

Hongding Gao

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Fields of Interest

- Statistical models in quantitative genetics and genomics
- Computational genetics and software development for genetic/genomic prediction
- New traits and high-throughput phenotyping in animal breeding

Education

- 2009 - 2012 Ph.D. Genetics, Aarhus University, Denmark
- 2007 - 2012 Ph.D. Quantitative Genetics, China Agricultural University, Beijing, China
- 2002 - 2006 B.S. Animal Science, China Agricultural University, Beijing, China

Research Experience

- 2021 - present Senior Scientist, Natural Resources Institute Finland (Luke), Finland
- 2018 - 2021 Assistant Professor/Researcher, Center for Quantitative Genetics and Genomics, Aarhus University, Denmark
- 2013 - 2018 Postdoc, Center for Quantitative Genetics and Genomics, Aarhus University, Denmark
- 02/2020 - 04/2020 Visiting scientist, University of New England, Australia
- 11/2016 - 01/2017 Visiting scientist, Natural Resources Institute Finland (Luke), Finland
- 12/2015 - 02/2016 Visiting scientist, Iowa State University, U.S.

Research Grants

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

Computer Skills

- Languages: C++, Fortran, R, Julia, Python
- Operating Systems: Linux

Software

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

Publications (sorted by first-author)

1. **Gao, H.**, Kudinov, A.A., Taskinen, M. et al. A computationally efficient method for approximating reliabilities in large-scale single-step genomic prediction. *Genet Sel Evol* 55, 1 (2023)
2. **Gao, H.**, G. Su, J. Jensen, P. Madsen, O. F. Christensen, B. Ask, B. G. Poulsen, T. Osterson and B. Nielsen. 2021. Genetic parameters and genomic prediction for feed intake recorded at group- and individual-level in different production systems for growing pigs. *Genetics Selection Evolution* 53:33
3. Li J., **Gao, H.***, P. Madsen, W. Liu, P. Bao, G. Xue, Y. Gao, X. Di and G. Su. 2020. Impact of the order of Legendre polynomials in random regression model on genetic evaluation for milk yield in dairy cattle population. *Frontiers in Genetics* 11:586155 (***co-first author**)
4. **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* 20:956
5. **Gao, H.**, B. Nielsen, G. Su, P. Madsen, J. Jensen, O. F. Christensen, T. Osterson and M. Shirali. 2019. Use of repeated group measurements with drop out animals for variance component estimation and genetic prediction. *G3: GENES, GENOMES, GENETICS* 9:2935-2940
6. **Gao, H.**, M. Koivula, I. Strandén, J. Jensen, P. Madsen, T. Pitkänen, G. P. Aamand, and Mäntysaari E. 2018. Genomic prediction using different single-step methods in the Finnish red dairy cattle population. *Journal of Dairy Science* 101:10082-10088

7. **Gao, H.**, P. Madsen, J. Pösö, G. P. Aamand, M. Lidauer and J. Jensen. 2018. Multivariate outlier detection for routine Nordic dairy cattle genetic evaluation in the Nordic Holstein and Red population. *Journal of Dairy Science* 101(12):11159-11164
8. **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
9. **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
10. **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* 130(5):333-40
11. **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
12. Li Y, Pu L, Shi L, **Gao, H.**, Zhang P, Wang L, Zhao F. 2021. Revealing New Candidate Genes for Teat Number Relevant Traits in Duroc Pigs Using Genome-Wide Association Studies. *Animals*. 11(3):806
13. Berg P., **Gao, H.**, J. R. Thomasen, A. C. Sørensen, L. Hjortø. 2021. Definition of relationship matrix used in optimal-contribution selection impacts genetic diversity maintained. *Genetics Selection Evolution* (under review)
14. Afiani F., **Gao, H.**, S. Joezy-Shekalgorabi, M. Afshar, S. Ali, P. Madsen, J. Jensen. 2021. Genotype by Climate Zone Interactions for Fertility, Somatic cell score, and Production in Iranian Holsteins. *Journal of Dairy Science* (under review)
15. Milkevych V., P. Madsen, **Gao, H.**, J. Jensen. 2020. The relative effect of genomic information on efficiency of Bayesian analysis of the mixed linear model with unknown variance. *Journal of Animal Breeding and Genetics* 138:14-22
16. Ma X., O. F. Christensen, **Gao, H.**, R. Huang, B. Nielsen, P. Madsen, J. Jensen, T. Ostensen, P. Li, M. Shirali, G. Su. 2020. Prediction of breeding values for group recorded traits including genomic information and an individually recorded correlated trait. *Heredity* 126:206–217
17. 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* 136(5):362-370
18. Fan H., Y. Hou, G. Sahana, **Gao, H.**, 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. *Animals* 9(9):655
19. Zhang Z., Q. Zhang, Q. Xiao, H. Sun, **Gao, H.**, Y. Yang, J. Chen, Z. Li, M. Xue, P. Ma, Y. Pan. 2018. The distribution of runs of homozygosity in Chinese and western pig breeds evaluated by reduced-representation sequencing data. *Animal Genetics* 49(6):579-591
20. Wang, X., **Gao, H.**, 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
21. Ma, P., J. Huang, W. Gong, X. Li, **Gao, H.**, 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