

Yang Da

Associate Professor

Appointment 75% Research, 25% Teaching

Research Area Quantitative and Molecular Genetics

Appointment History 2004-present Associate Professor
1999-2004 Assistant Professor

Graduate Program Affiliations

Animal Sciences – Senior Member
Bioinformatics – Member
Molecular Veterinary Biosciences – Senior Member

Professional and Honorary Societies

Member, American Dairy Science Association
Member, American Society of Animal Science

Five Most Significant Publications

Mao, Y. and Y. Da. 2005. Statistical power for detecting epistasis QTL effects under the F-2 Design. *Genetics, Selection, Evolution* (Accepted).

This is the first article to present analytical predictions for statistical and sample size requirements for mapping quantitative trait loci with epistasis effects.

Da, Y. 2003. Statistical methods and experimental designs for mapping genes of complex traits in domestic animals. *Acta Genetica Sinica* 30: 1183-1192.

This article reviews statistical methods and experimental designs available to complex trait gene mapping in domestic animals, and identifies future directions in this area.

London, N.R, J.R. Garbe, S.M. Schmutz, M.S. Abrahamsen, and Y. Da. 2003. Linkage analysis for mapping genes of sex-influenced traits. *Mammalian Genome* 14:261-267.

This article is the first article on linkage analysis for mapping genes of sex-influenced traits.

Da, Y., J. Garbe, N. London, and J. Xu. 2002. Linkage analysis using direct and indirect counting and relative efficiencies for codominant and dominant loci. *J. Animal Science* 80:2528-2539.

This article developed methods for rapid linkage analysis with codominant and dominant loci, which are useful for large scale gene mapping analysis when dominance is involved.

Da, Y., P.M. VanRaden, and L.B. Schook. 2000. Detection and parameter estimation for quantitative trait loci using regression models and multiple markers. *Genetics, Selection, Evolution* 32: 357-381.

This article developed methods for mapping linked quantitative trait loci with additive effects, and is the first the provided analytical solutions for estimating the effects and locations of quantitative trait loci.

Refereed Journal Publications and Book Chapters (Last Five Years)

Authored or co-authored 12 papers in peer-reviewed journals.

- Mao, Y. and **Y. Da**. 2005. Statistical power for detecting epistasis QTL effects under the F-2 Design. *Genetics, Selection, Evolution* (Accepted).
- Da, Y.** 2003. Statistical methods and experimental designs for mapping genes of complex traits in domestic animals. *Acta Genetica Sinica* 30: 1183-1192
- Garbe, J.R. and **Y. Da**. 2003. A software tool for the graphical visualization of large and complex populations. *Acta Genetica Sinica* 30: 2293-2295
- London, N.R., J.R. Garbe, S.M. Schmutz, M.S. Abrahamsen, and **Y. Da**. 2003. Linkage analysis for mapping genes of sex-influenced traits. *Mammalian Genome* 14:261-267.
- Patterson, E.E., J.R. Mickelson, **Y. Da**, M.C. Roberts, A. McVey, D. O'Brien, G. Johnson, and P.J. Armstrong. 2003. Clinical characteristics and inheritance of idiopathic epilepsy in Vizslas. *Journal of Veterinary Internal Medicine* 17:319-325.
- Reed, K.M., L.D. Chaves, J.R. Garbe, **Y. Da**, and D.E. Harry. 2003. Allelic variation and genetic linkage of avian microsatellites in a new turkey population for genetic mapping. *Cytogenetics and Genome Research* (In press).
- Da, Y.**, J. Garbe, N. London, and J. Xu. 2002. Linkage analysis using direct and indirect counting and relative efficiencies for codominant and dominant loci. *J. Animal Science* 80:2528-2539.
- Braunschweig, M.H., A.A. Paszek, J.I. Weller, **Y. Da**, R.J. Hawken, M.B. Wheeler, L.B. Schook, and L.J. Alexander. 2001. Generation and exploration of a dense genetic map in a region of a QTL affecting corpora lutea in a Meishan × Yorkshire cross. *Mammalian Genome* 12:719-723.
- Da, Y.**, P.M. VanRaden, and L.B. Schook. 2000. Detection and parameter estimation for quantitative trait loci using regression models and multiple markers. *Genetics, Selection, Evolution* 32:357-381.
- Da, Y.**, P.M. VanRaden, J.E. Beever, M. Ron, A.A. Paszek, J. Song, G.R. Wiggans, R.Z. Ma, J.I. Weller, and H.A. Lewin. 1999. Standardization and conversion of marker polymorphism measures. *Animal Biotechnology* 10:25-35.
- Da, Y.**, P.M. VanRaden, N. Li, J.I. Weller, L.B. Schook, and C.W. Beattie. 1999. Designs of resource families for mapping quantitative trait loci using genetic markers in domestic animals. *J. Agricultural Biotechnology* 7:31-48.
- Heyen, D.W., J.I. Weller, M. Ron, M. Band J.E. Beever, E. Feldmesser, **Y. Da**, G.R. Wiggans, P.M. VanRaden, and H.A. Lewin. 1999. A genome scan for quantitative trait loci influencing milk production and health traits in dairy cattle. *Physiological Genomics* 1:165-175.

Computer Software Packages

Locusmap, developed under my direction, is a computer software package designed for rapid linkage analysis and map construction of loci with a variety of inheritance modes. Version 1.0 of Locusmap was completed 1/18/2003 and is now available from <http://animalgene.umn.edu>.

Pedigraph, developed under my direction, is a pedigree/genealogy visualization program specifically designed to draw large, complex pedigrees. Pedigraph 1.0 was completed 1/18/2003, and Pedigraph 2.0 was completed 7/2004. Trial version 2.0 is now available from <http://animalgene.umn.edu>.

MiniInbred, developed under my direction, is a computer program to minimize inbreeding of breeding plans. Version 1.0 of MiniInbred was completed 5/2004 and was presented at the Animal/Dairy/Poultry meeting 7/2004.

Awards

Honorary professor and tutor of Ph.D. students, awarded by College of Animal Science and Technology, China Agricultural University, July 1997-1999.

Proceedings

- Da, Y.**, N. London, and J. Xu. 2002. Partition of genotypic variance for two linked loci under the F-2 design for QTL mapping. *In Proc. 7th World Cong. Genet. Appl. Livest. Prod.*, Montpellier, France 32: 737-740.
- London, N., J. Xu, J. Garbe, and **Y. Da**. 2002. Linkage analysis for the hypothesized interaction between the polled and scurred traits in cattle. *In Proc. 7th World Cong. Genet. Appl. Livest. Prod.*, Montpellier, France 29: 485-488.
- Xu, J., N. London, J. Garbe, and **Y. Da**. 2002. Bias in linkage analysis due to ignoring epistasis effects. *In Proc. 7th World Cong. Genet. Appl. Livest. Prod.*, Montpellier, France 32: 633-636.
- Da, Y.** 2001. Partitioning of genotypic value and variance for two quantitative trait loci with linkage. Symposium on Animal Breeding and Genetics in Honor of Professor Wu Zongxian's 90th Birthday, pp. 59-67, China Agricultural University, May 11-12, 2001.
- Da, Y.**, T. Sonstegard, B. Crooker, L. Hansen, H. Chester-Jones, M. Fahning, B. Seguin, G. Marx, G.C. Lamb, and F.A. Ponce de León. 2000. Designs of resource populations for dairy QTL mapping. W.E. Petersen Lecture. Dairy Genomics: Trends and Opportunities. University of Minnesota, St. Paul, December 11-12, 2000.
- Da, Y.**, M. Ron, A. Yanai, M. Band, R.E. Everts, D.W. Heyen, J.I. Weller, G.R. Wiggans, and H.A. Lewin. 1994. The dairy bull DNA repository: A resource for mapping quantitative trait loci. *The Fifth Congress of Genetics Applied to Livestock Production*. 21:229-232.

Invited Lectures, Short Course, Panel Discussion

- Bioinformatics needs in animal gene mapping – A panel discussion for the USDA electronic workshop on Animal Bioinformatics, 2002.
- Invited lectures: Statistical Analysis for Gene Mapping. China and Southern China Agricultural Universities, 2002.
- Special course: QTL Detection and Marker Assisted Selection, co-taught by J.I. Weller, A.A. Paszek, and **Y. Da**, 2000.

Funding (Last Five Years) – \$683,493

- NIH**. Comparative medicine and pathology training grant. C. Carlson (PI). 2003-08. \$945,423.
- USDA**. Genetic linkage map for the turkey. K. Reed (PI). 2003-06. \$382,028.
- Cargill**. Pedigree analysis large complex population. 2003-05. \$100,000.
- USDA**. Research training of veterinary students in microbial and animal health genomics. M. Abrahamsen (PI). 2003-05. \$100,000.
- USDA**. New statistical methods for QTL mapping. 2001-05. \$150,000.
- USDA**. Porcine Peyer's Patch expressed sequences associated with disease resistance. M. Murtaugh (PI). 2002-04. \$240,000.
- Cargill**. Development of analytical tools for animal genomics. 2001-04. \$299,800.
- UMN Grad School Grant in Aid**. Statistical and computational methods for animal genomics. 2001-03. \$18,693.
- USDA**. Development of an F-2 population for dairy QTL mapping. 1999-03. \$65,000.
- USDA**. Germplasm Conservation Program. \$50,000.

Dissertations and Theses (Last Five Years)

Name	Program	Degree	Thesis Title
Mathew A. Chrystal	Animal Sciences	Ph.D.	Marker assisted selection in dairy cattle using a mixed model approach.
Nicole R. London	Molecular Vet Biosci	Ph.D.	Statistical theory and methods for mapping gender affected genes and QTL.
Jie Xu	Animal Sciences	Ph.D.	Statistical analysis for mapping linked quantitative trait loci (QTL).

Graduate Student and Post-doctoral Supervision - Current Advisees

Yangcai Mao Post-doc Animal Sciences

Courses Taught (Last Five Years)

Designator	Name	Cr	% Effort	Term	Years
AnSc 5200	Statistical Genetics and Genomics	4	95%	Spring	2001, '02, '03
EEB 8980	Advanced Quantitative Genetics	1-3	50%	Spring	2002
AnSc 8141	Current Topics: Animal Breeding & Gen.	1	100%	Fall	2002

Service

Panelist, USDA electronic workshop on bioinformatics needs.

Reviewer, USDA-NRICGP grant proposals on animal genomics.

Member, Editorial Board, *Asian-Australasian J. of Animal Science*, 2000-2002

Reviewer, *Physiology Genomics*, *Mammalian Genome*, *J. Animal Science*, *J. Dairy Science*, *Asian-Australasian Journal of Animal Science*, *Genetics*, *Animal Genetics*, *GSE (Genetics, Selection, Evolution)*.

Service to National and Regional Research Committees

Co-organizer, NRSP-8 and NC-1010 workshop, Plant and Animal Genomics XIII.

Member, write-up group, renewal of multi-state NC-209 (now NC-1010) project.

Member, Genetics/Breeding Program Committee, Midwest ADS Meeting.

Chair, Breeding and Genetics Session IV Midwest ADS Meeting, 2005.