

# John B. Cole

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## *Education*

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Certificate in Legislative Studies, Government Affairs Institute at Georgetown University  
(December 2014)

Ph.D., Animal, Dairy, and Poultry Science, Louisiana State University, Baton Rouge (May 2003)  
Advisor: D. E. Franke

Dissertation: *Population structure and genetics of longevity in a colony of dog guides*

M.S., Animal and Dairy Science (Minor: Applied Statistics), Louisiana State University, Baton Rouge (August 1996)

Advisor: R. W. Adkinson

Thesis: *The effect of single and multiple trait selection on somatic cell count and clinical mastitis in dairy cattle*

B.S., Animal Systems (Dairy Production) (Minor: Microbiology), Louisiana State University  
(May 1994)

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## *Work Experience*

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January 2016–Present

Research Leader (Acting)

*Animal Genomics and Improvement Laboratory, Agricultural Research Service, United States Department of Agriculture, Beltsville, MD*

- Managed a Laboratory with four appropriated projects, 31.6 FTE, and an annual appropriated budget of \$8.2 million.
- Used simulation to study the impact of gene editing strategies on Mendelian recessive disorders.
- Estimated economic losses due to known recessive disorders carried by four breeds of US dairy cattle.
- Approximated gene content of non-genotyped animals for all known recessives carried by US Holsteins for use in selection indices.
- Developed a threshold animal model for the evaluation of calving traits in US dairy cattle.
- Created a biobank to collect DNA from calves that die at or near birth, or that have congenital defects, so that causal variants can be identified.

- Identified genomic regions that changed in response to 40 years of selection for divergent body size at comparable levels of production.

May 2014–January 2016

Research Geneticist (Animal)

*Animal Genomics and Improvement Laboratory, Agricultural Research Service, United States Department of Agriculture, Beltsville, MD*

Conducted research to develop procedures to enhance genetic improvement in the efficiency of the nation's dairy population for health and fitness traits.

- Led a project to patch the UMD3.1 *Bos taurus* reference assembly using PacBio long read data from DNA of three BAC clones.
- Used simulation to compare strategies for the management of multiple recessive haplotypes in a dairy cattle population.
- Implemented genetic evaluations for production and fertility (age at first calving and persistency of lactation).
- Researched multivariate statistical approaches for decomposing and comparing genomic (co)variance matrices.
- Used imputed high-density genotypes to identify genomic regions and gene networks associated with fertility in Holstein cattle.

December 2003–April 2014

Research Geneticist (Animal)

*Animal Improvement Programs Laboratory, Agricultural Research Service, United States Department of Agriculture, Beltsville, MD*

Conducted research to develop procedures to enhance genetic improvement in the efficiency of the nation's dairy population for health and fitness traits.

- Designed and carried out a DNA sequencing study to identify the causal variant(s) underlying a quantitative trait locus (QTL) associated with complex phenotypes (conformation and calving traits) on chromosome 18 in Holstein cattle.
- Developed a multi-breed genetic evaluation system for stillbirth in US Brown Swiss, Holstein, and Jersey cattle.
- Conducted genome-wide association studies to identify SNP associated with phenotypes associated with health, fertility, and fitness.
- Derived the first bounds on selection limits and Mendelian sampling effects using haplotypes derived from high-density DNA marker data.
- Developed methods for visualizing high-dimensionality genomics data, including implementation of new reports on the AIPL website to display chromosomal breeding values for net merit and its component traits, as well as SNP marker effects.

- Calculated multiplicative adjustment factors to correct milk, fat, and protein test-day data for effects of region- and season-of-calving, which are easier to compute than standardized lactation curves and provide similar benefits.
- Revised the net merit, fluid merit, and cheese merit selection indices to reflect current and predicted future economic conditions. Based on feed costs for the next five years, greater emphasis was placed on longevity, fertility, and efficiency relative to previous revisions.
- Identified a quantitative trait locus (QTL) associated with dystocia, conformation, longevity, and lifetime economic merit in Holsteins. Developed a physiological explanation for the QTL effect based on comparative bioinformatics with the human and the mouse.
- Enhanced best prediction methodology to account for lactations longer than 305 days. Updated 40 million lactation records in the national dairy database using the new calculations. Obtained industry and Interbull approval for routine use of the new methods for calculation of actual and mature equivalent lactation yields.
- Developed a routine national genetic evaluation for stillbirth in US Holsteins. Calculated economic values and variance components used to incorporate stillbirth into the USDA lifetime economic merit indices. Researched new models for genetic evaluation of dystocia and stillbirth.
- Conducted research into genetic evaluation of persistency of lactation for milk, fat, and protein. Demonstrated that 305 day mature equivalent yield and persistency can be used to predict yield beyond 305 days. Routine national evaluations for these traits have been requested by industry stakeholders.
- Extended the national calving ease genetic evaluation to provide proofs for Brown Swiss and Jersey bulls, as well as utilized records from crossbred offspring of Brown Swiss, Jersey, and Holstein sires. This was the first US evaluation to include data from crossbred animals.
- Developed data exchange format for the collection of producer-recorded health and management traits. Supervised development of edits for incoming data and the beginning of routine national data collection.
- Discovered data sources and implemented daily collection of climate data from 238 stations in the United States. Worked with scientists at the University of Georgia to develop best practices for use of climate data in management and genetic evaluation programs.
- Routinely presented research findings to groups of industry stakeholders, including dairy records processing centers, artificial insemination firms, breed associations, and National DHIA.

- Supervised animal scientists, biological laboratory technicians, computer analysts, and visiting scientists. Established performance objectives, tracked performance, and prepared annual evaluations documenting performance.

January 2011–December 2011

Legislative Fellow

*Senator Mark L. Pryor, United States Senate, Washington, DC*

Worked with staff to support Senator Pryor's legislative agenda, with an emphasis on regulatory reform. Prepared background memos, briefing materials, and vote recommendations. Met with representatives of trade and interest groups. Authored legislation on regulatory reform, scientific publishing, research funding, and tax incentives for volunteer fire and rescue personnel. Provided expert knowledge on issues related to science and agriculture.

Worked closely with Senator Portman's staff on S.1606, the Regulatory Accountability Act of 2011, which was co-sponsored by Senator Pryor and introduced with bipartisan support in the Senate and House of Representatives.

June 2002–December 2003

Data Manager

*Southern Regional Climate Center, Louisiana State University, Baton Rouge*

Data manager for one of six regional climate centers. Discovered, collected, and managed climate data for the southern United States. Designed and wrote several web-based systems for order management and delivery of climate data. Provided statistical and programming support to faculty in the Department of Geography and Anthropology.

June 2000–June 2002

Computer Analyst 2

*PT.NET, College of Education, Louisiana State University, Baton Rouge*

Webmaster for a multi-million-dollar collaborative grant among LSU, Southern University, and the East Baton Rouge Parish School System to develop best practices for the use of educational technology in elementary schools. Developed interactive web-based systems for the grant as well as departments within the College of Education. Provided technical support to grant personnel and faculty and staff at LSU.

January 2001–May 2001

Instructor

*Department of Dairy Science, Louisiana State University, Baton Rouge*

Taught a sophomore-level introductory genetics course to 70 undergraduates in the College of Agriculture. Scored above the College of Agriculture average on the end-of-semester Student Perception of Teaching evaluation.

Summer 1998 & 1999

Seminar Coordinator

*Life Sciences Summer Undergraduate Research Program, University of Minnesota, St. Paul*

Mentored groups of 12 undergraduates participating in a seven-week summer research program during which they participated in research projects in faculty laboratories.

Taught presentation skills during weekly seminars and assisted students with preparation of posters describing their research at the end of the summer. Worked with students to resolve laboratory and administrative issues.

September 1996–May 2000

Graduate Assistant

*Department of Animal Science, University of Minnesota, St. Paul*

Planned and conducted research under the supervision of a faculty advisor. Lectured and assisted with laboratory exercises as needed for classes in introductory animal science, animal breeding, biometrics, and dairy production.

June 1994–May 1996

Graduate Research Assistant

*Department of Dairy Science, Louisiana State University of Minnesota, Baton Rouge*

Conducted research under the supervision of a faculty advisor. Assisted with lectures and laboratory exercises for classes in introductory genetics and animal breeding.

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### ***Research Interests***

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Identification of causal variants associated with recessive genetic disorders in cattle.

Genetic improvement of health and fitness traits in dairy cattle

Use of genomic data to understand the biology of genes of large effect

Use of high-density SNP genotypes for mate selection and on-farm management decision-making

Population structure, systems of mating, and conservation genetics applied to livestock and companion animal species

Integration of whole-genome sequencing data and high-density SNP genotypes for identification of causative mutations underlying QTL associated with complex phenotypes

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### ***Refereed Journal Articles*** (23 first author, 67 co-author)

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2017

**Cole, J.B.** 2017. Managing recessive disorders in breeding programs by gene editing. *J. Dairy Sci.* (In preparation.)

**Cole, J.B.,** J.M. Bormann, C.A. Gill, H. Khatib, J.E. Koltas, C. Maltecca, and F. Miglior. 2017. Breeding and Genetics Symposium: Resilience of livestock to changing environments. *J. Animal Sci.* (In press.)

Dikmen, S., G.E. Dahl, **J.B. Cole**, D.J. Null, and P.J. Hansen. 2017. The Larson Blue coat color phenotype in Holsteins: characteristics and effects on body temperature regulation and production in lactating cows in a hot climate. *J. Animal Sci.* (Accepted.)

- Heringstad, B., C. Egger-Danner, A.J. Bradley, A.-M. Sogstad, D. Döpfer, A. Fiedler, F. Malchiodi, K.F. Stock, G. de Jong, T. Gilles, J. Burgstaller, K. Müller, M. Alsaod, F. Miglior, M. Holzhauser, N. Gengler, N. Charfeddine, and **J.B. Cole**. 2017. Invited Review: Genetics and claw health: opportunities to enhance claw health by genetic selection. *Animal* (In preparation.)
- Hutchison, J.L., P.M. VanRaden, D.J. Null, J.B. Cole, and D.M. Bickhart*. 2017. Benefits associated with reduced age at first calvingx for U.S. dairy cattle. *J. Dairy Sci.* (Submitted.)
- McClure, M.C., T.S. Sonstegard, C.W. Wolfe, *D.J. Null, D.M. Bickhart, L. Xu, H.J. Huson, H.D. Blackburn, G.R. Wiggans, G.E. Liu, J.B. Cole, and C.P. Van Tassell*. 2017. A rectovaginal constriction defect of Jersey cattle maps to the location of the Early B-Cell 1 Factor (*EBF1*) gene on chromosome 7. *Genet. Sel. Evol.* (Submitted.)
- Oliveira, Jr., G.A., T.C.S. Chud, R.V. Ventura, D.J. Garrick, **J.B. Cole**, D.P. Munari, J.B.S. Ferraz, E. Mullart, S. DeNise, and M.V.G.B. da Silva. 2017. Genotype imputation in a crossbred (*Bos primigenius indicus* × *Bos primigenius taurus*) dairy cattle population. *J. Dairy Sci.* (Submitted.)
- Ortega, M.S., A.C. Denicol, J.B. Cole, D.J. Null, J.F. Taylor, R.D. Schnabel, and P.J. Hansen*. 2017. Association of single nucleotide polymorphisms in candidate genes previously related to genetic variation in fertility with phenotypic measurements of reproductive function in Holstein cows. *J. Dairy Sci.* (Accepted.)
- Ortega, M.S., S. Wohlgenuth, P. Tribulo, L.G. Siqueira, D.J. Null, J.B. Cole, M.V.G.B. da Silva, and P.J. Hansen*. 2017. A single nucleotide polymorphism in *COQ9* affects mitochondrial and ovarian function, body weight change after calving, and fertility in Holstein cows. *Biol. Reprod.* (Accepted.)
- Parker Gaddis, K.L., S. Dikmen, J.B. Cole, and P.J. Hansen*. 2017. Evaluation of genetic components in traits related to superovulation, in vitro fertilization, and embryo transfer in Holstein cattle. *J. Dairy Sci.* (In press.) doi:<http://dx.doi.org/10.3168/jds.2016-11907>.
- Stafuzza, N.B., A. Zerlotini, F.P. Lobo, M.E.B. Yamagishi, M.E. Buzanskas, T.C.S. Chud, A.R. Caetano, D.P. Munari, D.J. Garrick, M.A. Machado, M.F. Martins, M.R. Carvalho, **J.B. Cole**, and M.V.G.B. da Silva. 2017. Identification of genetic variants with potential loss of function in Gyr, Girolando, and Guzerat cattle breeds by resequencing. *PLOS ONE* (Submitted.)
- Stafuzza, N.B., A. Zerlotini, F.P. Lobo, M.E.B. Yamagishi, T.C.S. Chud, A.R. Caetano, D.P. Munari, D.J. Garrick, M.A. Machado, M.F. Martins, M.R. Carvalho, **J.B. Cole**, and M.V.G.B. da Silva. 2017. Single nucleotide variants and indels identified from whole-genome resequencing of Guzerat, Gyr, and Girolando cattle breeds. *PLOS ONE* (Submitted.)

- Thompson, N.M., N.O. Widmar, M.M. Schutz, **J.B. Cole**, and C.A. Wolf. 2017. Economic and social considerations of breeding for polled dairy cows versus dehorning. *J. Dairy Sci.* (Accepted.)
- VanRaden, P.M., M.E. Tooker, J.R. O'Connell, D.M. Bickhart, and **J.B. Cole**. 2017. Selection of sequence variants to improve dairy cattle genomic predictions. *Genet. Sel. Evol.* (Submitted.)
- Wiggans, G.R., **J.B. Cole**, *S.M. Hubbard*, and T.S. Sonstegard. 2017. Genomic selection in dairy cattle: the USDA experience. *Ann. Rev. Anim. Biosci.* Review in Advance first posted online on November 16, 2016. doi:10.1146/annurev-animal-021815-111422.
- Zhou, Y., B. Shen, J. Jiang, A. Padhi, K.-E. Park, B.P. Telugu, H. Chen, **J.B. Cole**, G.E. Liu, and L. Ma. 2017. Construction of *PRDM9* allele-specific recombination maps in cattle using large-scale pedigree analysis and genome-wide single sperm genomics. *PLOS Genetics* (Submitted.)
- 2016 Bickhart, D.M., J.L. Hutchison, *D.J. Null*, P.M. VanRaden, and **J.B. Cole**. 2016. Reducing animal sequencing redundancy by preferentially selecting animals with low-frequency haplotypes. *J. Dairy Sci.* 99: 5526–5534. doi:10.3168/jds.2015-10347.
- Bickhart, D.M., L. Xu, J.L. Hutchison, **J.B. Cole**, *D.J. Null*, S.G. Schroeder, J. Song, J.F. Garcia, T.S. Sonstegard, C.P. Van Tassell, R.D. Schnabel, J.F. Taylor, H.A. Lewin, and G.E. Liu. 2016. Diversity and population-genetic properties of copy number variations and multicopy genes in cattle. *DNA Res.* 3:253–262. doi:10.1093/dnares/dsw013.
- Cole, J.B.**, *D.J. Null*, and P.M. VanRaden. 2016. Phenotypic and genetic effects of recessive haplotypes on yield, longevity, and fertility. *J. Dairy Sci.* 99: 7274–7288.
- Cole, J.B.**, and M.V.G.B. da Silva. 2016. Invited Review: Genomic selection in multi-breed dairy cattle populations. *Revista Brasil. Zootec.* 45:195–202. <http://dx.doi.org/10.1590/S1806-92902016000400008>.
- García-Ruiz, A.*, **J.B. Cole**, P.M. VanRaden, G.R. Wiggans, F.J. Ruiz-López, and C.P. Van Tassell. 2016. Changes in genetic selection differentials and generation intervals in US Holstein dairy cattle as a result of genomic selection. *Proc. Natl. Acad. Sci. USA.* 113:E3995–4004. doi:10.1073/pnas.1519061113.
- Kaniyamattam, K., M.A. Elzo, **J.B. Cole**, and A. De Vries. 2016. A stochastic dynamic simulation model including multi-trait genetics to estimate genetic, technical and financial consequences of dairy farm reproduction and selection strategies. *J. Dairy Sci.* 99:8187–8202. <http://dx.doi.org/10.3168/jds.2016-11136>.
- Ortega, M.S., A.C. Denicol, **J.B. Cole**, *D.J. Null*, and P.J. Hansen. 2016. Use of single nucleotide polymorphisms in candidate genes associated with daughter pregnancy rate for prediction of genetic merit for reproduction in Holstein cows. *Anim. Genet.* 47:288–297. doi: 10.1111/age.12420.



*Parker Gaddis, K.L., J.B. Cole, J.S. Clay, and C. Maltecca.* 2016. Benchmarking dairy herd health status using routinely recorded herd summary data. *J. Dairy Sci.* 99:1298–1314.

*Parker Gaddis, K.L., D.J. Null, and J.B. Cole.* 2016. Explorations in genome-wide association studies and network analyses with dairy cattle fertility traits. *J. Dairy Sci.* 99:6420–6435. doi:10.3168/jds.2015-10444.

*Pryce, J., K. Parker Gaddis, A. Koeck, C. Bastin, M. Abdelsayed, N. Gengler, F. Miglior, B. Heringstad, C. Egger-Danner, K. Stock, A. Bradley, and J. Cole.* 2016. Invited Review: Opportunities for genetic improvement of metabolic diseases. *J. Dairy Sci.* 99:6856–6873. doi:http://dx.doi.org/10.3168/jds.2016-10854.

2015 **Cole, J.B.** 2015. A simple strategy for managing many recessive disorders in a dairy cattle breeding program. *Genet. Sel. Evol.* 47:94. doi:10.1186/s12711-015-0174-9.

*Dikmen, S., X. Wang, M.S. Ortega, J.B. Cole, D.J. Null, and P.J. Hansen.* 2015. Single nucleotide polymorphisms associated with thermoregulation in lactating dairy cows exposed to heat stress. *J. Anim. Breed. Genet.* 132:409–419.

*Ma, L., J.R. O'Connell, P.M. VanRaden, B. Shen, A. Padhi, C. Sun, D.M. Bickhart, J.B. Cole, D.J. Null, Y. Da, and G.R. Wiggans.* 2015. Cattle sex-specific recombinations and their genetic control from a large pedigree analysis. *PLOS Genet.* 11:e1005387. doi:10.1371/journal.pgen.1005387.

*Parker Gaddis, K.L., F. Tiezzi, J.B. Cole, J.S. Clay, and C. Maltecca.* 2015. Genomic prediction of disease occurrence using producer-recorded health data: A comparison of methods. *Genet. Sel. Evol.* 47:41.

*Tiezzi, F., K.L. Parker Gaddis, J.B. Cole, J.S. Clay, and C. Maltecca.* 2015. A genome-wide association study for clinical mastitis in first parity US Holstein cows using single-step approach and genomic matrix re-weighting procedure. *PLoS ONE* 10:e0114919. doi:10.1371/journal.pone.0114919.

*Zavarez, L.B., Y.T. Utsunomiya, A.S. Carmo, H.H.R. Neves, R. Carneiro, M. Ferenčaković, A.M. Pérez O'Brien, I. Curik, J.B. Cole, C.P. Van Tassell, M.V.G.B. da Silva, T.S. Sonstegard, J. Sölkner, and J.F. Garcia.* 2015. Assessment of autozygosity in Nelore cows (*Bos indicus*) through high-density SNP genotypes. *Front. Livest. Gen.* 6(5):1–8. doi:10.3389/fgene.2015.00005.

2014 **Cole, J.B.,** B. Waurich, M. Wensch-Dorendorf, D.M. Bickhart, and H.H. Swalve. 2014. A genome-wide association study of calf birth weight in Holstein cattle using single nucleotide polymorphisms and phenotypes predicted from auxiliary traits. *J. Dairy Sci.* 97:3156–3172.

*Cooper, T.A., G.R. Wiggans, D.J. Null, J.L. Hutchison, and J.B. Cole.* 2014. Genomic evaluation, breed identification, and discovery of a haplotype affecting fertility for Ayrshire dairy cattle. *J. Dairy Sci.* 97:3878–3882. doi:10.3168/jds.2013-7427.



- da Silva, M.V.G.B., D.J.A. dos Santos, S.A. Boison, A.T.H. Utsunomiya, A.S. do Carmo, T.S. Sonstegard, **J.B. Cole**, and C.P. Van Tassell. 2014. The development of genomics applied to dairy breeding. *Livest. Sci.* 166:66–75. doi:10.1016/j.livsci.2014.05.017.
- Egger-Danner, C., **J.B. Cole**, J. Pryce, N. Gengler, B. Heringstad, A. Bradley, L. Andrews, and K.F. Stock. 2014. Invited review: overview of new traits and phenotyping strategies in dairy cattle with a focus on functional traits. *Animal* 9:191–207. doi:10.1017/S1751731114002614.
- Gay, K.D., N.J. Widmar, T.D. Nennich, A.P. Schinckel, **J.B. Cole**, and M.M. Schutz. 2014. Development of a lifetime merit-based selection index for US dairy grazing systems. *J. Dairy Sci.* 97:4568–4578. doi:10.3168/jds.2013-7474.
- Hutchison, J.L., J.B. Cole*, and D.M. Bickhart. 2014. Short Communication: Use of young bulls in the United States. *J. Dairy Sci.* 97:3213–3220. doi:10.3168/jds.2013-7525.
- Macciotta, N.P.P., C. Dimauro, D.J. Null, G. Gaspa, M. Cellesi, and **J.B. Cole**. 2014. Dissection of genomic correlation matrices of US Holsteins using multivariate factor analysis. *J. Anim. Breed. Genet.* 132:9–20. doi:10.1111/jbg.12113.
- McClure, M.C., D.M. Bickhart, D.J. Null, P.M. VanRaden, L. Xu, G.R. Wiggans, G. Liu, S.G. Schroeder, J. Glasscock, J. Armstrong, **J.B. Cole**, T.S. Sonstegard, and C. P. Van Tassell. 2014. Bovine exome sequence analysis and targeted SNP genotyping of recessive fertility defects HH2, HH3, and BH1 reveals causative mutation in SMC2 for HH3. *PLoS ONE* 9:e92769. doi:10.1371/journal.pone.0092769.
- McDaneld, T.G., L.A. Kuehn, M.G. Thomas, W.M. Snelling, T.P.L. Smith, E.J. Pollak, **J.B. Cole**, and J.W. Keele. 2014. Genome-wide association study of reproductive efficiency in female cattle. *J. Anim. Sci.* 92:1945–1957.
- Neves, H.H.R., R. Carvalheiro, A.M. Pérez O'Brien, Y.T. Utsunomiya, A.S. do Carmo, F.S. Schenkel, J. Sölkner, J.C. McEwan, C.P. Van Tassell, T.S. Sonstegard, **J.B. Cole**, M.V.G.B. da Silva, S.A. Queiroz, and J.F. Garcia. 2014. Accuracy of genomic predictions in *Bos indicus* (Nelore) cattle. *Genet. Sel. Evol.* 46:17. doi:10.1186/1297-9686-46-17.
- Parker Gaddis, K.L., J.B. Cole*, J.S. Clay, and C. Maltecca. 2014. Genomic selection for producer-recorded health event data in U.S. dairy cattle. *J. Dairy Sci.* 97:3190–3199.
- Sun, C., P.M. VanRaden, **J.B. Cole**, and J.R. O'Connell. 2014. Improvement of prediction ability for genomic selection of dairy cattle by including dominance effects. *PLoS ONE* 9(8):e103934. doi:10.1371/journal.pone.0103934.
- Utsunomiya, Y.T., A.S. do Carmo, H.H.R. Neves, R. Carvalheiro, L.B. Zavarez, P.K.R.K. Ito, A.M. Pérez O'Brien, J. Sölkner, L.R. Porto Neto, F.S. Schenkel, J. McEwan, **J.B. Cole**, M.V.G.B. da Silva, C.P. Van Tassell, T.S. Sonstegard, and J.F. Garcia. 2014. Genome-wide scan identifies putative genetic variants and genes associated with scrotal circumference in Nelore cattle. *PLoS ONE* doi:10.1371/journal.pone.0088561.

Weller, J.I., J.B. Cole, P.M. VanRaden, and G.R. Wiggans. 2014. Application of the *a posteriori* granddaughter design to the Holstein genome. *Animal* 8:511–519. <http://dx.doi.org/10.1017/S1751731114000111>.

Xu, L., D.M. Bickhart, **J.B. Cole**, P.M. VanRaden, J. Song, T.S. Sonstegard, C.P. Van Tassell, and G.E. Liu. 2014. Genomic signatures reveal new evidences for selection of important traits in domestic cattle. *Mol. Biol. Evol.* 32: 711–725. doi:10.1093/molbev/msu333.

Xu, L., **J.B. Cole**, Y. Hou, D.M. Bickhart, J. Song, P.M. VanRaden, T.S. Sonstegard, C.P. Van Tassell, and G.E. Liu. 2014. Genome wide CNV analysis reveals additional variants associated with milk production traits in Holsteins. *BMC Genomics* 15:683–692. doi:10.1186/1471-2164-15-683.

Yao, C., K.A. Weigel, and **J.B. Cole**. 2014. Short Communication: Genetic evaluation of stillbirth in US Brown Swiss and Jersey cattle. *J. Dairy Sci.* 97:2474–2480.

2013

Cochran, S.J., **J.B. Cole**, D.J. Null, and P.J. Hansen. 2013. Discovery of single nucleotide polymorphisms in candidate genes associated with fertility and production traits in Holstein cattle. *BMC Genetics* 14:49–71. doi:10.1186/1471-2156-14-49.

Cochran, S.J., **J.B. Cole**, D.J. Null, and P.J. Hansen. 2013. Single nucleotide polymorphisms in candidate genes associated with fertilizing ability of sperm and subsequent embryonic development in cattle. *Biol. Reprod.* 69:1–7. doi:10.1095/biolreprod.113.111260.

**Cole, J.B.**, R.M. Lewis, C. Maltecca, S. Newman, K.M. Olson, and R.G. Tait, Jr. 2013. Systems Biology in Animal Breeding: Identifying relationships among markers, genes, and phenotypes. *J. Anim. Sci.* 91:521–522. doi:10.2527/jas.2012-6166.

**Cole, J.B.**, and D.J. Null. 2013. Visualization of the transmission of direct genomic values for paternal and maternal chromosomes for fifteen traits in U.S. Brown Swiss, Holstein, and Jersey cattle. *J. Dairy Sci.* 96:2713–2726. doi:10.3168/jds.2012-6008.

Dikmen, S., **J.B. Cole**, D.J. Null, and P.J. Hansen. 2013. Genome-wide association mapping for identification of quantitative trait loci for rectal temperature during heat stress in Holstein cattle. *PLoS ONE* 8:e69202. doi:10.1371/journal.pone.0069202.

Hutchison, J.L., P.M. VanRaden, H.D. Norman, and **J.B. Cole**. 2013. Technical Note: Changes to herd cutoff date in conception rate evaluations. *J. Dairy Sci.* 96:1264–1268. doi:10.3168/jds.2012-6203.

Kim, E.-S., **J.B. Cole**, H. Huson, G.R. Wiggans, C.P. Van Tassell, B.A. Crooker, Y. Da, and T.S. Sonstegard. 2013. Effect of artificial selection on runs of homozygosity in U.S. Holstein cattle. *PLoS ONE* 8:e80813. doi:10.1371/journal.pone.0080813.

McClure, M.C., E.-S. Kim, D. Bickhart, D.J. Null, T.A. Cooper, **J.B. Cole**, G.R. Wiggans, P.A. Marsan, L. Colli, E. Santus, G. Liu, S.G. Schroeder, L.K. Matukumalli, C.P. Van Tassell, and T.S. Sonstegard. 2013. Fine mapping for Weaver Syndrome in the Brown Swiss breed with the identification of possible causal mutations across NRCAM, PNPLA8 and

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### *Software*

- Cole, J.B.** 2017. gene-editing: Programs for simulation of strategies for managing multiple recessives in a dairy cattle population using gene editing.

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- Cole, J.B.** 2010. PyPedal: A package for pedigree analysis using the Python programming language, v. 2.0.0. Website: <http://pypedal.sourceforge.net/>.
- Cole, J.B.**, and P.M. VanRaden. 2007. A Manual for Use of BESTPRED: A Program for Estimation of Lactation Yield and Persistency Using Best Prediction. Website: <http://www.aipl.arsusda.gov/software/bestpred/>.

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***Invited Presentations*** (26 domestic, 21 international)

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- 2017 June 2017. Possibilities in an age of genomics. The future of the breeding index in the ADSA Multidisciplinary and International Leadership Keynote (MILK) Symposium: The dairy cow in 50 years. ADSA, Pittsburgh, PA.
- 2016 October 2016. Updated guidelines for the recording, evaluation, and genetic improvement of udder health in dairy cattle. ICAR, Puerto Vargas, Chile.
- October 2016. Managing genetic disorders in cattle breeding programs. 18th State Congress of Veterinary Medicine, Canela, Brasil.
- May 2016. The role of phenotyping in dairy cattle improvement in the genomic era, Department of Dairy Science, University of Wisconsin, Madison.
- May 2016. Improving production efficiency through genetic selection. Large Dairy Herd Management Conference, Oak Brook, IL.
- March 2016. What direction should US dairy research take in the future? 51st National DHIA Annual Meeting, Orlando, FL.
- 2015 July 2015. Genomic selection in multiple-breed cattle populations. 52a Reunião Anual da Sociedade Brasileira de Zootecnia, Belo Horizonte, Brasil.
- May 2015. Genomic selection for traits other than production in dairy cattle. XX ANEMBE International Congress, Burgos, Spain.
- May 2015. What should you expect from genomic selection? XX ANEMBE International Congress, Burgos, Spain.
- April 2015. Using genotypes to construct phenotypes for dairy cattle breeding programs and beyond. Final OptiMIR Scientific and Expert Meeting, Namur, Belgium.
- March 2015. If we would see further than others: research & technology today and tomorrow. 50<sup>th</sup> National DHIA Annual Meeting, Columbus, OH.
- 2014 September 2014. Genetic improvement programs for US dairy cattle. Embrapa Gado de Leite, Juiz de Fora, MG, Brasil.

September 2014. Using genotyping and whole-genome sequencing to identify causal variants associated with complex phenotypes. Universidade Federal de Viçosa, Viçosa, MG, Brasil.

August 2014. The hunt for a functional mutation affecting conformation and calving traits on chromosome 18 in Holstein cattle. 10<sup>th</sup> World Congress on Genetics Applied to Livestock Production, Vancouver, BC, Canada.

May 2014. Phenotypes for novel functional traits of dairy cattle. International Committee for Animal Recording, Berlin, Germany.

March 2014. Health and fitness data – what might be possible for dairy cattle? and AIPL Update National DHIA Annual Meeting, St. Louis, MO.

2013

October 2013. Opportunities for Research on Applied Livestock Genomics. Department of Animal Sciences, Purdue University, West Lafayette, IN.

September 2013. Genomic Evaluation of Low-Heritability Traits: Dairy Cattle Health as a Model. 5<sup>th</sup> International Symposium on Animal Functional Genomics, Guarujá, SP, Brazil.

May 2013. Genomic Evaluation of Dairy Cattle Health. ICAR 2013 Health Data Conference, Aarhus, Denmark.

May 2013. Use of NGS to Identify the Causal Variant Associated with a Complex Phenotype. Wageningen University and Research Center, the Netherlands.

May 2013. Genomic Selection and Systems Biology – Lessons from Dairy Cattle Breeding. KeyGene nv, Wageningen, the Netherlands.

March 2013. Opportunities for Genetic Improvement of Health and Fitness Traits. 2013 National DHIA Annual Meeting, St. Pete Beach, Florida.

February 2013. The Use and Economic Value of Genomic Testing for Calves on Dairy Farms. ANAFI Genomics Workshop, Cremona, Italy.

2012

November 2012. Genomic Selection – Dairy Cattle Successes and Challenges. National Swine Improvement Federation, Kansas City, MO.

August 2012. Applications of Haplotypes in Dairy Farm Management. 63<sup>rd</sup> EAAP Meeting, Bratislava, Slovak Republic.

May 2012. Use of Dense SNP Chips for Gene Discovery. 16<sup>th</sup> QTL-MAS Workshop, Alghero, Italy.

May 2012. The U.S. Genetic Evaluation System. Department of Animal Sciences, University of Sassari, Sardinia, Italy.

May 2012. New Tools for Genomic Selection of Livestock. Department of Animal Sciences, University of Sassari, Sardinia, Italy.

April 2012. New Tools for Genomic Selection of Livestock. Department of Animal Science, North Carolina State University, Raleigh.

- March 2012. March 2012 AIPL Update. Select Sires Holstein Sire Evaluation Committee, Columbus, OH.
- February 2012. Genomics Beyond EBVs. 2nd International Workshop on Genomics Applied to Livestock, Araçatuba, SP, Brazil.
- 2011 July 2011. Data Structures and Visualization. 2011 ADSA/ASAS Joint Annual Meeting, New Orleans, LA.
- 2010 November 2010. What Can We Do With Dairy Cattle Genomics Other Than Predict More Accurate Breeding Values? Department of Animal Science, North Carolina State University, Raleigh.
- November 2010. Age at First Calving in Holstein Cattle in the United States. Dairy Cattle Reproduction Council, St. Paul, MN.
- 2009 November 2009. Biological Insights from the Implementation of a Genomic Selection Program in Dairy Cattle. Institute of Genetics, Vetsuisse Faculty, University of Berne, Switzerland.
- November 2009. Identifying Markers Associated with Thermal Tolerance. 18th DISCOVER Conference on Food Animal Agriculture: Effect of the Thermal Environment on Nutrient and Management Requirements of Cattle, Nashville, IN. (Declined)
- October 2009. Visualization of Results from Genomic Evaluation. Department of Animal Sciences, Colorado State University, Fort Collins.
- March, 2009. Distribution and Location of Genetic Effects for Dairy Traits. CRI Genomics Emerging Markets Program, Washington, D.C.
- 2008 June 2008. Best Predictions of Daily and Lactation Yields and Data Collection Ratings. International Committee for Animal Recording, Niagara Falls, NY.
- 2007 September 2007. Best Prediction of Actual Lactation Yields. AgriTech Analytics & Holstein Association USA Dairy Industry Event, Visalia, CA.
- September 2007. Overview of Animal Improvement Programs Laboratory. Department of Animal Sciences, Louisiana State University, Baton Rouge.
- September 2007. Genetic Evaluation of Calving Traits in U.S. Holsteins. Department of Animal Sciences, Louisiana State University, Baton Rouge.
- June 2007. Validation of Producer-Recorded Health Event Data and Use in Genetic Improvement of Dairy Cattle. Department of Animal Sciences, University of Florida, Gainesville.
- 2006 October 2006. Genetic Evaluation of Calving Traits in U.S. Holsteins. Breeding and Genetics group, Department of Animal Sciences, Colorado State University, Fort Collins.
- October 2006. Dairy Cattle Breeding in the United States. Department of Animal Sciences, Colorado State University, Fort Collins.



February 2006. Genetic Evaluation of Calving Traits. Department of Animal and Dairy Science, University of Georgia, Athens.

2003

August 2003. Genetics Applied to the Working Dog. International Seppala Siberian Sleddog Club Annual Meeting, Seeley, MT.

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### ***Grants Awarded*** (1 PD, 7 co-PD)

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Co-principal investigator on a \$350,000 AFRI foundational proposal “Sequence-Based Big Data Genomic Discovery and Application to Improve Dairy Fertility” (L. Ma, et al.).

Co-principal investigator on a \$174,000 CNPq “Science Without Borders” proposal titled “Genomic Selection for Dairy Cattle in Brazil” (M.V.G.B. Da Silva and J.B. Cole).

Co-principal investigator on a \$585,717 NSF grant titled “ABI Innovation: An Integrative Approach to Identifying Highly Heritable Subtypes of Complex Phenotypes” (J. Bi et al.).

Co-principal investigator on a \$3,000,000 Agriculture and Food Research Initiative integrated proposal titled “Improving Fertility of Dairy Cattle Using Translational Genomics” (T.E. Spencer, P.J. Hansen, J.B. Cole, J.C. Dalton, S. Dindot, J. McNamara, D.A. Moore, H. Neibergs, and S. Neibergs).

Co-principal investigator on an \$18,000 Southeast Milk, Inc. Milk Checkoff Program proposal titled “Development of tools to select cattle that are genetically resistant to heat stress” (P.J. Hansen, S. Dikmen, and J.B. Cole, 7/1/2011–6/30/2012).

Co-principal investigator on a \$1,000,000 integrated Agriculture and Food Research Initiative proposal titled “Improving Fertility During Heat Stress in Lactating Dairy Cows” (Grant No. 2009-05159).

Co-principal investigator on a \$450,000 Cooperative State Research, Extension, and Education Service National Research Initiative grant for a proposal titled “Genomic Signature of Artificial Selection and Genome-Wide Association Analysis in Holstein Cows” (Grant No. 2008-35205-18846).

Principal investigator on a \$500 grant from The Seeing Eye, Inc., Morristown, NJ, USA, for a proposal titled “Genetic Analysis in a Colony of Guide Dogs”.

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### ***Teaching Experience***

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Guest Lecturer, ANEQ575: Computational Biology in Animal Breeding, Colorado State University, Spring 2009.

Instructor, DARY 2072: Introductory Agricultural Genetics, LSU, Spring 2001.

Lecturer, AGRI 2072: Plant and Animal Genetics, LSU, Spring 1996.

Lecturer, ANSC 1101: Introductory Animal Science, University of Minnesota, 1996–2000.

Lecturer, ANSC 2211: Biometrics for Livestock, University of Minnesota, 2000.



Lecturer, ANSC 3221: Animal Breeding, University of Minnesota, 1996–2000.

Lecturer, DARY 4018: Applied Animal Breeding and Genetics, LSU, 1995.

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### *Graduate Committees*

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Mike Donnelly, University of Minnesota, M.S. (Advisors: L.B. Hansen and A.J. Seykora)  
(External Reviewer)

Allison Fleming, University of Guelph, Ph.D. (Advisor: F. Miglior) (External Reviewer)

Sofia Ortega, University of Florida, Ph.D. (Advisor: P.J. Hansen)

Kristen L. Parker Gaddis, North Carolina State University, Ph.D. (Advisor: C. Maltecca)

Chen Yao, University of Wisconsin, Ph.D. (Advisor: K.A. Weigel)

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### *Postdoctoral Scientists Supervised*

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Kristen L. Parker Gaddis (2014-2016)

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### *Training*

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“Committees and Parties in Congress”, The Government Affairs Institute at Georgetown University, Washington, D.C., September 17–December 12, 2014.

“Congressional Power and Presidential Authority”, The Government Affairs Institute at Georgetown University, Washington, D.C., September 25–December 24, 2013.

“Appropriations and the Federal Agencies”, The Government Affairs Institute at Georgetown University, Washington, D.C., November 21–22, 2011.

“Preparing and Delivering Congressional Testimony”, The Government Affairs Institute at Georgetown University, Washington, D.C., March 28–29, 2011.

“Executive-Legislative Branch Relations”, The Government Affairs Institute at Georgetown University, Washington, D.C., February 24–25, 2011.

“Advanced Budget and Appropriations Process”, The Government Affairs Institute at Georgetown University, Washington, D.C., January 20–21, 2011.

“Collateral Duty Course for Federal Employees (OSHA 6000)”, SOHES-BARC-ARS-USDA, Beltsville, MD, June 9–29, 2010.

“ARS Congressional Briefing Conference”, The Government Affairs Institute at Georgetown University, Washington, D.C., March 8–11, 2010.

“Writing Winning Grants”, University of Maryland, College Park, MD, November 13, 2008.

“Presenting Data and Information”, Edward Tufte, Arlington, VA, May 24, 2007.

“Seminar for New Managers: Blended Course”, United States Office of Personnel Management, Western Management Development Center, Aurora, CO, April 3–May 19, 2006.

- “Fast Track to ColdFusion MX7”, Fig Leaf Software, Washington, DC, June 6–8, 2005.
- “Longitudinal Data Analysis with Continuous and Discrete Responses”, The SAS Institute, Inc., Rockville, MD, September 16–17, 2004.
- “Mixed Models Analysis Using the SAS System”, The SAS Institute, Inc., Rockville, MD, November 17–19, 2004.
- “Predictive Modeling Using Logistic Regression”, The SAS Institute, Inc., Rockville, MD, December 2–3, 2004.

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### *Professional Affiliations*

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- Chair of the Breeding and Genetics Program Committee for the 2016 American Dairy Science Association/American Society for Animal Science Joint Annual Meeting (2015–2016)
- Chair of the Breeding and Genetics Program Committee for the 2012 American Dairy Science Association/American Society for Animal Science Joint Annual Meeting (2011–2012)
- Member of the American Dairy Science Association (2000–present)
- Member of the Dairy Health Data Recording Project Advisory Board (2010–present)
- Member of the Editorial Board for Frontiers in Livestock Genomics (2010–present)
- Member of the Editorial Board for the Journal of Animal Science (2006–2010)
- Member of the Functional Traits Working Group of the International Committee for Animal Recording (2010–present)
- Member of Gamma Sigma Delta, The Honor Society of Agriculture (1998–present)
- Member of National Dairy Shrine (2004–present)
- Member of the Breeding and Genetics Program Committee for the 2010, 2011, 2014, and 2015 American Dairy Science Association Joint Annual Meetings (2009–2011; 2013–2015)
- Member of the Planning Committee for the 2013 International Committee for Animal Recording Health Data Conference in Aarhus, Denmark (2012–2013).
- Non-voting member of Holstein Association USA's Genetic Advancement Committee (2006–2007)
- Secretary and President of the S-1040 regional research project (“Genetic Selection and Crossbreeding to Enhance Reproduction and Survival of Dairy Cattle”) (2009–2010)
- Secretary and President of the SCC-084 coordinating committee (“Genetic selection and mating strategies to improve the well-being and efficiency of dairy cattle”) (2014–2015)

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### *Awards and Honors*

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- 2016 Editor’s Choice Article of the Month in Genetics and Breeding (co-author), Journal of Dairy Science, October 2016.

2016 Editor's Choice Article of the Month in Genetics and Breeding (senior author), Journal of Dairy Science, September 2016.

2015 Jay L. Lush Award in Animal Breeding and Genetics, American Dairy Science Association, for outstanding research in animal breeding with the potential for improvement of dairy cattle.

2015 Award of Recognition, Council on Dairy Cattle Breeding, for international development of genomic predictions for dairy cattle (group award).

2014 Editor's Choice Article of the Month in Our Industry Today (co-author), Journal of Dairy Science, July 2014.

2014 Editor's Choice Article of the Month in Genetics and Breeding (senior author), Journal of Dairy Science, May 2014.

2014 High Impact Research Publication (one of eight publications selected, co-author), Institute of Food and Agricultural Sciences, University of Florida.

2013 Editor's Choice Article of the Month in Genetics and Breeding (co-author), Journal of Dairy Science, February 2013.

2010 USDA Secretary's Honor Award, Cattle Genomics Consortium, for helping America promote sustainable agricultural production and biotechnology exports as America works to increase food security (group award).

2008 President's Volunteer Service Award, Silver Award

1994 Southern ADSA-SAD Undergraduate Paper Presentation Contest, Production, 3rd Place

1993 Southern ADSA-SAD Undergraduate Paper Presentation Contest, Manufacturing, 1st Place

1990 Recipient of the J. B. Frye, Jr. Scholarship in Dairy Science