

Hongding Gao | Curriculum Vitae

☎ + (45) 6090 9996 • 📞 + (45) 8715 7696
✉ hongding.gao@mbg.au.dk • 🌐 www.hongdinggao.com
Born: 19. October, 1984

Fields of Interest

- o Statistical methods of genetic evaluation and genomic selection
- o Computational biology in quantitative genetics and genomics
- o Animal breeding and genetics

Professional Experience

- o Researcher, Center for Quantitative Genetics and Genomics, Dept. of Molecular Biology and Genetics, Aarhus University, Denmark, 2018 -
- o Postdoc, Center for Quantitative Genetics and Genomics, Dept. of Molecular Biology and Genetics, Aarhus University, Denmark, 2013 - 2018
- o Industrial Postdoc, Breakthrough Leadership Program, Harvard Business School, Apr. 2015 - Jan. 2016
- o Visiting scientist, Dept. of Animal Science (Rohan Fernando & Dorian Garrick), Iowa State University, U.S. Dec. 2015 - Feb. 2016
- o Visiting scientist, Natural Resources Institute Finland (Luke) (Ismo Strandén & Esa Mäntysaari), Finland, Nov. 2016 - Jan. 2017
- o Director, Dairy Cattle Genetic Evaluation, Dairy Association of China, Beijing, P.R.China, 2012 - 2013

Education Background

- o Ph.D. Center for Quantitative Genetics and Genomics, Dept. of Molecular Biology and Genetics, Aarhus University, Denmark 2009 - 2012
- o Ph.D. Dept. of Animal Science and Technology, China Agricultural University, P.R.China 2007 - 2012
- o B.Sc. Dept. of Animal Science and Technology, China Agricultural University, P.R.China 2002 - 2006

Research Grants

- o Danish National Advanced Technology Foundation no.140-2013-6, 2014-2017

Computer Skills

- o Languages: C++, Fortran, R, Julia, Python, SAS
- o Operating Systems: Mac OS X, Linux

- o Applications: L^AT_EX, Emacs

Software

- o ssBr: A software toolbox for genomic prediction and variance component estimation based on single-step model using Bayesian methods for large-scale data (Fortran 90). Software has been developed for parallel computing

Selected Publications

- o **Gao H.**, M. Koivula, I. Strandén, J. Jensen, P. Madsen, T. Pitkänen, G. P. Aamand, and Mäntysaari E. 2018. Short communication: Genomic prediction using different single-step methods in the Finnish red dairy cattle population. *Journal of Dairy Science* (In press)
- o **Gao H.**, P. Madsen, J. Pösö, G. P. Aamand, M. Lidauer and J. Jensen. 2018. Short communication: Multivariate outlier detection for routine Nordic dairy cattle genetic evaluation in the Nordic Holstein and Red population. *Journal of Dairy Science* (In press)
- o Zhang T., **H. Gao**, S. Goutam, H. Fan, . . . , F. Zhao. 2018. Genome-wide association studies reveal candidate genes for fat deposition in tails and body size in Hulun Buir sheep. *Journal of Animal Breeding and Genetics* (submitted)
- o Li J., **Gao H.***, P. Madsen, W. Liu, P. Bao, G. Xue, J. Yang, Y. Gao and G. Su. 2018. Comparison of different orders of Legendre polynomials in random regression model for estimation of genetic parameters and breeding values of milk yield in the Chinese Holstein population. *Animal Science Journal* (submitted, *co-first author)
- o Zhang Z., Q. Zhang, . . . , **H. Gao**, . . . , Y. Pan. 2018. The distribution of runs of homozygosity in Chinese and western pig breeds evaluated by reduced-representation sequencing data. *Animal Genetics* (In press)
- o Wang, X., **H. Gao**, K. G. Gebremedhin, B. S. Bjerg, J. Van Os, C. B. Tucker, and G. Zhang. 2018. A Predictive Model of Equivalent Temperature Index for Dairy Cattle (ETIC). *Journal of Thermal Biology* 76:165-170
- o Ma, P., J. Huang, W. Gong, X. Li, **H. Gao**, Q. Zhang, X. Ding and C. Wang. 2018. The impact of genomic relatedness between populations on the genomic estimated breeding values. *Journal of Animal Science and Biotechnology* 9:64
- o **Gao, H.**, P. Madsen, G. P. Aamand, and J. Jensen. 2018. Estimation of variance components in populations under genomic selection. Page 486 in 11th World Congr. Genet. Appl. Livest. Prod. Vol. Methods and Tools - Models and Computing Strategies 2, Auckland, New Zealand
- o Madsen, P., V. Milkevych, **H. Gao**, O. F. Christensen, and J. Jensen. 2018. DMU - A Package for Analyzing Multivariate Mixed Models in Quantitative Genetics and Genomics. Page 525 in 11th World Congr. Genet. Appl. Livest. Prod. Vol. Electronic Poster Session - Methods and Tools - Software, Auckland, New Zealand
- o Milkevych, V., P. Madsen, **H. Gao**, and J. Jensen. 2018. Efficient block-Gibbs sampling in variance component estimation for predictions which combine phenotypic and genomic information. Page 468 in 11th World Congr. Genet. Appl. Livest. Prod. Vol. Method and Tools - Models and Computing Strategies 1, Auckland, New Zealand
- o **Gao, H.**, P. Madsen, U. S. Nielsen, G. P. Aamand, G. Su, K. Byskov, and J. Jensen. 2015. Including different groups of genotyped females for genomic prediction in a Nordic Jersey population. *Journal of Dairy Science* 98(12):9051-9059

- o **Gao, H.**, P. Madsen, J. Pösö, J. Pedersen, M. Lidauer, and J. Jensen. 2014. Multivariate outlier detection in genetic evaluation in Nordic Jersey cattle. Page 835 in 10th World Congr. Genet. Appl. Livest. Prod., Vancouver, Canada
- o **Gao, H.**, G. Su, L. Janss, Y. Zhang, and M. S. Lund. 2013. Model comparison on genomic predictions using high-density markers for different groups of bulls in the Nordic Holstein population. *Journal of Dairy Science* 96(7):4678-4687
- o **Gao, H.**, M. Lund, Y. Zhang, and G. Su. 2013. Accuracy of genomic prediction using different models and response variables in the Nordic Red cattle population. *Journal of Animal Breeding and Genetics*
- o **Gao, H.**, O. F. Christensen, P. Madsen, U. S. Nielsen, Y. Zhang, M. S. Lund, and G. Su. 2012. Comparison on genomic predictions using three GBLUP methods and two single-step blending methods in the Nordic Holstein population. *Genetics Selection Evolution* 44:8