Hongding Gao | Curriculum Vitae

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

Education Background

o Ph.D. Center for Quantitative Genetics and Genomics, Dept. of Molecular Biology and Genetics, Aarhus University, Denmark, 2012

o Ph.D. Dept. of Animal Science and Technology, China Agricultural University, P.R.China, 2012

o B.Sc. Dept. of Animal Science and Technology, China Agricultural University, P.R.China, 2006

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

Research Grants

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

Teaching

o Course "Linear Models" at Copenhagen University (Master students) since 2018

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

Publications

- Milkevych V., P. Madsen, **H. Gao**, J. Jensen. 2019 The relative effect of genomic information on efficiency of Bayesian analysis of the mixed linear model with unknown variance. Genetics Selection Evolution (Submitted)

- **Gao H.**, P. Madsen, G. P. Aamand, J. R. Thomasen, A. C. Sørensen and J. Jensen. 2019 Effects of genomic selection on estimation of variance components: a simulation study. BMC Genomics

- Ma X., O. F. Christensen, **H. Gao**, R. Huang, B. Nielsen, P. Madsen, J. Jensen, T. Ostersen, P. Li, M. Shirali, G. Su. 2019 Prediction of breeding values for group recorded traits including genomic information and an individually recorded correlated trait. Heredity (Submitted)

- **Gao H.**, B. Nielsen, G. Su, P. Madsen, J. Jensen, O. F. Christensen, T. Ostersen and M. Shirali. 2019 Use of repeated group measurements with drop out animals for variance component estimation and genetic prediction. G3: GENES, GENOMES, GENETICS

- Zhang T., **Gao H.**, S. Goutam, H. Fan, ..., F. Zhao. 2019. 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

- Fan H., Y. Hou, G. Sahana, **H. Gao**, C. Zhu, L. Du, L. Wang, and F. Zhao. 2019. The metabolism of tail fat in two types of Hulun Buir sheep according to tail size and sex. Animal (submitted)

- Li J., **Gao H.***, P. Madsen, W. Liu, P. Bao, G. Xue, J. Yang, Y. Gao and G. Su. 2019. 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. PLOS ONE (submitted, *co-first author)

- **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

- **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

- 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

- 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

- 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

- **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

- 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