influenza virus infection in two genetically distinct chicken lines
- Refined mapping of several developmental mutants including: coloboma, wingless-2,

diplopodia-1, talpid-2, and cleft primary palate

- Conducted RNA-seq analysis to identify differentially expressed genes in the liver between broiler chickens with high and low feed efficiencies
- Designed a 6K LD panel based from 60K SNP genotypes of three parental pure lines. Then used the LD panel to impute genotypes of crossbreds using the pure lines, crossbreds or a 50:50 mix of pure lines and crossbreds as reference populations. Accuracy of imputation was over 96% for most scenarios, indicating that breeders can impute high-density genotypes of crossbred chickens with high accuracy.
- Investigated the genetics and developmental expression of the avian mTOR pathway and its affect on feed efficiency
- Initiated an exploratory study on the potential influence of Marek's disease virus (MDV) exposure on epigenetic regulation as it relates to MD incidences and disease risk.
- Determined that administration of the adrenal glucocorticoid (GC) corticosterone (CORT) during embryonic development can induce premature GH cell differentiation and increase growth of broiler chickens after hatch.
- Used RNA-seq to investigate the genomics of aflatoxin resistance in turkeys.
- Employed an integrated genomics approach for identification of genes and pathways that confer genetic resistance to Marek's disease. These include genome wide allele specific expression, RNA-seq, CHIP-seq, SNP arrays, profiling global gene expression.
- Analyzed expression of the peptide transporters, PepT1, PepT2, and PHT1 in the embryonic and post-hatch chick. A tissue by age interaction was observed for all genes. Determined that uptake of peptides in the developing chick is regulated by peptide transporters that are expressed in a tissue-and development-specific manner.

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#### **4. Summary of impact statements**

- Provided three significant insights into the genetics associated with GGA16. With continued effort these findings may lead to better means of selection of poultry for disease resistance and better strategies for initiating immune responses to vaccines.
- Identified genes and pathways associations with important biological traits in chickens.
- Identified genetic variation in commercial research chicken lines, and developed statistical methodology for the use of high-density SNP genotypes in genetic improvement, both of which are of potential value in genetic selection to improve commercial populations.
- Validated an experiment heat-stress model for study of the genomics of resistance to heat stress.
- Generated a comparative map on which the first draft of the turkey genome was assembled.
- New chicken genome sequences will provide data that can be used to improve the current draft assembly, which is deficient in several aspects.
- The culture and germline transmission avian of PGCs will have significant applications in reproductive biology, developmental biology, transgenics and conservation biology.
- Characterization of epigenetic regulatory mechanisms and genome elements responsible for variation in immune response from resource population genetic

information will provide new insights into genetic control of important health and production traits.

- Identification of signatures of selection and domestication will determine origins of domestication, elucidate the nature of genetic variation in inbred lines, and fine map genes associated with aggression in poultry.
- Developed software to call SNPs, find LD,  $F_{st}$ ,  $F_{is}$ , and Tajima D from sequencing data. This software has been used to find signatures of selection for a number of traits, including aggression and MD resistance
- The finding that the infinitesimal model is the most correct approximation to the true biological genetic variation for these traits implies the following: 1) ssGBLUP is more accurate than any SNP based method, such as BayesA, BayesB, or other such methods. Those methods assume a relatively small number of SNPs where effects can be estimated and selected for. In contrast, the infinitesimal model implies that genomic selection improves accuracy by increasing the precision with which relationships are estimated.
- Determined that GWAS for economic traits will find relatively few large effect QTLs
- Identified key parameters deriving from and affecting GWAS in poultry. The results imply that for some traits it will be possible to do genotype only selection for several generations before retraining will be necessary.
- Provided training, outreach and support for poultry researchers via AgBase to assist them to better leverage their functional genomics data to understand key economic traits for poultry.
- Provided fundamental annotation information (both structural and functional) for functional modeling of genomic data sets. This enables poultry researchers to more accurately identify genes involved in the systems they are studying and translate long lists generated by functional genomics into a biological model that they can use to improve poultry production.
- Telomere/telomerase dysregulation and Marek's disease virus (MDV). MDV is a major cause of mortality leading to substantial economic losses to the poultry industry. Interestingly, the oncogenic MDV genome (which is circular and has no need for a telomere-maintenance system) contains two copies of the chicken telomerase RNA gene as well as several sets of telomere repeats. We hypothesize the MDV is utilizing aspects of the telomere-telomerase system to integrate into the chicken genome at the site of telomeres, and that this contributes to aspects of the disease state – pathology, persistence and/or oncogenesis.
- Genetic developmental mutants under study are common to poultry and are similar to common human congenital malformations affecting limb, heart, and craniofacial features. The analyses will contribute to our understanding of genes and genetic mechanisms important to skeletal, limb and organ development.
- Preliminary results indicate there is differential gene expression between the broiler chickens with high and low feed efficiencies. The information will be useful in characterizing the biological basis of variability in broilers feed efficiency.
- Understanding the genetic and cellular mechanisms regulating GH production is

essential to develop novel strategies for improving broiler growth and feed efficiency through enhanced secretion of endogenous GH.

- Assembly of the turkey MHC has significantly advanced understanding of this locus in poultry. Three MHC regions have been assembled and compared with the closely related Ocellated turkey.
- A shared set of genes and SNPs that exhibit allele specific expression in response to MDV infection have been identified between experimental layers and broilers, which suggests common pathways and possibly causative polymorphisms for MD response. These SNPs can be used as genetic markers in resource populations to directly test whether the associated genes confer genetic resistance and incorporated into genetic selection programs.
- Furthered our understanding of host genetics influences over MD vaccine efficacy which is important for vaccine development and usage.
- Understanding the functional roles of peptide transporters is fundamental for assessing the uptake and utilization of peptides for growth and development. Some are important for uptake of dietary peptides in the intestine, while others are important in the reabsorption of peptides in the kidney and regulation of neuropeptide concentrations in the brain.

## **5. Publications for 2012**

### Journal Articles, and Book Chapters

- Ammari M, McCarthy FM, Nanduri B, Pinchuk G, Pinchuk L (2012). Understanding the Pathogenesis of Cytopathic and Noncytopathic Bovine Viral Diarrhea Virus Infection Using Proteomics. Book Chapter in: Proteomic Applications in Biology, ISBN: 978-953-307-613-3, InTech. Edited by: Joshua L. Heazlewood and Christopher J. Petzold, Subject editors: Tsz-Kwong Man, Ricardo J. Flores.
- Baurhoo B, Ferket P, Ashwell CM, de Oliveira J, Zhao X. 2012. Cell Walls of *Saccharomyces cerevisiae* Differentially Modulated Innate Immunity and Glucose Metabolism during Late Systemic Inflammation. *PLoS One*. 7(1):e30323.
- Bhatti M, Fan R, Muir WM, Pruett SB, Nanduri B. Transcriptomic analysis of peritoneal cells in a mouse model of sepsis: confirmatory and novel results in early and late sepsis. *BMC Genomics*. 2012 Sep 25;13(1):509.
- Bignardi, A. B., El Faro, L., Rosa, G. J. M., Cardoso, V. L., Machado, P. F., and Albuquerque, L. G. Bayesian analysis of random regression models using B-splines to model test-day milk yield of Holstein cattle in Brazil. *Livestock Science* 150: 401-406, 2012.
- Bignardi, A. B., El Faro, L., Rosa, G. J. M., Cardoso, V. L., Machado, P. F., and Albuquerque, L. G. Principal components and factor analytic models for test-day milk yield in Brazilian Holstein cattle. *Journal of Dairy Science* 95(4): 2157-2164, 2012.
- Bottje WG, Kong BW, Song JJ, Lee J, Hargis BM, Lassiter K, Wing T and Hardiman J. 2012. Gene expression in breast muscle associated with feed efficiency in a single male broiler line using a chicken 44k microarray II. Differentially expressed focus genes. *Poultry Science*. 91(10):2576-87.



- Carlson, D. F., W. Tan, A. M. Geurts, C. R. Long, W. Muir et al. 2012 Adding and subtracting livestock genes with transposons and nucleases. *Transgenic Research* 21: 901-902
- Chandra YG, Lee JY, and Kong BW. 2012. Genome sequence comparison of two vaccine infectious laryngotracheitis virus (ILTV) strains. *Virus Genes*. 44(3):470-4
- Chang, S., J.R. Dunn, M. Heidari, L. Lee, C.W. Ernst, J. Song, H.M. Zhang. 2012. Vaccine by chicken line interaction alters the protective efficacy against challenge with a very virulent plus strain of Marek's disease virus in White Leghorn chickens. *World J. Vaccines* 2:1-11.
- Cheng, H. H., S. MacEachern, S. Subramaniam, and W. M. Muir, 2012 Chicks and single-nucleotide polymorphisms: an entree into identifying genes conferring disease resistance in chicken. *Animal Production Science* 52: 151-156
- Coble, D.J., Sandford, E. E., Ji, T., Abernathy, J., Fleming, D., Zhou, H., and Lamont, S.J. 2012. Impacts of *Salmonella enteritidis* infection on liver transcriptome in broilers. *Genesis* (on line) DOI: 10.1002/dvg.22351
- Dekkers, J.C.M., 2012. Application of genomics tools to animal breeding. *Curr. Genomics* 13: 207-212.
- Dorshorst B, Molin AM, Rubin CJ, Johansson AM, Strömstedt L, Pham MH, Chen CF, Hallböök F, Ashwell C, Andersson L. 2011. A complex genomic rearrangement involving the endothelin 3 locus causes dermal hyperpigmentation in the chicken. *PLoS Genet.* Dec;7(12):e1002412.
- Duan, KM, Ware, T. McCullough, WM. Surette, MG. Song, JZ. 2012 Comprehensive Analysis of Gene-Environmental Interactions with Temporal Gene Expression Profiles in *Pseudomonas aeruginosa*. *Plos One* 7(4): e35993
- Ek, W., Marklund, S., Ragavendran, A., Siegel, P.B., Muir, W., Carlborg, O. 2012. Generation of a multi-locus chicken introgression line to study the effects of genetic interactions on metabolic phenotypes in chickens. *Frontiers in Genetics-Genetic Architecture* 3:1-4.
- Ellestad LE, Porter TE (2013) Ras-dva is a novel Pit-1- and glucocorticoid-regulated gene in the embryonic anterior pituitary gland. *Endocrinology* 154:308-319
- Fang, HB. Deng, D. Tian, GL. Shen, L. Duan, K. and Song, JZ. 2012 Analysis for Temporal Expressions under Multiple Biological Conditions. *Statistics in Biosciences*. (2012) 4:282–
- Froman, D. P., and D. D. Rhoads. 2012. A systems biology definition for chicken semen quality. *Journal of Animal Science*. Published online before print October 16, 2012, doi: 10.2527/jas.2012-5681
- Froman, D. P., and D. D. Rhoads. 2012. Validation of a spectrophotometer-based method for estimating daily sperm production and deferent duct transit. *Poultry Science* 91: 2621- 2627.
- Garcia, D. A., Pereira, I. G., Silva, F. F. E., Rosa, G. J. M., Pires, A. V., and Leandro, R. A. Generalized linear mixed models for the genetic evaluation of binary reproductive traits: a simulation study. *Brazilian Journal of Animal Science* 41(1): 52-57, 2012.
- Gianola, D., Rosa, G. J. M. and Allison, D. B. Humble thanks to a gentle giant (an obituary for James F. Crow) *Frontiers in Genetics* 3: 93, 2012. doi: 10.3389/fgene.2012.00093

- He Y, Yu, Y. Zhang, Y. Song, JZ. Mitra, A. Zhang, Y. Wang, Y. Sun, D. Zhang, S. 2012 Genome-wide Bovine H3K27me3 Modifications and the Regulatory Effects on Genes Expressions in Peripheral Blood Lymphocytes. *Plos One* 7(6): e39094.
- Heuck-Knubel K, Proszkowiec-Weglarz M, Narayana J, Ellestad LE, Prakobsaeng N, Porter TE (2012) Identification of cis-elements necessary for glucocorticoid induction of growth hormone gene expression in chicken embryonic pituitary cells. *Am J Physiol* 302:R606-619
- Kaiser, M.G., Block, S.S., Ciraci, C., Fang, W., Sifri, M., and Lamont, S.J. 2012. Effects of dietary vitamin E type and level on LPS-induced cytokine mRNA expression in broiler chicks. *Poultry Sci.*91:1893-1898.
- Kanayeva, D.A., R Wang, D Rhoads, GF Erf, MF Slavik, S Tung, Y Li. 201. Efficient separation and sensitive detection of *Listeria monocytogenes* using an impedance immunosensor based on magnetic nanoparticles, microfluidic chip and interdigitated microelectrode. *Journal of Food Protection* 75:1951-1959.
- Kogut, M, Hsin-I Chiang, Christi Swaggerty, Huaijun Zhou. 2012. Gene Expression Analysis of Toll-like Receptor Pathways in Heterophils from Genetic Chicken Lines That Differ In Their Susceptibility to *Salmonella enteritidis*. *Frontiers in Epigenomics* accepted
- Korrida, A., S. Jadallah, F. Chbel, A. Amin-Alami, M. Ahra and S.E. Aggrey, 2012. Patterns of genetic diversity and population structure of the threatened Houbara and Macqueen's bustard as revealed by microsatellite markers. *Genetics and Molecular Research (GMR)* 11: 3207-21.
- Korrida, A., S.N. Nahashon, A. Amin-Alami, S. Jadallah, and S.E. Aggrey, 2012. Modeling absolute and allometric growth in Houbara Bustard (*Chlamydotis undulate undulate*) in captivity. *Atlas J. Biol.* 2: 110-115.
- Kumar R, Lawrence ML, Watt J, Cooksey AM, Burgess SC, Nanduri B. RNA-seq based transcriptional map of bovine respiratory disease pathogen "*Histophilus somni* 2336". *PLoS One.* 2012;7(1):e29435.
- Kumar S, Kunec D, Buza JJ, Chiang HI, Zhou H, Subramaniam S, Pendarvis K, Cheng HH, Burgess SC. (2012). Nuclear Factor kappa B is central to Marek's disease herpesvirus induced neoplastic transformation of CD30 expressing lymphocytes in-vivo. *BMC Syst Biol.* 14;6:123. doi: 10.1186/1752-0509-6-123.
- Lee JY, Bottje WG, and Kong BW. 2012. Genome-wide host responses against infectious laryngotracheitis virus vaccine infection in chicken embryo lung cells. *BMC Genomics* 13:143.
- Lee, L.F., M. Heidari, H.M. Zhang, B. Lupiani, S. Reddy and A. Fadly, 2012. Cell culture attenuation eliminates rMd5deltaMeq-induced bursal and thymic atrophy and renders the mutant virus as an effective and safe vaccine against Marek's disease. *Vaccine* 30:5151-5158.
- Li, H., J. Ji, Q.M. Xie, H. Shang, H.M. Zhang, X. Xin, F. Chen, B. Sun, C. Xue, J. Ma, Y. Bi. 2012. Aberrant expression of liver microRNA in chickens infected with subgroup J avian leukosis virus. *Virus Res.* 169:268-271.
- Lian, L., Ciraci, C., Chang, G., Hu, J., and Lamont, S.J. 2012. NLRC5 knockdown in chicken macrophages alters response to LPS and poly (I:C) stimulation. *BMC Vet. Res.* 8:23

doi:10.1186/1746-6148-8-23

- Lian, L., Qu, L., Chen, Y., Lamont S. J., and Yang, N. 2012. A systematic analysis of miRNA transcriptome in Marek's disease virus-induced lymphoma reveals novel and differentially expressed miRNAs. *PLoS ONE* 7(11): e51003. doi:10.1371/journal.pone.0051003
- Lian, L., Sun, H. Qu, L., Chen, Y., Lamont, S., Yang, N. 2012. Gene expression analysis of host responses to Marek's disease virus infection in susceptible and resistant spleens of chickens. *Poultry Sci.* 91: 2130-2138.
- Luo, J. Mitra, A., Tian F. Chang S. Zhang H. Cui K. Zhao, K. Yu, Y. and Song, JZ. 2012 Genome-wide Histone Methylation Analysis and New Pathway Predictions in MD-resistant and MD-susceptible Chickens after MDV Infection. *Plos One* 7(7): e41849.
- Luo, J. Yu, Y. Chang, S. Zhang H. Tian, F. and Song JZ. 2012 Analysis of DNA methylation and virus induced DNA methylation change in MD-resistant and – susceptible chickens. *Frontiers in Epigenomics* doi: 10.3389
- Luo, J., Y. Yu, S. Chang, F. Tian, H.M. Zhang, and J. Song, 2012. DNA methylation fluctuation induced by virus infection differs between MD-resistant and – susceptible chickens. *Frontiers Genetics* 3:1-15.
- MacEachern S. ,WM Muir, SD Crosby, and HH.Cheng 2012. Genome-wide identification and quantification of cis- and trans- regulated genes responding to Marek's disease virus infection via analysis of allele-specific expression. *Frontiers in Genetics.* 2:1-11.
- Manda P., Ozkan S., Wang H., McCarthy FM and Bridges SM. (2012). Cross-ontology Multi-level Association Rule Mining in the Gene Ontology. *PLoS One* 7(10):e47411. doi: 10.1371/journal.pone.0047411.
- Meisenberg C, Tait PS, Dianova II, Wright K, Edelmann MJ, Ternette N, Tasaki T, Kessler BM, Parsons JL, Kwon YT, Dianov GL. Ubiquitin ligase UBR3 regulates cellular levels of the essential DNA repair protein APE1 and is required for genome stability. *Nucleic Acids Res.* 2012 Jan;40(2):701-11.
- Mitra, A. and Song, JZ. 2012 WaveSeq: A Novel Data-driven Method of Detecting Histone Modifications using Wavelets. *Plos One* 7(9): e45486.
- Mitra, A., J. Luo, H.M. Zhang, K. Zhao, J. Song, and K. Cui, 2012. Marek's disease virus infection induces widespread differential chromatin marks in inbred chicken lines. *BMC Genomics* 13:557.
- Morota, G., Valente, B. D., Rosa, G. J. M., Weigel, K. A. and Gianola, D. An assessment of linkage disequilibrium in Holstein cattle using a Bayesian network. *Journal of Animal Breeding and Genetics* 129: 474-487, 2012.
- Mukherjee M, Porter TE (2012) Differential abilities of chicken Pit1 isoforms to regulate the GH promoter: Evidence for synergistic activation. *Endocrinology* 153:3320-3330
- Nanduri B, Suvarnapunya AE, Venkatesan M, Edelmann MJ. Deubiquitinating Enzymes as Promising Drug Targets for Infectious Diseases. *Curr Pharm Des.* 2012 Nov 2
- NG, C.S., P. Wu, J. Foley, A. Foley, M. McDonald, S. Leal, W. Juan, C. Huang, Y. Lai, W. Lo, C. Chen, H.M. Zhang, R. Widelitz, P. Patel, W. Li, and C.M. Chuong, 2012. The chicken frizzle feather is due to an  $\alpha$ -keratin (KRT75) mutation that causes a defective rachis. *PLoS Genet.* 8:e1002748.

- Nie, Q., Sandford, E.E., Nolan, L.K., Zhang, X., Lamont, S.J. 2012. Deep sequencing-based transcriptome analysis of chicken spleen in response to avian pathogenic *Escherichia coli* (APEC) infection, PLoS ONE 7(7): e41645. doi:10.1371/journal.pone.0041645
- Payne A, Schmidt TB, Nanduri B, Pendarvis K, Pittman JR, Thornton JA, Grissett J, Donaldson JR. Proteomic analysis of the response of *Listeria monocytogenes* to bile salts under anaerobic conditions. J Med Microbiol. 2013 Jan;62(Pt 1):25-35.
- Pérez-Cabal, M. A., Vazquez, A. I., Gianola, D., Rosa, G. J. M., and Weigel, K. A. Accuracy of genome-enabled prediction in a dairy cattle population using different cross-validation layouts. Frontiers in Genetics 3:27, 2012. doi: 10.3389/fgene.2012.00027
- Petite, J.N. and Pardue, S.L. Depletion of endogenous primordial germ cells in avian species. US Patent #7,994,388.
- Pillai L, Chouvarine P, Tudor CO, Schmidt CJ, Vijay-Shanker K, McCarthy FM. (2012). Developing a biocuration workflow for AgBase, a non-model organism database. Database 2012:bas038. doi: 10.1093/database/bas038.
- Piyasatian, N., R.L. Fernando, and J.C.M. Dekkers. 2012. QTL detection and marker-assisted composite line development. Livestock Sci. 143: 233-241.
- Powell, J. E., Kranis, A., Floyd, J., Dekkers, J. C. M., Knott, S. and Haley, C. S. 2012. Optimal use of regression models in genome-wide association studies. Animal Genetics, 43: 133–143.
- Pungpapong , V. W.M. Muir, X Li, D Zhang, and M. Zhang. A Fast and Efficient Approach for Genomic Selection with High-Density Markers. G3 Genes, Genomes, Genetics 2012. 2: 1179–1184
- Qiu R, Croom J, Ali RA, Ballou AL, Smith CD, Ashwell CM, Hassan HM, Chiang CC, Koci MD. 2012. Direct fed microbial supplementation repartitions host energy to the immune system. J Anim Sci. Aug;90(8):2639-51.
- Qu, L., D. Nettleton, and J.C.M. Dekkers. 2012. Improved estimation of the noncentrality parameter distribution from a large number of t-statistics, with applications to false discovery rate estimation in microarray data analysis. Biometrics. doi: 10.1111/j.1541-0420.2012.01764.x
- Reddy JS, Kumar R, Watt JM, Lawrence ML, Burgess SC, Nanduri B. Transcriptome profile of a bovine respiratory disease pathogen: *Mannheimia haemolytica* PHL213. BMC Bioinformatics. 2012;13 Suppl 15:S4.
- Robb, E., and M.E. Delany. 2012. Polydactyly in an avian biomedical model: A genetic study of pre-axial variation and genomic maintenance. Cytogenetic and Genome Research 136:50-68.
- Robb, E.A., and M.E. Delany. 2012. Case study of sequence capture enrichment technology: Identification of variation underpinning developmental syndromes in an amniote model. Genes. 3:233-247
- Rosa, G. J. M. Foundations of Animal Breeding. In: Encyclopedia of Sustainability Science and Technology. Meyers, R. A. (Editor). New York: Springer, 2012
- Ross, M. K., & Edelman, M. J. (2012). Carboxylesterases: A Multifunctional Enzyme Involved in Pesticide and Lipid Metabolism. Parameters for Pesticide QSAR and PBPK/PD models for Human Risk Assessment. ACS Books. 1099.

- Samuel, D., S. Trabelsi, A. B. Karnuah, N. B. Anthony and S.E. Aggrey, 2012. The use of dielectric spectroscopy as a tool for predicting meat quality in poultry. *Int. J. Poultry Sci.* 11: 551-555.
- Sandford E, M. Orr , M. Shelby, X. Li , H. Zhou , T. J Johnson , S. Kariyawasam , P. Liu , L K Nolan and S. J Lamont. 2012. Leukocyte transcriptome from chickens infected with avian pathogenic *Escherichia coli* identifies pathways associated with resistance. *Results in Immunology*, 2:44-53
- Sandford, E.E., Orr, M., Li, X., Zhou, H., Johnson, T.J., Kariyawasam, S., Liu, P., Nolan, L.K., Lamont, S.J. 2012. Strong concordance between transcriptomic patterns of spleen and peripheral blood leukocytes in response to avian pathogenic *Escherichia coli* infection. *Avian Diseases* 56:732-736.
- Selvam, R., A. Jurkevich, S. Kang, M. Mikhailova, L. Cornett, and W. Kuenzel. 2013. Distribution of the vasotocin subtype four receptor (VT4R) in the anterior pituitary gland of the chicken, *Gallus gallus*, and its possible role in the avian stress response. *Journal of Neuroendocrinology* 25:56-66.
- Shi F, Kong BW, Song JJ, Lee JY, Dienglewicz RL and Erf GF. 2012. Understanding mechanisms of vitiligo development in Smyth line of chickens by transcriptomic microarray analysis of evolving autoimmune lesions. *BMC Immunology*. 13:18.
- Shim, M, A. B. Karnuah, N.B. Anthony, and S. E. Aggrey, 2012. The effects of broiler chicken growth rate on valgus, varus and tibial dyschondroplasia. *Poultry Sci.* 91: 62-65.
- Shim, M., A.B. Karnuh, A.D. Mitchell, N. B. Anthony, G.M. Pesti and S.E. Aggrey, 2012. The effect of growth rate on leg morphology, tibia breaking strength, mineral density, mineral content and bone ash in broilers. *Poultry Science* 91: 1790-5.
- Shim, M.Y., M. Tahir, A. B. Karnuah, M. Miller, T.D. Pringle, S.E. Aggrey and G.M. Pesti, 2012. Strain and sex effects on growth performance and carcass traits of contemporary commercial crosses of broilers. *Poultry Science* 91: 2942-8
- Shiotsuki, L., Cardoso, F. F., Silva, J. A. I. V., Rosa, G. J. M., and Albuquerque, L. G. Evaluation of an average numerator relationship matrix model and a Bayesian hierarchical model for growth traits in Nellore cattle with uncertain paternity. *Livestock Science* 144: 89- 95, 2012.
- Simon J, Milenkovic D, Godet E, Cabau C, Collin A, Métayer-Coustard S, Rideau N, Tesseraud S, Derouet M, Crochet S, Cailleau-Audouin E, Hennequet-Antier C, Gespach C, Porter TE, Duclos MJ, Dupont J, Cogburn LA (2012) Insulin immuno-neutralization in fed chickens: effects on liver and muscle transcriptome. *Physiol Genomics* 44:283-292
- Speier, J.S., Yadgary, L., Uni, Z., and Wong, E.A. 2012. Gene expression of nutrient transporters and digestive enzymes in the yolk sac membrane and small intestine of the developing embryonic chick. *Poult. Sci.* 91: 1941-1949.
- Sun, C., Wu, X. L., Weigel, K. A., Rosa, G. J. M., Bauck, S., Woodward, B. W., Schnabel, R. D., Taylor, J. F. and Gianola, D. An ensemble-based approach to imputation of moderate- density genotypes for genomic selection with application to Angus cattle. *Genetics Research* 94: 133–150, 2012.
- Tian, F. Luo, J. Zhang, H. and Song JZ. 2012 Marek's Disease Virus Challenge Induced Immune-Related Gene Expression and Chicken Repeat 1 (CR1) Methylation Alterations

in Chickens. *American Journal of Molecular Biology* 2, 232-241

- Tian, F., J. Luo, H.M. Zhang, S. Chang, and J. Song. 2012. MiRNA expression signatures induced by Marek's disease virus infection in chickens. *Genomics* 99:152-159.
- Van Eenennaam, A. and W.M. Muir 2012. *Animal Biotechnologies And Agricultural Sustainability*. In *The Role of Biotechnology in a Sustainable Food Supply*. Eds Jennie Popp, Marty Matlock, Nathan Kemper, Molly Jahn. Cambridge University Press
- Vazquez, A. I., de los Campos, G., Klimentidis, Y. C., Rosa, G. J. M., Gianola, D., Yi, N. and Allison, D. B. A Comprehensive genetic approach for improving prediction of skin cancer risk in humans. *Genetics* 192: 1493-1502, 2012.
- Vazquez, A. I., Perez-Cabal, M. A., Heringstad, B., Rodrigues-Motta, M., Rosa, G. J. M., Gianola, D., and Weigel, K. A. Predictive ability of alternative models for genetic analysis of clinical mastitis. *Journal of Animal Breeding and Genetics* 129(2): 120-128, 2012.
- Velleman SG, Sporer KRB, Ernst CW, Reed KM, and Strasburg GM. 2012. Versican, matrix Gla protein, and death-associated protein expression affect muscle satellite cell proliferation and differentiation. *Poultry Science*, 91:1964- 1973.
- Wang, Y., Vinayak Brahmakshatriya, Blanca Lupiani, Sanjay M Reddy, Benjamin Soibam, Ashley L Benham, Preethi Gunaratne, Hsiao-ching Liu, Mares Trakooljul, Nancy Ing, Ron Okimoto and Huaijun Zhou 2012. Integrated Analysis of microRNA Expression and mRNA Transcriptome in Lungs of Avian Influenza Virus Infected Broilers. *BMC Genomics* 13:278
- Wang,H, I. Misztal, I. Aguilar, A. Legarra, and W. M. Muir Genome-wide association mapping including phenotypes from relatives without genotypes. 2012. *Genetics Research* 94:73-83
- Wideman, RF, D. D. Rhoads, G. F. Erf, and N. B. Anthony. 2013. Pulmonary Arterial Hypertension (PAH, Ascites Syndrome) in Broilers: A Review. *Poultry Science* 92:64- 83.
- Wolc, A., J. Arango, P. Settar, J.E. Fulton, N.P. O'Sullivan, R. Preisinger, D. Habier, R. Fernando, D.J. Garrick, W.G. Hill and J.C.M. Dekkers. 2012. Genome-wide association analysis and genetic architecture of egg weight and egg uniformity in layer chickens. *Animal Genetics* 47: 87-96.
- Wolc, A., J. Arango, P. Settar, N.P. O'Sullivan, V.E. Olori, I.M.S. White, W.G. Hill, and J.C.M. Dekkers. 2012. Genetic parameters of egg defects and egg quality in layer chickens. *Poultry Sci.* 91: 1292-1298.
- Wu, X.-L., Sun, C., Beissinger, T. M., Rosa, G. J. M., Weigel, K. A., de Leon, N. and Gianola, D. Parallel Markov chain Monte Carlo - bridging the gap to high-performance Bayesian computation in animal breeding and genetics. *Genetics Selection Evolution* 44: 29, 2012.
- Xie, X., Zheng, L., Yu, Y., Liang, L., Guo, M., Song JZ. And Yuan, Z. 2012 Protein sequence analysis based on hydropathy profile of amino acids. *Journal of Zhejiang University - Science B* Volume 13, Number 2, 152-158,
- Xu, M., S. Fitzgerald, H.M. Zhang, D. Karcher, M. Heidari, 2012. Very virulent plus strains of MDV induce acute form of transient paralysis in both susceptible and resistant chicken lines. *Viral Immunol.* 25:306-323.
- Yokoo, M. J., Magnabosco, C. U., Rosa, G. J. M., Lobo, R. B., and Albuquerque, L. G. Reproductive traits and their associations with other economically important traits in Nelore. *Arquivo Brasileiro de Medicina Veterinaria e Zootecnia* 64(1): 91-100, 2012.

- Yuan, P. Yu, Y. Luo, J. Tian, F. Zhang, H. Chang, S. Ramachandran, R. Song JZ. 2012 Comparative study of lipoprotein metabolism in Marek's disease susceptible and resistant chickens. *Poultry Science* 91:2598-2605.
- Yuan, P., Y. Yu, J. Luo, F. Tian, H.M. Zhang, S. Chang, R. Ramachandran, L. Zhang, J. Song. 2012. Lipoprotein metabolism differs between Marek's disease susceptible and resistant chickens. *Poultry Sci.* 91:2598-2605.
- Zhang L, Katselis GS, Moore RE, Lekpor K, Goto RM, Hunt HD, Lee TD, Miller MM. 2012. MHC class I target recognition, immunophenotypes and proteomic profiles of natural killer cells within the spleens of day-14 chick embryos. *Dev Comp Immunol* 37:446-56.

#### Dissertations

- Chouvarine, Philippe. Genomic and functional analysis of next-generation sequencing data. PhD dissertation, Mississippi State University, Starkville MS, June 2012.
- Prashanti Manda. Novel algorithms for cross-ontology, multi-level data mining. PhD dissertation, Mississippi State University, Starkville MS, October 2012.
- Krishnamoorthy, S. (2012) Investigation of a Locus on Chromosome 9 for Contributions to Pulmonary Hypertension Syndrome in Broilers. PhD Dissertation. University of Arkansas
- Jeeyoung Lee. Molecular basis of feed efficiency in meat-type birds, 2012, University of Georgia Library.
- Amal Korrida. Houbara bustards "Chlamydotis undulate and Macqueen's bustards "Chlamydotis macqueni: Genetic, morphometric and phylogeographic studies., 2012. Ibn Zohr University Library, Agadir, Morocco.
- Fei Tian: Genome-wide analysis of chicken miRNAs and DNA methylation and their roles in Marek's disease resistance and susceptibility. Doctor of Philosophy, 2012, University of Maryland

#### **6. Leveraging and Funding**

- MHC-Y Class I Determinants in Innate and Adaptive Immune Responses to Marek's Disease, USDA NIFA-AFRI 09/09-8/13, \$370,000; role: PI Miller.
- USDA-NIFA-AFRI competitive research grant. "Use of high-density SNP genotyping for genetic improvement of livestock" Dekkers et al.
- USDA-NIFA-AFRI competitive research grant. "Adapting chicken production to climate change through breeding" Schmidt et al.
- USDA-NRI competitive research grant. "Pathogen Interactions in Avian Colibacillosis: a Systems-Based, Functional Genomics Approach, Nolan et al.
- Poultry coordinator funds, \$65,000; PI: Dodgson
- EPSCoR Research Infrastructure Improvement Program Source of support: National Science Foundation. 09/01/11 - 06/30/13 co-PI: Edelman
- Identification of biological networks responsive to metal oxide nanoparticles in human bronchial epithelial cells. NSF EPSCoR. 2/01/2011-6/30/2013 co PI: Edelman
- Role of the ubiquitin proteasome system in foodborne disease – proteomic analysis of deubiquitinating enzymes and ubiquitinated substrates in Salmonella infection. MAFES

Strategic Research Initiative Program. 01/01/2012-12/30/2012. PI: M.J Edelman

- Novel Approaches for Biomarker and Drug Target Discovery in The Foodborne Illness Shigellosis. MAFES Strategic Research Initiative Program. 01/01/2011-6/30/2012. PI: Edelman
- Physiological Functions of Deubiquitinating Enzymes as Potential Drug Targets in Foodborne Disease Salmonellosis. USDA ARS. 07/01/11 - 06/30/12 PI: MJ Edelman
- Quantitative Studies of the Effects of Oil Exposure on the Pelagic Microbial Community and Sheepshead Minnow, Using a Global Proteomics Approach. BP America. 01/01/11 - 5/31/12PI: MJ Edelman, T Pechan
- NIH-NCI-2007-0617, Comparative proteomics applied to the avian model of ovarian cancer USDA-NIFA- 2010-04201 Adapting chicken production to climate change through breeding
- National Research Initiative Competitive Grant no. 2008-35205-04723. PI Muir
- Agriculture and Food Research Initiative Competitive Grant no. 2009-65205-05665 USDA-AFRI Enhancing genetic resistance to Marek's disease in chicken via allele-specific expression screens and genome-wide selection
- NIH NIGMS Project Number: 07111084: Experimental annotation of the Chicken Genome. 2009-2013.
- USDA AFRI Competitive grant 0224891: Knowledge representation resources for agricultural researchers. 2011-2013.
- The chicken anatomy ontology project is paid for in part by NRSP8 Bioinformatics funds and by the Mississippi State University Institute for Genomics, Biocomputing & Biotechnology (IGBB).
- A Gene-Based, Quantitative Definition for Semen Quality. NIFA-AFRI, 11/10-10/13, \$500,000; PI: Froman.
- REU Site: Applied Biotechnology in the Life Sciences. NSF, \$332,865, 5/11-4/14, PI Rhoads
- SNP chip mapping of REL line samples. Arkansas Biosciences Institute, \$29,612; 7/12-6/13; PI Rhoads
- Funding for the Poultry Workshop at Plant and Animal Genome. NIFA-AFRI Food Security; 1/13-12/14; \$36,000,PI Schmidt
- Central neural plasticity of the avian vasotocinergic system during stress. NSF; 1/1/2009-12/31/2012; \$348,473; PI, PI Kuenzel
- Identification of stress receptor blockers in an avian biomedical model of stress. AR Biosciences Institute (ABI), 7/1/2011- 6/30/2012; \$50,000 PI Kuenzel
- Whole-genome sequencing for genetically selected chicken lines important for both biomedical models and agriculture in Arkansas. AR Biosciences Institute (ABI) 7/2011-6/2012, \$50,000 PI Kong
- Effects of non-ventilation during early incubation of broiler eggs on bioenergetics and oxidative stress in broilers pre- and post-hatch. Poultry & Egg Assoc., Research Project #669. 07/2011-06/2012; \$34,435 PI: Bottje, coPI Kong
- Ultra-sensitive, low-cost nanorod sensors to detect blood serum microRNA biomarkers.



AR Biosciences Institute (ABI), 7/2011-6/2012; \$26,900 PI: Ji, Co-PI: B. Kong.

- System Biology Analysis & Modeling of Complex “OMIC” Data: A Service Center Approach. Agriculture and Food Research Initiative Competitive Grant no. 2011-67015-30196
- USDA NRI Competitive research grant: “Integration of Gene expression, SNP and Nutrient Digestibility analysis to improve feed efficiency in meat-type birds. S.E. Aggrey et al.
- Adisseo “Molecular mechanisms underlying methionine utilization in meat type chickens. S.E. Aggrey and G. M Pesti.
- National Research Initiative Competitive Grant no. USDA-NRI/NIFA 2008-35204-04660 National Institute of Food and Agriculture Grant no. USDA-NRI/NIFA 2010-65205-20588
- Minnesota Agricultural Experiment Station. Multi-State Project, RNA-Seq in horse and turkey transcriptomics. 2010-2013. \$80,700 (co-PI Reed, w/J. Mickelson, M. McCue and S. Valberg).
- Minnesota Agricultural Experiment Station. Application of new sequencing technologies to investigate locus remodeling and CNV in the MHC of turkey. 2012-2013 \$24,969. PI Reed
- CVM Emerging Zoonotic Disease Signature Program Pilot Grant, Elucidating the complexities of Escherichia coli Peritonitis in Commercial Laying Hens. 2013- 2014 \$48,215. (coPI Reed, w/Johnson).
- United States Department of Agriculture, AFRI. Reference genome sequence for the turkey, Meleagris gallopavo. 2010-2013. \$908,280 (Reed co-PI w/ R. Dalloul, O. Folkerts and E. Smith).
- United States Department of Agriculture, NRICGP. The turkey MHC: Sequence, haplotype structure and gene expression. 2009-2013. \$447,663 (PI Reed w/ M. Rutherford).
- Inferring Causal Phenotype Networks Using Genomic Information. NIFA-AFRI, 03/11-02/14, \$467,290; PI Rosa.
- Development of Efficient Design and Statistical Analysis Strategies for Genome-Wide Association Studies in Livestock. NIFA-HATCH, 10/09-09/13, \$146,344; PI Rosa.
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marker-assisted selection (GWMAS) over multiple generations in commercial poultry.

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- Nutrition of the developing chick embryo: nutrient uptake systems of the yolk sac membrane and embryonic intestine. Wong, E.A. and Uni, Z. Binational Agricultural Research and Development (BARD), 2008-2012.

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