

Hongding Gao | Curriculum Vitae

– Chinese citizen

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Fields of Interest

- o Statistical methods of genetic evaluation and genomic selection
- o Programming in quantitative genetics

Professional Experience

- o Postdoc, Dept. of Molecular Biology and Genetics, Aarhus University, Denmark, Oct. 2013 - Present
- o Industrial Postdoc, Breakthrough Leadership Program, Harvard Business School, Apr. 2015 - Jan. 2016
- o Visiting scientist, Dept. of Animal Science, Iowa State University, U.S. Dec. 2015 - Feb. 2016
- o Visiting scientist, Natural Resources Institute Finland (Luke), Finland, Nov. 2016 - Jan. 2017
- o Geneticist, Dairy Association of China, Beijing, P.R.China, Jul. 2012 - Sep. 2013

Research Grants

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

Education Background

- o Ph.D. 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

Computer Skills

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

Publications

- o **Gao H.**, Madsen P, Nielsen US, Aamand GP, Su G, Byskov K & Jensen, J. Including different groups of genotyped females for genomic prediction in a Nordic Jersey population. J Dairy Sci. 2015

- o **H. Gao**, P. Madsen, J. Pösö, J. Pedersen, M. Lidauer and J. Jensen 10th World Congress on Genetics Applied to Livestock Production (WCGALP) 2014
- o **H. Gao**, G. Su, L. Janss, Y. Zhang, and M. S. Lund: Model comparison on genomic predictions using high-density markers for different groups of bulls in the nordic Holstein population J. Dairy Sci.2013, 96:7
- o **H. Gao**, M.S. Lund, Y. Zhang & G. Su: Accuracy of genomic prediction using different models and response variables in the Nordic Red Cattle population. J. Anim. Breed. Genet. 2013, 10.1111/jbg.12039
- o **Hongding Gao**, Ole F Christensen, Per Madsen, Ulrik S Nielsen, Yuan Zhang, Mogens S Lund, Guosheng Su: Comparison on genomic predictions using three GBLUP methods and two single-step blending methods in the Nordic Holstein population. Genet Sel Evol 2012, 44:8
- o **Gao, H.**, Christensen, O., Madsen, P., Nielsen, U., Lund, M., and Su, G.,: Genomic prediction in Nordic Holstein population using one-step approach. EAAP 62nd Annual Meeting, Stavanger, Norway. 2011
- o Su, G., **Gao, H.**, Lund, M.,: Contributions of different sources of information to reliability of genomic prediction for Danish Jersey population. EAAP 62nd Annual Meeting, Stavanger, Norway. 2011