

NRSP8 Journal Publications for 2012

AQUACULTURE

Beck BH, Farmer BD, Straus D, Li C, Peatman E (2012) Putative roles for a rhamnose binding lectin in *Flavobacterium columnare* pathogenesis in channel catfish *Ictalurus punctatus*. *Fish Shellfish Immunology* 33:1008-1015

Arias CR, Cai W, Peatman E, Bullard SA (2012) Channel Catfish x Blue Catfish Hybrid Exhibits Higher Resistance to *Columnaris* Disease as Compared to Its Parental Species. *Diseases of Aquatic Organisms* 100(1):77-81.

Li C, Zhang Y, Wang R, Lu J, Nandi S, Mohanty S, Terhune S, Liu Z, and Peatman E (2012) RNA-seq analysis of mucosal immune responses reveals signatures of intestinal barrier disruption and pathogen entry following *Edwardsiella ictaluri* infection in channel catfish, *Ictalurus punctatus*. *Fish Shellfish Immunology* 32(5):816-27

Sun* F, Peatman* E, Li C, Liu S, Jiang Y, Zhou Z, Kucuktas H, Liu Z (2012) Host Signatures of Attachment, NF- κ B Suppression and IFN Stimulation in the Channel Catfish (*Ictalurus punctatus*) Gill Transcriptome Following *Flavobacterium Columnare* Challenge. *Dev Comp Immunol* 38(1):169-80

Ninwichian, Peatman E, Perrera D, Liu S, Dunham R, Liu Z (2012) Identification of a sex-linked marker in channel catfish. *Animal Genetics* 43(4):476

Rajendran KV, Zhang J, Liu S, Peatman E, Kucuktas H, Wang X, Liu H, Wood T, Terhune J, Liu Z (2012) Pathogen recognition receptors in channel catfish: II. Identification, phylogeny and expression of retinoic acid-inducible gene I (RIG-I)-like receptors. *Dev Comp Immunol* 37(3-4):381-9

Zhang H, Peatman E, Liu H, Feng T, Chen L, Liu Z (2012) Molecular characterization of three L-type lectin genes from channel catfish, *Ictalurus punctatus* and their responses to *Edwardsiella ictaluri* challenge. *Fish Shellfish Immunology* 32(4):598-608.

Rajendran KV, Zhang J, Liu S, Kucuktas H, Wang X, Liu H, Sha Z, Terhune J, Peatman E, Liu Z (2012) Pathogen recognition receptors in channel catfish: I. Identification, phylogeny and expression of NOD-like receptors. *Dev Comp Immunol* 37(1):77-86

Zhou Z, Liu H, Liu S, Sun F, Peatman E, Kucuktas H, Kaltenboeck L, Feng T, Zhang H, Niu D, Lu J, Waldbieser G, Liu Z (2012) Alternative complement pathway of channel catfish (*Ictalurus punctatus*): Molecular characterization, mapping and expression analysis of factors Bf/C2 and Df. *Fish Shellfish Immunol* 32:186-95.

Zhang H, Peatman E, Liu H, Niu D, Feng T, Kucuktas H, Waldbieser G, Chen L, Liu Z (2012) Characterization of a mannose-binding lectin from channel catfish (*Ictalurus punctatus*). *Research in Veterinary Medicine* 92(3):408-13

Lu J, Peatman E, Tang H, Lewis J, and Liu Z (2012) Genome expansion in zebrafish is mediated by recent tandem duplications. *BMC Genomics* 13:246

Lu J, Peatman E, Tang H, Lewis J, Liu ZJ. 2012. Profiling of gene duplication patterns of teleost genomes: Evidence for rapid lineage-specific genome expansion mediated by recent tandem duplications. *BMC Genomics* 13:246.

Ninwichian* P, Peatman* E, Liu H, Kucuktas H, Somridhivej B, Liu S, Li P, Jiang Y, Sha Z, Kaltenboeck M, Abernathy JA, Wang W, Chen F, Lee Y, Wong L, Wang S, Lu J, Liu Z (2012) Second Generation Genetic Linkage Map of Catfish and Its Integration with the BAC-based Physical Map. *G3: Genes, Genomes, Genetics* 2(10):1233-41.

Liu S, Zhang S, Zhou Z, Waldbieser G, Sun F, Lu J, Zhang J, Jiang Y, Zhang H, Wang X, Rajendran KV, Khoo L, Kucuktas H, Peatman E, Liu Z (2012) Efficient assembly and annotation of the transcriptome of catfish by RNA-Seq analysis of a doubled haploid homozygote. *BMC Genomics* 13 (1), 595

Zhang, G., Fang, X., Guo, X., Li, L., Luo, R., Xu, F., Yang, P., Zhang, L., Wang, X., Qi, H., Xiong, Z., Que, H., Xie, Y., Holland, P.W.H., Paps, J., Zhu, Y., Wu, F., Chen, Y., Wang, J., Peng, C., Meng, J., Yang, L., Liu, J., Wen, B., Zhang, N., Huang, Z., Zhu, Q., Feng, Y., Mount, A., Hedgecock, D., Xu, Z., Liu, Y., Domazet-Loso, T., Du, Y., Sun, X., Zhang, S., Liu, B., Cheng, P., Jiang, X., Li, J., Fan, D., Wang, W., Fu, W., Wang, T., Wang, B., Zhang, J., Peng, Z., Li, Y., Li, N., Wang, J., Chen, M., He, Y., Tan, F., Song, X., Zheng, Q., Huang, R., Yang, H., Du, X., Chen, L., Yang, M., Gaffney, P.M., Wang, S., Luo, L., She, Z., Ming, Y., Huang, W., Zhang, S., Huang, B., Zhang, Y., Qu, T., Ni, P., Miao, G., Wang, J., Wang, Q., Steinberg, C.E.W., Wang, H., Li, N., Qian, L., Zhang, G., Li, Y., Yang, H., Liu, X., Wang, J., Yin, Y. & Wang, J. (2012). The oyster genome reveals stress adaptation and complexity of shell formation. *Nature*, 490: 49-54.

Burki, R., Krasnov, A., Bettge, K., Rexroad, C.E., 3rd, Afanasyev, S., Antikainen, M., Burkhardt-Holm, P., Wahli, T. & Segner, H. (2012). Pathogenic infection confounds induction of the estrogenic biomarker vitellogenin in rainbow trout. *Environ Toxicol Chem*, 31: 2318-2323.

Aussanasuwannakul A, Weber GM, Salem M, Yao J, Slider S, Manor ML, Kenney PB. 2012. Effect of sexual maturation on thermal stability, viscoelastic properties, and texture of female rainbow trout, *Oncorhynchus mykiss*, fillets. *J Food Sci* 77: S77-83.

Bernardi, G., Wiley, E.O., Mansour, H., Miller, M.R., Orti, G., Haussler, D., O'brien, S.J., Ryder, O.A. & Venkatesh, B. (2012). The fishes of Genome 10K. *Marine Genomics*, 7: 3-6.

Braden, L.M., Barker, D.E., Koop, B.F. & Jones, S.R.M. (2012). Comparative defense-associated responses in salmon skin elicited by the ectoparasite *Lepeophtheirus salmonis*. *Comparative Biochemistry and Physiology Part D: Genomics and Proteomics*, 7: 100-109.

Bridle, A.R., Koop, B.F. & Nowak, B.F. (2012). Identification of Surrogates of Protection against Yersiniosis in Immersion Vaccinated Atlantic Salmon. *PLoS ONE*, 7: e40841.

Everett, M., Miller, M. & Seeb, J. (2012). Meiotic maps of sockeye salmon derived from massively parallel DNA sequencing. *BMC Genomics*, 13: 521.

Faber-Hammond, J., Phillips, R.B. & Park, L.K. (2012). The Sockeye Salmon Neo-Y Chromosome Is a Fusion between Linkage Groups Orthologous to the Coho Y Chromosome and the Long Arm of Rainbow Trout Chromosome 2. *Cytogenetic and Genome Research*, 136: 69-74.

Campbell, M.R., C.C. Kozfkay, T. Copeland, W.C. Schrader, M.W. Ackerman, and S.R. Narum. 2012. Estimating abundance and life history characteristics of threatened wild Snake River steelhead stocks by using genetic stock identification. *Transactions of the American Fisheries Society* 141:1310-1327.

Campbell, N. R., Amish, S. J., Pritchard, V. L., McKelvey, K. S., Young, M. K., Schwartz, M. K., Garza, J. C., Luikart, G. and Narum, S. R. 2012. Development and evaluation of 200 novel SNP assays for population genetic studies of westslope cutthroat trout and genetic identification of related taxa. *Molecular Ecology Resources*, 12: 942-949.

Gomez-Uchida, D., Seeb, James e., Habicht, C. & Seeb, Lisa w. (2012). Allele frequency stability in large, wild exploited populations over multiple generations: insights from Alaska sockeye salmon (*Oncorhynchus nerka*). *Canadian Journal of Fisheries and Aquatic Sciences*, 69: 916-929.

Hecht, B.C., Thrower, F.P., Hale, M.C., Miller, M.R. & Nichols, K.M. (2012b). Genetic Architecture of Migration-Related Traits in Rainbow and Steelhead Trout, *Oncorhynchus mykiss*. *G3: Genes|Genomes|Genetics*, 2: 1113-1127.

Hess, M.A., Rabe, C.D., Vogel, J.L., Stephenson, J.J., Nelson, D.D. & Narum, S.R. (2012). Supportive breeding boosts natural population abundance with minimal negative impacts on fitness of a wild population of Chinook salmon. *Molecular Ecology*, 21: 5236-5250.

Johnstone, K.A., Lubieniecki, K.P., Koop, B.F. & Davidson, W.S. (2012). Identification of olfactory receptor genes in Atlantic salmon *Salmo salar*. *Journal of Fish Biology*, 81: 559-575.

- Lai, Y.Y.Y., Lubieniecki, K.P., Koop, B.F. & Davidson, W.S. (2012). Characterization of the Atlantic salmon (*Salmo salar*) brain-type fatty acid binding protein (*fabp7*) genes reveals the fates of teleost *fabp7* genes following whole genome duplications. *Gene*, 504: 253-261.
- Limborg, M.T., Blankenship, S.M., Young, S.F., Utter, F.M., Seeb, L.W., Hansen, M.H.H. & Seeb, J.E. (2012). Signatures of natural selection among lineages and habitats in *Oncorhynchus mykiss*. *Ecology and Evolution*, 2: 1-18.
- Liu, S., Rexroad, C., Iii, Couch, C., Cordes, J., Reece, K. & Sullivan, C. (2012). A Microsatellite Linkage Map of Striped Bass (*Morone saxatilis*) Reveals Conserved Synteny with the Three-Spined Stickleback (*Gasterosteus aculeatus*). *Marine Biotechnology*, 14: 237-244.
- Ma, H., Hostuttler, M., Wei, H., Rexroad, C.E., Iii & Yao, J. (2012). Characterization of the Rainbow Trout Egg MicroRNA Transcriptome. *PLoS ONE*, 7: e39649.
- Manor ML, Weber GM Salem M, Yao J, Aussanasuwannakul, Kenney PB. 2012. Effect of sexual maturation and triploidy on chemical composition and fatty acid content of energy stores in female rainbow trout, *Oncorhynchus mykiss*. *Aquaculture* 364–365: 312–321.
- Matala, A.P., W. Young, J.L. Vogel, and S.R. Narum. 2012. Influences of hatchery supplementation, spawner distribution, and habitat on genetic structure of Chinook salmon in the South Fork Salmon River, Idaho. *North American Journal of Fisheries Management* 32:346-359.
- Miller, M.R., Brunelli, J.P., Wheeler, P.A., Liu, S., Rexroad, C.E., Palti, Y., Doe, C.Q. & Thorgaard, G.H. (2012). A conserved haplotype controls parallel adaptation in geographically distant salmonid populations. *Molecular Ecology*, 21: 237-249.
- Overturf, K., Vallejo, R., Palti, Y., Barrows, F. & Parsons, J. (2012). Microarray analysis of differential utilization of plant-based diets by rainbow trout. *Aquaculture International*, 20: 213–232.
- Palti, Y., Genet, C., Gao, G., Hu, Y., You, F., Boussaha, M., Rexroad, C. & Luo, M.-C. (2012). A Second Generation Integrated Map of the Rainbow Trout (*Oncorhynchus mykiss*) Genome: Analysis of Conserved Synteny with Model Fish Genomes. *Marine Biotechnology*, 14: 343-357.
- Rexroad, C., Vallejo, R., Liu, S., Palti, Y. & Weber, G. (2012). QTL affecting stress response to crowding in a rainbow trout broodstock population. *BMC Genetics*, 13: 97.
- Salem, M., Vallejo, R.L., Leeds, T.D., Palti, Y., Liu, S., Sabbagh, A., Rexroad, C.E., Iii & Yao, J. (2012). RNA-Seq Identifies SNP Markers for Growth Traits in Rainbow Trout. *PLoS ONE*, 7: e36264.
- Storer, C.G., Pascal, C.E., Roberts, S.B., Templin, W.D., Seeb, L.W. & Seeb, J.E. (2012). Rank and Order: Evaluating the Performance of SNPs for Individual Assignment in a Non-Model Organism. *PLoS ONE*, 7: e49018.
- Sutherland, B.J.G., Jantzen, S.G., Yasuike, M., Sanderson, D.S., Koop, B.F. & Jones, S.R.M. (2012). Transcriptomics of coping strategies in free-swimming *Lepeophtheirus salmonis* (Copepoda) larvae responding to abiotic stress. *Molecular Ecology*, 21: 6000-6014.
- Yasuike, M., Leong, J., Jantzen, S., Schalburg, K., Nilsen, F., Jones, S.M. & Koop, B. (2012). Genomic Resources for Sea Lice: Analysis of ESTs and Mitochondrial Genomes. *Marine Biotechnology*, 14: 155-166.
- Aranguren LF, Salazar M, Tang K, Caraballo X, Lightner D. 2013. Characterization of a new strain of Taura syndrome virus (TSV) from Colombian shrimp farms and the implication in the selection of TSV resistant lines. *J Invertebr Pathol*. 112:68-73.

- Aranguren LF, Tang KF, Lightner DV. 2012. Protection from yellow head virus (YHV) infection in *Penaeus vannamei* pre-infected with Taura syndrome virus (TSV). *Dis Aquat Organ.* 98:185-92.
- Bartholomay LC, Loy DS, Dustin Loy J, Harris DL. 2012. Nucleic-acid based antivirals: augmenting RNA interference to 'vaccinate' *Litopenaeus vannamei*. *J Invertebr Pathol.* 110:261-6.
- Gui L, Wang B, Li FH, Sun YM, Luo Z, Xiang JH. 2012. Blocking the large extracellular loop (LEL) domain of FcTetraspanin-3 could inhibit the infection of white spot syndrome virus (WSSV) in Chinese shrimp, *Fenneropenaeus chinensis*. *Fish Shellfish Immunol.* 32:1008-15.
- Li F, Xiang J. 2013. Recent advances in researches on the innate immunity of shrimp in China. *Dev Comp Immunol.* 39:11-26.
- Li F, Xiang J. 2012. Signaling pathways regulating innate immune responses in shrimp. *Fish Shellfish Immunol.* doi: 10.1016/j.fsi.2012.08.023.
- Li S, Li F, Wen R, Xiang J. 2012. Identification and characterization of the sex-determiner transformer-2 homologue in Chinese shrimp, *Fenneropenaeus chinensis*. *Sex Dev.* 6:267-78.
- Li S, Li F, Sun Z, Xiang J. 2012. Two spliced variants of insulin-like androgenic gland hormone gene in the Chinese shrimp, *Fenneropenaeus chinensis*. *Gen Comp Endocrinol.* 177(2):246-55.
- Lightner DV, Redman RM, Pantoja CR, Tang KF, Noble BL, Schofield P, Mohny LL, Nunan LM, Navarro SA. 2012. Historic emergence, impact and current status of shrimp pathogens in the Americas. *J Invertebr Pathol.* 110:174-83.
- Loy JD, Mogler MA, Loy DS, Janke B, Kamrud K, Scura ED, Harris DL, Bartholomay LC. 2012. dsRNA provides sequence-dependent protection against infectious myonecrosis virus in *Litopenaeus vannamei*. *J Gen Virol.* 93:880-8.
- Moss SM, Moss DR, Arce SM, Lightner DV, Lotz JM. 2012. The role of selective breeding and biosecurity in the prevention of disease in penaeid shrimp aquaculture. *J Invertebr Pathol.* 110:247-50.
- Qian Z, Liu X, Wang L, Wang X, Li Y, Xiang J, Wang P. 2012. Gene expression profiles of four heat shock proteins in response to different acute stresses in shrimp, *Litopenaeus vannamei*. *Comp Biochem Physiol C Toxicol Pharmacol.* 156):211-20.
- Stentiford GD, Neil DM, Peeler EJ, Shields JD, Small HJ, Flegel TW, Vlak JM, Jones B, Morado F, Moss S, Lotz J, Bartholomay L, Behringer DC, Hauton C, Lightner DV. 2012. Disease will limit future food supply from the global crustacean fishery and aquaculture sectors. *J Invertebr Pathol.* 110:141-57.
- Tang KF, Navarro SA, Pantoja CR, Aranguren FL, Lightner DV. 2012. New genotypes of white spot syndrome virus (WSSV) and Taura syndrome virus (TSV) from the Kingdom of Saudi Arabia. *Dis Aquat Organ.* 99:179-85
- Wang D, Li F, Chi Y, Xiang J. 2012. Potential relationship among three antioxidant enzymes in eliminating hydrogen peroxide in penaeid shrimp. *Cell Stress Chaperones.* 17:423-33.
- Wang L, Li F, Wang B, Xiang J. 2012. Structure and partial protein profiles of the peritrophic membrane (PM) from the gut of the shrimp *Litopenaeus vannamei*. *Fish Shellfish Immunol.* 33:1285-91.
- Wen R, Li F, Xie Y, Li S, Xiang J. 2012. A homolog of the cell apoptosis susceptibility gene involved in ovary development of Chinese shrimp *Fenneropenaeus chinensis*. *Biol Reprod.* 86:1-7.
- Zhang J, Wang J, Li F, Sun Y, Yang C, Xiang J. 2012. A trehalose-6-phosphate synthase gene from Chinese shrimp, *Fenneropenaeus chinensis*. *Mol Biol Rep.* 39:10219-25.

Zhao C, Zhang X, Li F, Huan P, Xiang J. 2013. Functional analysis of the promoter of the heat shock cognate 70 gene of the Pacific white shrimp, *Litopenaeus vannamei*. *Fish Shellfish Immunol.* 34:397-401.

Beck, B.H., Fuller, S.A., Peatman, E., McEntire, M.E., Darwish, A., and Freeman, D.W. 2012. Chronic exogenous kisspeptin administration accelerates gonadal development in basses of the genus *Morone*. *Comp. Biochem. Physiol. A.* 162:265-273.

Liu, S., Rexroad III, C.E., Couch, C.R., Cordes, J., Reece, K., and C.V. Sullivan. 2012. A microsatellite linkage map of striped bass (*Morone saxatilis*) reveals conserved synteny with the threespined stickleback (*Gasterosteus aculeatus*). *Mar Biotechnology* 14(2):237-244. doi: 10.1007/s10126-011-9407-2.

Reading, B.J., Chapman, R.W., Schaff, J.E., Scholl, E.H., Opperman, C.H., and Sullivan, C.V. 2012. An ovary transcriptome for all maturational stages of the striped bass (*Morone saxatilis*), a highly advanced perciform fish. *BMC Research Notes* 5:111 doi:10.1186/1756-0500-5-111.

BIOINFORMATICS

Zhi-Liang Hu, Carissa A. Park, Xiao-Lin Wu and James M. Reecy (2013). Animal QTLdb: an improved database tool for livestock animal QTL/association data dissemination in the post-genome era. *Nucleic Acids Research*, 41(D1):D871-9.

Martien Groenen, Alan Archibald, Hirohide Uenishi, Christopher Tuggle, Yasuhiro Takeuchi, Max Rothschild, Claire Rogel-Gaillard, Chankyu Park, Denis Milan, Hendrik-Jan Megens, Shengting Li, Denis Larkin, et al. (2012). Analyses of pig genomes provide insight into porcine demography and evolution. *Nature*, 491, 393-398 (15 November 2012).

Marie-Laure Endale Ahanda, Eric R Fritz, Jordi Estellé, Zhi-Liang Hu, Ole Madsen, Martien AM Groenen, Dario Beraldi, Ronan Kapetanovic, David A Hume, Robert RR Rowland, Joan K Lunney, Claire Rogel-Gaillard, James M Reecy, Elisabetta Giuffra (2012). Prediction of Altered 3'-UTR miRNA-Binding Sites from RNA-Seq Data: The Swine Leukocyte Antigen Complex (SLA) as a Model Region. *PLoS One*. 2012; 7(11):e48607. doi: 10.1371/journal.pone.0048607. Epub 2012 Nov 6

Xiao-Lin Wu and Zhi-Liang Hu (2012). *Methods in molecular biology* (Clifton, NJ), 871: 145.

ZL Hu, JM Reecy, and XL Wu (2012). Design database for quantitative trait loci (QTL) data warehouse, data mining, and meta-analysis. *Methods in molecular biology* (Clifton, NJ) 871, 121

CATTLE

Allen C., B. Alves, X. Li, L. Tedeschi, H. Zhou, J. Paschal, P.K. Riggs, U. Brag-Neto., D. Keisler, G. Williams, M. Amstalden. 2012 Gene expression in the arcuate nucleus of heifers is affected by controlled intake of high- and low-concentrate diets. *J. Anim. Sci.* 90:2222–2232.

Baeza, M.C., P.M. Corva, L.A. Soria, E. Pavan, G. Rincon and J. F. Medrano 2012. Genetic variants in a lipid regulatory pathway as potential tools for improving the nutritional quality of grass-fed beef. *Animal Genetics* 2012 Jun 13. doi: 10.1111/j.1365-2052.2012.02386.x. [Epub ahead of print]

Barboza M, J Pinzon, S Wickramasinghe, JW Froehlich, I Moeller, JT Smilowitz, LR Ruhaak, J Huang, B Lönnerdal, JB German, JF Medrano, BC Weimer, CB Lebrilla 2012. Glycosylation of Human Milk Lactoferrin exhibits dynamic changes during early lactation enhancing its role in pathogenic bacteria-host interactions. *Mol Cell Proteomics* 11(6):M111.015248, Epub 2012 Jun 19.

Brannan JL., P.J. Holman, P.M. Olafson, J.H. Pruett, and P.K. Riggs. 2012 Extraction of high quality RNA from bovine and cervine hide biopsies for ectoparasite-host studies. *J. Parasitology*. <http://dx.doi.org/10.1645/GE-3132.1>

- Brown, D. E., Dechow, C. D., Liu, W.-S., Harvatine, K.J., Ott, T. (2012) Association of telomere length with age, herd and culling in lactating Holsteins. *J. Dairy Sci.* 95, 6384-6387.
- Casellas, J., R. J. Gularte, C.R. Farber, L. Varona, M. Mehrabian, E.E. Schadt, A. J. Lusk, A.D. Attie, B.S. Yandell and J.F. Medrano 2012. Genome Scans for Transmission Ratio Distortion Regions in Mice. *Genetics* 191(1):247-59.
- Chen, C., C.T.A. Herzig, L.J. Alexander, J.C. Telfer and C.L. Baldwin. Genomic copy number determination and genetic polymorphism of the gamma delta T cell co-receptor WC1 genes. *BMC Genetics*, 2012 13:86. doi: 10.1186/1471-2156-13-86.
- Clifford, A.J., K. Chen, L. McWade, G. Rincon, S-H. Kim, D.M. Holstege, J.E. Owens, B.Liu, H-G. Muller, J.F. Medrano, J.G. Fadel, A. J. Moshfegh, D. J. Baer, J. A. Novotny 2012. Gender and single nucleotide polymorphisms in MTHFR, BHMT, SPTLC, CRBP2, CETP, and SCARB1 are significant predictors of plasma homocysteine normalized to red blood cell folate concentrations in healthy adults. *Journal of Nutrition* 142(9):1764-71.
- Elzo, M.A., G.C. Lamb, D.D. Johnson, M.G. Thomas, I. Misztal, D.O. Rae, C.A. Martinez, J.G. Wasdin, and J.D. Driver. 2012. Genomic-polygenic evaluation of Angus-Brahman multibreed cattle for feed efficiency and postweaning growth using the Illumina3k chip. *J. Anim. Sci.* 90:2488-2497.
- Fisher, C.A., E. K. Bhattarai, J. B. Osterstock, S. E. Dowd, P. M. Seabury, M. Vikram, R. H. Whitlock, Y. H. Schukken, R. D. Schnabel, J. F. Taylor, J. E. Womack, C. M. Seabury. 2011. Evolution of the bovine TLR gene family and member associations with *Mycobacterium avium* subspecies paratuberculosis infection. *PLoS One.* 6:e27744.
- Fortes, M. R. S , W. M. Snelling, A. Reverter, Shivashankar H. Nagaraj, S. Lehnert, R. J. Hawken, K. L. DeAtley, S. O. Peters, G. A. Silver, G. Rincon, J. F. Medrano, A. Islas-Trejo, M. G. Thomas 2012. Gene network analyses of first service conception in Brangus heifers: use of genome and trait associations, hypothalamic-transcriptome information, and transcription factors. *J Anim Sci.* 90(9):2894-906.
- Jones, B.C. and J. E. Womack. 2012. Polymorphism and Haplotype Structure in River Buffalo (*Bubalus bubalis*) Toll-Like Receptor 5 (TLR5) Coding Sequence. *Anim Biotechnol.* 23:132-140.
- Luna-Nevárez, P., G. Rincón, J.F. Medrano, D.G. Riley, C. C. Chase Jr., S. W. Coleman, K. L. DeAtley, A. Islas-Trejo, G. A. Silver and M. G. Thomas 2012. Identificación de un polimorfismo del gen PAPP-A2 asociado a la fertilidad en vaquillas de la Raza Romosinuano criadas bajo un ambiente subtropical. *Revista Mexicana de Ciencias Pecuarias* 3(2):185-200.
- McDaneld, T.G., L.A. Kuehn, M.G. Thomas, W.M. Snelling, T.S. Stonstegard, L.K. Matukumalli, T.P.L. Smith, E.J. Pollak, and J.W. Keele. 2012. Y are you not pregnant: identification of Y chromosome segments in female cattle with decreased reproductive efficiency. *J. Anim. Sci.* 90:2142-2151.
- Minozzi, G., J.L. Williams, A. Stella, F.S.M. Luini, M. Settles, J.F. Taylor, R.H. Whitlock, R. Zanella, H.L. Neiberghs. 2012. Meta-analysis of two genome wide association studies of bovine paratuberculosis. *PLoS One* 7(3):e32578. Epub 2012 Mar 2.
- Peters, S.O., K. Kizilkaya, D.J. Garrick, R.L. Fernando, J.M. Reecy, R.L. Weaber, G.A. Silver, and M.G. Thomas. 2012. Heritability and Bayesian genome-wide association study of first service conception and pregnancy in Brangus heifers. *J. Anim. Sci.* 90:(doi:10.2527/jas.2012-5580).
- Peters, S.O., K. Kizilkaya, D.J. Garrick, R.L. Fernando, J.M. Reecy, R.L. Weaber, G.A. Silver, and M.G. Thomas. 2012. Bayesian quantitative loci inference from whole genome analyses of growth and yearling ultrasound measures of carcass traits in Brangus heifers. *J. Anim. Sci.* 90:3398-3409.
- Russell, M.L., D. W. Bailey, M. G. Thomas, and B.K. Whitmore. 2012. Grazing distribution and diet quality of Angus, Brangus, and Brahman cows in the Chihuahuan Desert. *Range Ecol. Mgt.* 65:371-381.

Shen J., E. L. Abel, P. K. Riggs, J. Repass, S. C. Hensley, L.J. Schroeder, A. Temple, A. Chau, A. McClellan, O. Rho, K. Kiguchi, M. Ward, O. J. Semmes, M. D. Person, J. M. Angel, and J. DiGiovanni. 2012. Proteomic and pathway analyses reveal a network of inflammatory genes associated with differences in skin tumor promotion susceptibility in DBA/2 and C57BL/6 mice. *Carcinogenesis*. 33:2208–2219.

Snelling, W.M., R.A. Cushman, J.W. Keele, C. Maltecca, M.G. Thomas, M.R.S. Fortes, and A. Reverter. 2012. Networks and pathways to guide genomic selection. *J. Anim. Sci.* 90(E-2012-5784-R1):accepted 10/9/2012.

Snelling, W.M., R.A. Cushman, M.R.S. Fortes, A. Reverter, G.L. Bennett, J.W. Keele, L.A. Kuehn, T.G. McDanel, R.M. Thallman, and M.G. Thomas. 2012. How SNP chips will advance our knowledge of factors controlling puberty and aid in selecting replacement females. *J. Anim. Sci.* 90:1152-1165.

Stafuzza, N. B., A. J. Greco, J. R. Grant, C. A. Abbey, C. A. Gill, T. Raudsepp, L. C. Skow, J. E. Womack, P. K. Riggs and M. E. J. Amaral. 2012. A high resolution radiation hybrid map of the river buffalo major histocompatibility complex (MHC) and comparison with BoLA. *Animal Genomics*. doi: 10.1111/age.12015.

Stafuzza, N. B., C. A. Abbey, C. A. Gill, J. E. Womack, and M. E. J. Amaral. 2012. Construction and preliminary characterization of a river buffalo bacterial artificial chromosome library. *Genet. Mol. Res.* 11: 3013-3019

Warden, C.H., R. Gularte-Mérida, J.S. Fisler, S. Hansen, N. Shibata, A. Le, J.F. Medrano and J.S. Stern 2012. Leptin receptor interacts with rat chromosome 1 to regulate renal disease traits. *Physiological Genomics* 2012 Sep 11. [Epub ahead of print]

Weber, K. L., D.J. Drake, J. F. Taylor, D.J. Garrick, L.A. Kuehn, R.M. Thallman, R.D. Schnabel, W.M. Snelling, E.J. Pollak, A.L. Van Eenennaam. 2012. The accuracies of DNA-based genetic merit prediction equations derived from Angus- and multi-breed beef cattle training populations. *Journal of Animal Science*. 90:4191-4202.

Weber, K. L., R. M. Thallman, J. W. Keele, W. M. Snelling, G. L. Bennett, T. P. L. Smith, T. G. McDanel, M. F. Allan, A. L. Van Eenennaam, and L. A. Kuehn. 2012. Accuracy of genomic breeding values in multi-breed beef cattle populations derived from deregressed breeding values and phenotypes. *Journal of Animal Science*. 90:4177-4190.

Wei S, Duarte MS, Du M, Jiang Z, Paulino PVR, Chen J, Fernyhough-Culver ME, Hausman GJ, Zan L, Dodson MV. 2012. Like pigs, and unlike other breeds of cattle examined, mature Angus-derived adipocytes may extrude lipid prior to proliferation in vitro. *Adipocyte* 1(4):1-5.

Wickramasinghe, S., G. Rincon, A. Islas-Trejo, J.F. Medrano 2012. Transcriptional profiling of bovine milk using RNA sequencing. *BMC Genomics* 13:45

Womack, J.E. 2012. First steps: bovine genomics in historical perspective. *Anim Genet.* 43:2.

EQUINE

ACHILLI A., OLIVIERI A., SOARESC P., LANCIONI H., HOOSHIAR KASHANI B., PEREGO U.A., NERGADZE S.G., CAROSSA V., SANTAGOSTINO M., CAPOMACCIO S., FELICETTI M., AL-ACHKAR W., PENEDO M.C.T., VERINI-SUPPLIZI A., HOUSHMANDH M., WOODWARD S.R., c O., SILVESTRELLI M., GIULOTTO E., PEREIRAC L., BANDELT H.J. , TORRONI A. Mitochondrial genomes from modern horses reveal the major haplogroups that underwent domestication
PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES -PNAS, 2012, 109:7, 2449-2454.

Andersson LS, Larhammar M, Memic F, Wootz H, Schwochow D, Rubin CJ, Patra K, Arnason T, Wellbring L, Hjälms G, Imsland F, Petersen JL, McCue ME, Mickelson JR, Cothran G, Ahituv N, Roepstorff L, Mikko S, Vallstedt A, Lindgren L, Andersson L and Kullander K. (2012). Mutations in DMRT3 affect locomotion in horses and spinal circuit function in mice. *Nature*. 2012 Aug 30;488 (7413):642-6. doi: 10.1038/nature11399.

Andersson LS, Swinburne JE, Meadows JR, Broström H, Eriksson S, Fikse WF, Frey R, Sundquist M, Tseng CT, Mikko S, Lindgren G. 2012. The same ELA class II risk factors confer equine insect bite hypersensitivity in two distinct populations. *Immunogenetics*. 2012 Mar;64(3):201-8. doi: 10.1007/s00251-011-0573-1. Epub 2011 Sep 23. Erratum in: *Immunogenetics*. 2012 Feb;64(2):163. Swinburne, June E [corrected to Swinburne, June E].

Andersen K, Bird KL, Rasmussen M, Haile H, Breuning-Madsen H, Kjaer K, Orlando L, Gilbert MTP, Willerslev E. 2012. Meta-barcoding of 'dirt' DNA from soil reflects vertebrate biodiversity. *Mol Ecol* 21:1966-79.

Biagini P, Thèves C, Balaesque P, Géraut A, Cannet C, Keyser C, Nikolaeva D, Gérard P, Duchesne S, Orlando L, Willerslev E, Alekseev AN, de Micco P, Ludes B, Crubézy E. 2012. Variola virus in a 300-year-old Siberian mummy. *N Engl J Med* 367:2057-9.

Bower MA, Whitten M, Nisbet RER, Spencer M, Dominy KM, Murphy AM, Cassidy R, Barrett E, Hill EW, Binns M. Thoroughbred racehorse mitochondrial DNA demonstrates closer than expected links between maternal genetic history and pedigree records. *Journal of Animal Breeding and Genetics*. Article first published online: 24 JUL 2012 DOI: 10.1111/j.1439-0388.2012.01018.x

Bower MA, Campana MG, Nisbet RER, Weller R, Whitten M, Edwards CJ, Stick F, Barrett E, O'Connell TC, Hill EW, Wilson AW, Howe CJ, Barker G, Binns M. Truth in the bones: resolving the identity of the founding elite Thoroughbred racehorses. *Archaeometry*, 2012, doi: 10.1111/j.1475-4754.2012.00666.x

Bower MA, McGivney BA, Campana MG, Gu J, Andersson LS, Barrett E, Davis CR, Mikko S, Stock F, Voronkova V, Bradley DG, Fahey AG, Lindgren G, MacHugh DE, Sulimova G, Hill EW The genetic origin and history of speed in the Thoroughbred racehorse. *Nature Communications*, 2012, 3:643 doi: 10.1038/ncomms1644

Brosnahan MM, Miller DC, Adams M, Antczak DF. (2012) IL-22 is expressed by the invasive trophoblast of the equine (*Equus caballus*) chorionic girdle. *J Immunol*. 188:4181-4187.

CAPPELLI K. , FELICETTI M., CAPOMACCIO S., NOCELLI C., SILVESTRELLI M., VERINI SUPPLIZI A. Effect of training status on immune defence related gene expression in Thoroughbred: Are genes ready for the sprint?. *THE VETERINARY JOURNAL*, 2012, Article first published online: 16 JUL 2012.

Cappelini E, Jensen L, Szklarczyk D, Ginolhac A, da Fonseca R, Stafford T, Holven S, Collins M, Orlando L, Willerslev E, Gilbert MTP, Olsen JV. 2012. Proteomic analysis of a Pleistocene mammoth femur reveals more than one hundred ancient bone proteins. *J Proteome Res* 11:917-926.

COLLI L., PERROTTA G., NEGRINI R., BOMBA L., BIGI D., ZAMBONELLI P., VERINI SUPPLIZI A., AJMONE MARSAN P. Detecting population structure and recent demographic history in endangered livestock breeds: the case of the Italian autochthonous donkeys *ANIMAL GENETICS*, 2012, Article first published online: 17 APR 2012,

Dalen L, Orlando L, Shapiro B, Brandstrom-Durling M, Quam R, Gilbert MT, Diez Fernandez-Lomana JC, Willerslev E, Arsuaga JL, Gotherstrom A. 2012. Partial genetic turnover in Neandertals: continuity in the East and population replacement in the West. *Mol Biol Evol* 29:1893-7.

Das, P.J., Lyle, S.K., Beehan, D., Chowdhary, B.P., Raudsepp, T. 2012. Cytogenetic and molecular characterization of Y isochromosome in a 63XO/64Xi(Yq) mosaic karyotype of an intersex horse. *Sex Dev* 6 (1-3): 117-127.

Doan R, Cohen N, Harrington J, Veazy K, Juras R, Cothran G, McCue ME, Skow L, Dindot SV. (2012). Identification of copy number variants in horses. *Genome Res*. 2012 May;22(5):899907. doi: 10.1101/gr.128991.111. Epub 2012 Mar 1.

Finno, CJ, Famula, T., Aleman, M., Higgins, R., Madigan, J., Bannasch, D. Pedigree analysis and exclusion of alpha-tocopherol transfer protein (TTPA) as a candidate gene for neuroaxonal dystrophy in the American Quarter horse *J Vet Intern Med*. 2012 Nov 27.

- Finno CJ, Aleman M, Ofri R, Hollingsworth SR, Madigan JE, Winfield L, Bannasch DL. Electrophysiological studies in American Quarter horses with neuroaxonal dystrophy. *Vet Ophthalmol.* 2012 Sep;15 Suppl 2:3-7. doi: 10.1111/j.1463-5224.2012.00997.x. Epub 2012 Mar 20.
- Foote AD, Thomsen PF, Sveegaard S, Wahlberg M, Kielgast J, Kyhn LA, Salling AB, Galatius A, Orlando L, Gilbert MT. 2012. Investigating the potential use of environmental DNA (eDNA) for genetic monitoring of marine mammals. *PLoS One* 7:e41781.
- Fritz KL, McCue ME, Valberg SJ, Rendahl AK, and Mickelson JR. (2012). Genetic mapping of recurrent exertional rhabdomyolysis in a population of North American Thoroughbred horses. *Animal Genetics* 2012 Mar 23. doi: 10.1111/j.1365-2052.2012.02351.x. Epub 2012 Mar 23.
- Gabreski, N., Haase, B., Armstrong, C., Distl, O., BROOKS, S.(2012). Investigation of allele frequencies for Lavender foal syndrome in the horse. *Animal Genetics*, 43 (5), 650.
- Ghosh, S., Das, P.J., Qu, Z., Fang, E., Arnold, C., Adelson, D.L., Chowdhary, B.P., Raudsepp, T. 2012. Array CGH Studies in Equine Disorders of Sexual Development – SRY-Positive Sex Reversal and Cryptorchidism. *Cytogenet. Genome Res.* 136 (4), 314.
- Ginolhac A, Vilstrup J, Stenderup J, Rasmussen M, Stiller M, Shapiro B, Zazula G, Froese D, Steinmann KE, Thompson JF, Al-Rasheid K, Gilbert TMP, Willerslev E, Orlando L. 2012. Improving the performance of true-Single Molecule Sequencing for ancient DNA. *BMC Genomics* 13:177.
- Hauswirth, R., Haase, B., Blatter, M., BROOKS, S.A., Burger, D., Drögemüller, C., Gerber, V., Henke, D., Janda, J., Jude, R., Magdesian, K. G., Matthews, J. M., Poncet, P. A., Svansson, V., Tozaki, T., Wilkinson-White, L., Penedo, M. C., Rieder, S., Leeb, T. (2012). Mutations in MITF and PAX3 Cause "Splashed White" and Other White Spotting Phenotypes in Horses. *PLoS Genetics*, 4 (e1002653), 9pp.
- Holl, H., Lear, T., Nolen-Walston, R., Slack, J., Wade, C., BROOKS, S. (2013). Detection of two equine trisomies using SNP-CGH. *Mammalian Genome*, In Review.
- Jacobsen MW, Hansen MM, Orlando L, Bekkevold D, Bernatchez L, Willerslev E, Gilbert MT. 2012. Mitogenome sequencing reveals shallow evolutionary histories and recent divergence time between morphologically and ecologically distinct European whitefish (*Coregonus* spp.). *Mol Ecol* 21:2727-42.
- Janecka JE, Chowdhary BP, Murphy WJ (2012) Exploring the correlations between sequence evolution rate and phenotypic divergence across the Mammalian tree provides insights into adaptive evolution. *Journal of Bioscience* 37:1–13.
- Jorgensen T, Kjaer KH, Haile J, Rasmussen M, Boessenkool S, Andersen K, Coissac E, Taberlet P, Orlando L, Gilbert MTP, Willerslev E. 2012. Islands in the ice: detecting past vegetation on Greenlandic Nunataks using historical records and sedimentary DNA meta-barcoding. *Mol Ecol* 21:1980-8.
- Jorgensen T, Haile J, Moller P, Kjaer KH, Andreev Andrei, Boessenkool S, Rasmussen M, Kienast F, Coissac E, Taberlet P, Brochmann C, Bigelow NH, Andersen K, Orlando L, Gilbert MTP, Willerslev E. 2012. A comparative study of macrofossils, pollen and ancient plant DNA from permafrost sediments of northern Siberia reveals long-term vegetational stability. *Mol Ecol* 21:1989-2003.
29. Makvandi-Nejad, S., Allen, J., Chu, E., Gu, E., Chandler, A., Loredano, A., Bellone, R., Mezey, J. G., BROOKS, S., Sutter, N. (2012). Four Loci Explain 83% of Size Variation in the Horse. *PLoS One*, 7 (e39929), 6pp.
- McGivney BA, Browne JA, Fonseca RG, Katz LM, MacHugh DE, Whiston R, Hill EW. MSTN genotypes in Thoroughbred horses influence skeletal muscle gene expression and racetrack performance. *Animal Genetics*, 2012 Early View 27 Feb 2012 doi: 10.1111/j.1365-2052.2012.02329.x [Short communication]

- McCue, DL Bannasch, JL Petersen, J Gurr, E Bailey, MM Binns, O Distl, G Guérin, T Hasegawa, EW Hill, T Leeb, G Lindgren, MCT Penedo, KH Røed, OA Ryder, JE Swinburne, T Tozaki, SJ Valberg, M Vaudin, K Lindblad-Toh, CM Wade, JR Mickelson (2012) A high density SNP array for the domestic horse and extant perissodactyla: Utility for association mapping, genetic diversity and phylogeny studies. *PLoS Genet* 8, e1002451.
- Moridi M, Masoudi AA, Vaez Torshizi R, Hill EW. Mitochondrial DNA D-loop sequence variation in maternal lineages of Iranian native horses. *Animal Genetics*. 2012 Jun 26. doi: 10.1111/j.1365-2052.2012.02389.x. [Epub ahead of print] [Short communication]
- Mourier T, Ho SY, Gilbert MT, Willerslev E, Orlando L. 2012. Statistical guidelines for detecting past population shifts using ancient DNA. *Mol Biol Evol* 29:2241-51.
- Parducci L, Jorgensen T, Tollesfrud MM, Elverland E, Alm T, Fontana SL, Bennett KD, Haile J, Matetovici I, Suyama Y, Edwards ME, Andersen K, Rasmussen M, Boessenkool S, Coissac E, Brochmann C, Taberlet P, Houmark-Nielsen M, Larsen NK, Orlando L, Gilbert MT, Kjaer KH, Alsos IG, Willerslev E. 2012. Glacial survival of boreal trees in northern Scandinavia. *Science* 335:1083-6.
- Noronha LE, Harman RM, Wagner B, Antczak DF. (2012) Generation and characterization of monoclonal antibodies to equine NKp46. *Vet Immunol Immunopathol*. 147:60-68
- Noronha LE, Harman RM, Wagner B, Antczak DF. (2012) Generation and characterization of monoclonal antibodies to equine CD16. *Vet Immunol Immunopathol*. 146(2):135-142.
- Noronha LE, Huggler KE, de Mestre AM, Miller DC, Antczak DF. (2012) Molecular evidence for natural killer-like cells in equine endometrial cups. *Placenta*. 33:379-386
- Overballe-Petersen S, Orlando L, Willerslev E. 2012. Next-generation sequencing offers new insights into DNA degradation. *Trends Biotechnol* 30:364-8.
- Raudsepp, T., McCue, M.M., Das, P.J., Dobson, L., Vishnoi, M., Fritz, K.L., Schaefer, R., Rendahl, A.K., Derr, J.N., Love, C.C., Varner, D.D., Chowdhary, B.P. 2012. Genome-Wide Association Study Implicates Testis-Sperm Specific FKBP6 as a Susceptibility Locus for Impaired Acrosome Reaction in Stallions. *PLoS GENETICS*, Dec;8(12):e1003139. Epub 2012 Dec 20.
- Raudsepp T, Das PJ, Avila F, Chowdhary BP. 2012. The Pseudoautosomal Region and Sex Chromosome Aneuploidies in Domestic Species. *Sex Dev*. 6:72-83.
- Sánchez-Quinto F, Schroeder H, Ramirez O, Avila-Arcos MC, Pybus M, Olalde I, Velazquez AM, Marcos ME, Encinas JM, Bertranpetit J, Orlando L, Gilbert MT, Lalueza-Fox C. 2012. Genomic affinities of two 7,000-year-old Iberian hunter-gatherers. *Curr Biol* 22:1494-9.
- Sato F, Hirota K, Tozaki T, Ito K, Dhakal P, Taya K, Endo Y, Murase H, Nambo Y. A case of ambiguous external genitalia in a Thoroughbred male horse with the 63,XO/64,XY mosaic karyotype. *J Vet Med Sci*. 2012 74(10):1327-31.
- Schubert M, Ginolhac A, Lindgreen S, Thompson JF, Al-Rasheid KA, Willerslev E, Krogh A, Orlando L. 2012. Improving ancient DNA read mapping against modern reference genomes. *BMC Genomics* 13:178.
- Shakhsi-Niaei, J Klukowska-Rötzler, C Drögemüller, J Swinburne, C Ehrmann, D Saftic, A Ramseyer, V Gerber, G Dolf, T Leeb (2012) Replication and fine-mapping of a QTL for recurrent airway obstruction (RAO) in European Warmblood horses. *Anim Genet* 43, 627-631.
- Signer-Hasler, C Flury, B Haase, D Burger, H Simianer, T Leeb, S Rieder (2012) A genome-wide association study reveals loci influencing height and other conformation traits in horses. *PLoS One* 7, e37282.

- Steelman, S.M. and B.P. Chowdhary. 2012. Plasma proteomics shows alterations in clotting and complement cascades in chronic equine laminitis. *BMC Vet. Res.* – Sep 27; 8(1):179. (Epub ahead of print).
- Steelman, SM, Chowdhary, BP, Dowd S, Suchodolski, J, Janečka, JE. 2012. Pyrosequencing of 16S rRNA genes in fecal samples reveals high diversity of hindgut microflora in horses and potential links to chronic laminitis. *BMC Vet Res* 8, 231, 1-11.
- Swinburne, T. Tozaki, S. J. Valberg, M. Vaudin, K. Lindblad-Toh, C. M. Wade and J. R. Mickelson (2012). "A high density SNP array for the domestic horse and extant *Perissodactyla*: utility for association mapping, genetic diversity, and phylogeny studies." *PLoS Genet* 8(1): e1002451.
- Tachibana Y, Nakano Y, Nagaoka K, Kikuchi M, Nambo Y, Haneda S, Matsui M, Miyake YI, Imakawa K. Expression of Endometrial Immune-related Genes Possibly Functioning During Early Pregnancy in the Mare. *J Reprod Dev.* 2012 Nov 9. [Epub ahead of print]
- Takasu M, Hiramatsu N, Tozaki T, Kakoi H, Nakagawa T, Hasegawa T, Huricha, Maeda M, Murase T, Mukoyama H. Genetic characterization of the endangered Kiso horse using 31 microsatellite DNAs. *J Vet Med Sci.* 2012 74(2):161-6.
- Tallmadge RL, Such KA, Miller KC, Matychak MB, Felipe MJ. (2012) Expression of essential B cell development genes in horses with common variable immunodeficiency. *Mol Immunol.* 51(2):169-76.
- Tallmadge RL, Stokol T, Gould-Earley MJ, Earley E, Secor EJ, Matychak MB, Felipe MJ. (2012) Fell Pony syndrome: characterization of developmental hematopoiesis failure and associated gene expression profiles. *Clin Vaccine Immunol.* 19(7):1054-64.
- Thomsen PF, Kielgast J, Iversen LL, Wiuf C, Rasmussen M, Gilbert MT, Orlando L, Willerslev E. 2012. Monitoring endangered freshwater biodiversity using environmental DNA. *Mol Ecol* 21:2565-73.
- Tozaki T, Kurosawa M, Hill EW. The Influence of the Myostatin Gene on Thoroughbred Racehorses *Hippophile* 2012 48: 24-32 [Japanese]
- Tozaki T, Hill EW, Hirota K, Kakoi H, Gawahara H, Miyake T, Sugita S, Hasegawa T, Ishida N, Nakano Y, Kurosawa M. A cohort study of racing performance in Japanese Thoroughbred racehorses using genome information on ECA18. *Anim Genet.* 2012 43(1):42-52.
- Tozaki T, Miyake T, Kakoi H, Gawahara H, Hirota K, Nakano Y, Kurosawa M. Heritability estimates for racing performance in Japanese Thoroughbred racehorses using linear and non-linear model analyses. *J Anim Breed Genet.* 2012 129(5):402-8.
- Velie, B. D., P. K. Knight, P. C. Thomson, C. M. Wade and N. A. Hamilton (2012). "The association of age at first start with career length in the Australian Thoroughbred racehorse population." *Equine Vet J.*
- Velie, B. D., C. M. Wade and N. A. Hamilton (2012). "Profiling the careers of Thoroughbred horses racing in Australia between 2000 and 2010." *Equine Vet J.*
- Wang X, Miller DC, Clark AG, Antczak DF. (2012) Random X inactivation in the mule and horse placenta. *Genome Res.* 10:1855-1863.
- Yoccoz N, Brathen KA, Gielly L, Haile J, Edwards M, Goslar Tm von Stedingk J, Brysting A, Coissac E, Pompanon F, Sonstebø J, Miquel C, Valentini A, De Bello F, Chave J, Thuillier W, Wincker P, Craud C, Gavory F, Rasmussen M, Gilbert MTP, Orlando L, Brochmann C, Willerslev E, Taberlet P. 2012. DNA from soil mirrors plant taxonomic and growth form diversity. *Mol Ecol* 2:3647-55.

POULTRY

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. doi: 10.1016/j.dci.2012.03.007.

Dekkers, J.C.M., 2012. Application of genomics tools to animal breeding. *Curr. Genomics* 13: 207-212.

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.

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.

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

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.

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

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.

Sandford, E.E., Orr, M., Shelby, M., Li, X., Zhou, H., Johnson, T.J., Kariyawasam, S., Liu, P., Nolan, L.K., and Lamont, S.J. 2012. Transcriptome response of leukocytes from chickens infected with avian pathogenic *Escherichia coli* identifies pathways associated with resistance. *Results in Immunol.* 2: 44-53.

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.

Nanduri B, Suvarnapunya AE, Venkatesan M, Edelman MJ. Deubiquitinating Enzymes as Promising Drug Targets for Infectious Diseases. *Curr Pharm Des.* 2012 Nov 2. [Epub ahead of print] PubMed PMID: 23151130.

- 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.
- 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. doi: 10.1186/1471-2105-13-S15-S4. Epub 2012 Sep 11. PubMed PMID: 23046475; PubMed Central PMCID: PMC3439734.
- Bhatty 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. [Epub ahead of print] PubMed PMID: 23009705.
- 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. doi: 10.1099/jmm.0.049742-0. Epub 2012 Sep 13. PubMed PMID: 22977076.
- 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. doi: 10.1371/journal.pone.0029435. Epub 2012 Jan 20. PubMed PMID: 22276113; PubMed Central PMCID: PMC3262788.
- 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.
- Baurhoo B, Ferket P, Ashwell CM, de Oliviera 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.
- 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.
- 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.
- 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.
- 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
- 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
- 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
<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3464110>
- 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
- 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.

- 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.
- 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.
- 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.
- Chandra YG, Lee JY, and Kong BW. 2012. Genome sequence comparison of two vaccine infectious laryngotracheitis virus (ILT) strains. *Virus Genes.* 44(3):470-4
- 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.
- 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.
- 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.
- 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.
- Ying Wang, 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
- 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
- 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 doi:10.3390/genes3020233 <http://www.mdpi.com/2073-4425/3/2/233/>
- 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.
- 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.

- 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.
- 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.
- 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.
- 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 broilers. *Poultry Science* 91: 2942-8
- 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/fgene.2012.00020
- 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.
- 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 doi:10.4236/ajmb.2012.23024
- 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. doi:10.1371/journal.pone.0035993
- 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) 4:282–299 doi: 10.1007/s12561-012-9063-8
- 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. doi:10.1371/journal.pone.0039094
- 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. doi:10.1371/journal.pone.0041849
- Mitra, A. and *Song, JZ. 2012 WaveSeq: A Novel Data-driven Method of Detecting Histone Modifications using Wavelets. *Plos One* 7(9): e45486. doi:10.1371/journal.pone.0045486
- Mitra, A., Luo, J., Zhang H. Zhao K. and *Song, JZ. 2012 Marek's Disease Virus Infection Induces Differential Chromatin Marks and Tissue-specific effects in inbred chicken lines. *BMC Genomics* 13:557 doi:10.1186/1471-2164-13-557
- 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

- 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
- Mukherjee M, Porter TE (2012) Differential abilities of chicken Pit1 isoforms to regulate the GH promoter: Evidence for synergistic activation. *Endocrinology* 153:3320-3330
- 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.
- Eimes JA, Reed KM, Mendoza KM, Bollmer JL, Whittingham LA, Bateson ZW and PO Dunn. Greater prairie-chickens have a compact MHC-B with a single class IA locus. *Immunogenetics*, 2012 Nov 20.
- 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.
- 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.
- 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.
- 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.
- 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.
- 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.
- 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.
- 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 Nelore cattle with uncertain paternity. *Livestock Science* 144: 89-95, 2012.
- 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.
- 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.
- 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

MacEachern, S., W.M. Muir, S. Crosby, and H.H. 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. *Frontier Live. Gen.* 2:113.

Cheng, H.H., S. MacEachern, S. Subramaniam, and W.M. Muir. 2012. Chicks and SNPs – an entrée into identifying genes conferring disease resistance in chicken. *Anim. Prod. Sci.* 52:151-156.

Kumar, S., D. Kunec, J. Buza, H.-I. Chiang, H. Zhou, S. Subramaniam, K. Pendarvis, H.H. Cheng, and S.C. Burgess. 2012. Nuclear factor kappa B is central to Marek's disease herpesvirus induced neoplastic transformation of CD30 expressing lymphocytes in-vivo. *BMC Systems Biol.* 6:123.

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.

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.

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.

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 α -keratin (KRT75) mutation that causes a defective rachis. *PloS Genet.* 8:e1002748.

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.

Luo, J., A. Mitra, F.Tian, S. Chang, H.M. Zhang, K. Cui, Y. Yu, K. Zhao, J. Song. 2012. Histone methylation analysis and pathway predictions in chickens after MDV infection. *PLoS One* 7:e41849.

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.

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.

Tian, F., J. Luo, H.M. Zhang, S. Chang, and J.Z. Song. 2012. Marek's disease virus challenge induced immune-related gene expression and chicken repeat 1 (CR1) methylation alterations in chickens. *Amer. J. Mol. Biol.* 2:232-241.

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.

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.

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.

SHEEP AND GOAT

Brown, D. E., Dechow, C. D., Liu, W.-S., Harvatine, K.J., Ott, T. (2012) Association of telomere length with age, herd and culling in lactating Holsteins. *J. Dairy Sci.* 95, 6384-6387.

- Chen, C., C.T.A. Herzig, L.J. Alexander, J.C. Telfer and C.L. Baldwin. Genomic copy number determination and genetic polymorphism of the gamma delta T cell co-receptor WC1 genes. *BMC Genetics*, 2012 13:86. doi: 10.1186/1471-2156-13-86.
- Dong, Y, M. Xie, Y. Jiang, N. Xiao, X. Du, G. Zhang, G. Tosser-Klopp, J. Wang, S. Yang, J. Liang, W. Chen, J. Chen, P. Zeng, Y. Hou, C. Bian, S. Pan, Y. Li, X. Liu, W. Wang, B. Servin, B. Sayre, B. Zhu, D. Sweeney, R. Moore, W. Nie, Y. Shen, R. Zhao, G. Zhang, J. Li, T. Faraut, J. Womack, Y. Zhang, J. Kijas, N. Cockett, S. Su, S. Zhao, J. Wang and W. Wang (2013) A reference genome of the domestic goat (*Capra hircus*) generated by Illumina sequencing and whole genome mapping. *Nature Biotechnology* doi:10.1038/nbt.2478.
- Du XY, Womack JE, Owens KE, Elliott JS, Sayre B, Bottcher PJ, Milan D, Garcia Podesta M, Zhao SH, Malek M. A whole-genome radiation hybrid panel for goat. *Small Ruminant Research* 2012, 105:114-116.
- Kijas, J. W., J. E. Miller, T. Hadfield, R. McCulloch, E. Garcia-Gamez, L. R. Porto Neto, N. E. Cockett and the International Sheep Genomics Consortium (2012) Tracking the emergence of a new breed using 49,034 SNP in sheep. *PLoS* 7(7):e41508.doi:10.1371/journal.pone.0041508.
- Kijas J.W., Lenstra J.A., Hayes B., Boitard S., Porto Neto L.R., San Cristobal M., Servin B., McCulloch R., Whan V., Gietzen K., Paiva S., Barendse W., Ciani E., Raadsma H., McEwan J., Dalrymple B., International Sheep Genomics Consortium Members (2012) Genome wide analysis of the world's sheep breeds reveals high levels of historic mixture and strong recent selection. *PLoS Biol.* Feb;10(2):e1001258.
- Heaton, M. P., Clawson, M. L., Chitko-Mckown, C. G., Leymaster, K. A., Smith, T. P. L., Harhay, G. P., White, S. N., Herrmann-Hoesing, L. M., Mousel, M. R., Lewis, G. S., Kalbfleisch, T. S., Keen, J. E., and Laegreid, W. W. Reduced lentivirus susceptibility in sheep with TMEM154 mutations. *PLoS Genet.* 8 (1):e1002467. 2012.
- Herrmann-Hoesing, L.M., White, S.N., Broughton-Neiswanger, L.E., Johnson, W.C., Noh, S.M., Schneider, D.A., Li, H., Taus, N.S., Reynolds, J., Truscott, T., Dassanayake, R.P., and Knowles, D.P. Ovine progressive pneumonia virus is transmitted more effectively via aerosol nebulization than oral administration. *Open Journal of Veterinary Medicine* 2(3):113-119. 2012.
- Leeds, T. D., Notter, D. R., Leymaster, K. A., Mousel, M. R., and Lewis, G. S. Evaluation of Columbia, USMARC-Composite, Suffolk, and Texel rams as terminal sires in an extensive rangeland production system: I. Ewe productivity and crossbred lamb survival and preweaning growth. *J. Anim. Sci.* 90 (9):2931-2940. 2012.
- Malherbe, C., T.N. Holt, J. Marquard, K.M. Cammack, and D. O'Toole. 2012. Right ventricular hypertrophy with heart failure in Holstein heifers at 1,600 m. *J. Vet. Diagn. Invest.* 24(5):867-877.
- Mousel, M. R., Leymaster, K. A., Christenson, R. K., Nonneman, D. J., and Rohrer, G. A. Validation and fine mapping of a QTL for ovulation rate on swine chromosome 3. *Anim. Genet.* 43 (2):220-224. 2012.
- Mousel, M. R., Notter, D. R., Leeds, T. D., Zerby, H. N., Moeller, S. J., and Lewis, G. S. Evaluation of Columbia, USMARC-Composite, Suffolk, and Texel rams as terminal sires in an extensive rangeland production system: III. Prefabrication carcass traits and organ weights. *J. Anim. Sci.* 90 (9):2953-2962. 2012.
- Notter, D. R., Leeds, T. D., Mousel, M. R., Taylor, J. B., Kirschten, D. P., and Lewis, G. S. Evaluation of Columbia, USMARC-Composite, Suffolk, and Texel rams as terminal sires in an extensive rangeland production system: II. Postweaning growth and ultrasonic measures of composition for lambs fed a high-energy feedlot diet. *J. Anim. Sci.* 90 (9):2941-2952. 2012.
- Subramaniam, R., White, S.N., Herrmann-Hoesing, L.M., and Subramaniam, S. MHC class II DR allelic diversity in bighorn sheep. *GENE* 506(1):217-222. 2012.

Tellam, R. L., N. E. Cockett and C. A. Bidwell (2012) Genes contributing to genetic variation of muscling in sheep. *Frontiers in Anim. Genomics* 3:Article 164. doi:10.3389/fgene.2012.00164.

Wang, M., H. Yu, Y.S. Kim, C.A. Bidwell, and S. Kuang. 2012. Myostatin facilitates slow and inhibit fast myosin heavy chain expression during myogenic differentiation. *Biochemical and Biophysical Research Communications* 426(1):83-8.

White, S.N., Reynolds, J.O., Waldron, D.F., Schneider, D.A., and O'Rourke, K.I. Extended scrapie incubation time in goats singly heterozygous for PRNP S146 or K222. *GENE* 501(1):49-51. 2012.

White, S.N., Mousel, M.R., Herrmann-Hoesing, L.M., Reynolds, J. O., Leymaster, K.A., Neiberger, H.L., Lewis, G.S., and Knowles, D.P. Genome-wide association identifies multiple genomic regions associated with susceptibility to and control of ovine lentivirus. *PLoS ONE* 7 (10):e47829. 2012.

SWINE

Badke, Y.M., R.O. Bates, C.W. Ernst, C. Schwab, and J.P. Steibel. 2012. Estimation of linkage disequilibrium in four US pig breeds. *BMC Genomics*. 13:24

Bates, R.O., M.E. Doumit, N.E. Raney, E.E. Helman and C.W. Ernst. 2012. Association of halothane sensitivity with growth, carcass merit and meat quality. *Animal*. 6:1537-1542.

Bennett AC, Loyd H, Hellams L, Lunney JK, Rowland RRR, Dorman KS, Carpenter S. 2012. Longitudinal analysis of genetic variation in ORF2-6 in pigs experimentally infected with porcine reproductive and respiratory syndrome virus. *IPRRSS NSIF 2012*. Abstract #62.

Boddicker N, Garrick DJ, Reecy JM, Rowland B, Lunney JK, Dekkers JCM. 2012. Validation of a major quantitative trait locus associated with host response to experimental infection with PRRS virus. *PAG*. P0636.
<http://pag.confex.com/pag/xx/webprogram/Paper3384.html>

Boddicker N, Reecy JM, Rowland RRR, Lunney JK, Dekkers JCM. 2012. Region on *Sus scrofa* chromosome 1 associated with viremia in pigs infected with porcine reproductive and respiratory syndrome virus. *IPRRSS NSIF 2012*. Abstract #63.

Boddicker N, Garrick DJ, Rowland RRR, Lunney JK, Reecy JM, Dekkers JCM. 2013. Validation of a major quantitative trait locus associated with host response to experimental infection with Porcine Reproductive and Respiratory Syndrome virus. *Animal Genetics*. In revision.

Boddicker N, Rowland R, Lunney JK, Garrick DJ, Reecy J, Dekkers JCM. 2012. A major QTL associated with host response to Porcine Reproductive and Respiratory Syndrome virus challenge. *J. Anim. Sci.* 90: 1733 - 46.

Butler JE, Wertz N Sun XZ, Lunney JK, Muyldermans S. 2013. Resolution of an immunodiagnostic dilemma: Heavy chain chimeric antibodies. *Molec. Immunol.* 53: 140– 148.

Chase C, Lunney JK. 2012. Swine Immune System. Chapter 16 In: *Diseases of Swine (10th Edition)* Editors: Zimmerman J, Karriker L, Ramirez A, Schwartz K, Stevenson G. John Wiley & Sons, Inc., Hoboken, NJ. Chp.16. p.227-250.

Choi, I., R.O. Bates, N.E. Raney, J.P. Steibel and C.W. Ernst. 2012. Evaluation of QTL for carcass merit and meat quality traits in a US commercial Duroc population. *Meat Science*. 92:132-138.

Choi, I., J.P. Steibel, R.O. Bates, N.E. Raney and C.W. Ernst. 2012. Identification and evaluation of quantitative trait loci influencing growth, carcass composition, and meat quality traits in pigs. *J. Anim. Sci.* 90(E-Suppl. 2):22.

- Endale Ahanda ML, Fritz ER, Estellé J, Zhi-Liang Hu, Madsen O, Groenen MA, Beraldi D, Kapetanovic R, Hume DA, Rowland RR, Lunney JK, Rogel-Gaillard C, Reecy JM, Giuffra E. (2012). Prediction of Altered 3'-UTR miRNA-Binding Sites from RNA-Seq Data: The Swine Leukocyte Antigen Complex (SLA) as a Model Region. *PLoS One*. 2012;7 (11).
- Freeman, T.C., A. Ivens, K. J. Baillie, D. Beraldi, M.W. Barnett, D. Dorward, A. Downing, L. Fairbairn, R. Kapetanovic, A. Tomoiu, R. Alberio, C. Wu, A. I. Su, K. M. Summers, C.K. Tuggle, A.L. Archibald, D.A. Hume. 2012. A Gene Expression Atlas of the Domestic Pig. *BMC Biology* 10:90.
- Godnic I, Calin GA, Horvat S, Jiang Z, Jevsinek Skok D, Zorc M, Dovc P, Kunej T. 2012. Catalog of microRNA seed polymorphisms in vertebrates. *PLoS ONE* 7: e30737.
- Groenen MAM, Archibald AL, Uenishi H, Tuggle CK, Takeuchi Y, Rothschild MF, Rogel-Gaillard C, Park C, Milan D, Megens HJ, Li S, Larkin DM, Kim H, Frantz LAF, Caccamo M, Ahn H, Aken BL, Anselmo A, Anthon C, Auvil L, Badaoui B, Beattie CW, Bendixen C, Berman D, Blecha F, Blomberg J, Bolund L, Mirte Bosse1, Botti S, Bujie Z, Bystrom M, Capitanu B, Carvalho-Silva D, Chardon P, Chen C, Cheng R, Choi S-H, Chow W, Clark RC, Clee C, Crooijmans RPMA, Dawson HD, Dehais P, De Sapio F, Dibbitts B, Nizar Drou13, Zhi-Qiang Du4, Kellye Eversole26, Fadista J, Fairley S, Faraut T, Faulkner GJ, Fowler KE, Fredholm M, Fritz E, Gilbert JGR, Giuffra E, Gorodkin J, Griffin DK, Harrow JL, HaywardA, Howe K, Hu Z-L, Humphray SJ, Hunt T, Jensen HH, Jeon JT, Jern P, Jones M, Jurka J, Kanamori H, Kapetanovic R, Kim J, Kim J-H, Kim K-W, Kim T-H, Larson G, Lee K, Lee K-T, Leggett R, Lewin HA, Li Y, Liu W, Loveland JE, Lu Y, Lunney JK, Ma J, Madsen O, Mann K, Matthews L, McLaren S, Morozumi T, Murtaugh M, Narayan J, Nguyen DT, Ni P, Oh S-J, Onteru S, Panitz F, Park E-W, Park HS, Pascal G, Paudel Y, Perez-Enciso M, Gonzalez RR, Reecy JM, Rodriguez-Zas S, Rohrer GA, Rund L, Sang Y, Schachtschneider K, Schraiber JG, Schwartz J, Scobie L, Scott C, Searle S, Servin B, Southey BR, Sperber G, Stadler P, Sweedler J, Tafer H, Thomsen B, Wali R, Wang J, Wang J, White S, Xu X, Yerle M, Zhang G, Zhang J, Zhang J, Zhao S, Rogers J, Churcher C, Schook LB. 2012. Pig genomes provide insight into porcine demography and evolution. *Nature*. 491: 393-8.
- Kapetanovic, R., Fairbairn, L., Beraldi, D., Sester, D.P., Tuggle, C.K., and D.A. Hume. 2012. Pig bone marrow-derived macrophages resemble human macrophages in their response to bacterial lipopolysaccharide. *J. Immunology* 188:3382-94.
- Kunej T, Jevsinek Skok D, Zorc M, Ogrinc A, Michal JJ, Kovac M, Jiang Z. 2012. Obesity gene atlas in mammals. *Journal of Genomics* 1: 45-55.
- Li RS, Sun QW, Jia YM, Cong RH, Ni YD, Yang XJ, Jiang Z, Zhao RQ. 2012. Coordinated miRNA/mRNA expression profiles for understanding breed-specific metabolic characters of liver between Erhualian and Large White Pigs. *PLoS ONE* 7: e38716.
- Liu J, Bai J, Lu Q, Zhang L, Jiang Z, Michal JJ, He Q, Jiang P. 2012. Two-dimensional liquid chromatography-tandem mass spectrometry coupled with isobaric tags for relative and absolute quantification (iTRAQ) labeling approach revealed first proteome profiles of pulmonary alveolar macrophages infected with porcine circovirus type 2. *Journal of Proteomics* 79C:72-86.
- Liu, X.L., S.B. Yang, M.F. Rothschild, Z.W. Zhang and B.Fan. 2012. Genome-wide association study of total number born and number born alive in pigs using both compressed mixed linear model and Bayes model. *Yi Chuan*. 34:1261-1270. (Chinese).
- Lu Q, Bai J, Zhang LL, Liu J, Jiang Z, Michal JJ, Jiang P. 2012. Two-dimensional liquid chromatography-tandem mass spectrometry coupled with isobaric Tags for relative and absolute quantification (iTRAQ) labeling approach revealed first proteome profiles of pulmonary alveolar macrophages infected with porcine reproductive and respiratory syndrome virus. *Journal of Proteome Research* 11: 2890–2903.
- Lunney JK. 2012. Genomics and Animal Health. *Advances in Pork Production*. 23: 155-166.
- McCulloch, R.S., Ashwell, M.S., O’Nan, A.T., and Mente, P.L. (2012) Identification of stable normalization genes for quantitative real-time PCR in porcine articular cartilage. *Journal of Animal Science and Biotechnology*. 3:36.

- McKnite, A., Perez-Munoz, M. E., Lu, L., Williams, E., Brewer, S., Andreux, P., Bastiaansen, J., Wang, X., Kachman, S., Auwerx, J., Williams, R., Benson, A., Peterson, D., Ciobanu, D. (2012). Murine Gut Microbiota is Defined by Host Genetics and Modulates Variation of Metabolic Traits. *PLoS One*, 7(6):e39191. Epub 2012 Jun 18.
- Onteru, S.K., B. Fan, Z.Q. Du, D.J. Garrick, K.J. Stalder and M.F. Rothschild. 2012. A whole-genome association study for pig reproductive traits. *Anim Genet*. 43:18-26.
- Rowland R, Lunney JK, Dekkers JCM. 2012 Control of porcine reproductive and respiratory syndrome (PRRS) through genetic improvements in disease resistance and tolerance. *Frontiers in Livestock Genomics*. 3: 260.
- Telugu, B.P.V.L., T. Ezashi, S. Sinha, A.P. Alexenko, L. Spate, R.S. Prather, R.M. Roberts. LIF-dependent, pluripotent stem cells established from inner cell mass of porcine embryos. *Transgenic Research* 21:906.
- Wilke, V.L., Nettleton, D., Wymore, M.J., Gallup, J.M., Demirkale C.Y., Ackermann M.R., Tuggle C.K., Ramer-Tait A.E., Wannemuehler M.J., Jergens A.E. 2012. Gene expression in intestinal mucosal biopsy specimens obtained from dogs with chronic enteropathy. *Am J Vet Res*. 73:1219-29.
- Wysocki, M., H. Chen, J.P. Steibel, D. Kuhar, D. Petry, J. Bates, R. Johnson, C.W. Ernst and J.K. Lunney. 2012. Identifying putative candidate genes and pathways involved in immune responses to porcine reproductive and respiratory syndrome virus (PRRSV) infection. *Anim. Genet*. 43:328-332.
- Yang, C.X., Z.Q. Du, E.C. Wright, M.F. Rothschild, R.S. Prather and J.W. Ross. 2012. Small RNA profile of the cumulus-oocyte complex and early embryos in the pig. *Biol Reprod*. 87:117.
- Zhou X, Michal JJ, Zhang LF, Ding B, Lunney JK, Liu B, Jiang Z. 2013. Interferon-induced IFIT family in host antiviral defense. *International Journal of Biological Sciences* 9(2): 200-208.
- Zhou X, Jiang T, Du X, Zhou P, Jiang Z, Michal JJ, Liu B. 2013. Molecular characterization of porcine SARM1 and its role in regulating TLRs signaling during highly pathogenic porcine reproductive and respiratory syndrome virus infection in vivo. *Developmental & Comparative Immunology* 39:117-26.