

Scott C. Fahrenkrug

Associate Professor

Appointment 75% Research, 25% Teaching

Research Area Functional Genomics, Molecular Genetics

Appointment History 2001-present Associate Professor

Graduate Program Affiliations

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

Professional and Honorary Societies

Member, Society for Developmental Biology
Member, International Society for Differentiation
Member, International Society for Animal Genetics

Five Most Significant Publications

Klee, E.W., D.F. Carlson, S.C. Fahrenkrug, S.C. Ekker, and L.B. Ellis. 2004. Identifying secretomes in people, pufferfish and pigs. *Nucleic Acids Res.* 2004 32(4):1414-1421.

The proteins processed by the secretory pathway (secretome) are critical players in the development of multi-cellular eukaryotic organisms but have yet to be comprehensively studied at the genomic level. In this study, we used a computer-to-bench pipeline to predict human, Fugu, and porcine secretomes. The methods developed here are specifically designed to accept partial open reading frames and improve secreted protein predictions in eukaryotic transcriptomes, and are valuable for the analysis and annotation of eukaryotic EST databases.

Fahrenkrug, S.C., B.A. Freking, T.P.L. Smith, G.A. Rohrer, and J.W. Keele. 2002. Single nucleotide polymorphism (SNP) discovery in porcine expressed genes. *Anim. Genet.* 2002 33(3):186-195.

This paper described a novel method for locus-specific amplification and resequencing to identify single nucleotide polymorphisms in swine. This work represents the first and largest SNP discovery effort yet undertaken for pigs. It also established for the first time a genome-wide estimate as to the frequency of SNPs in pig genes.

Fahrenkrug, S.C., T.P. Smith, B.A. Freking, J. Cho, J. White, J. Vallet, T. Wise, G. Rohrer, G. Pertea, R. Sultana, J. Quackenbush, and J.W. Keele. 2002. Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly. *Mamm. Genome.* 2002 13(8):475-478.

This paper describes the construction and sequencing of two normalized cDNA libraries from pig tissues. The results of this work represent the single largest contribution of pig ESTs to the porcine gene index (45,000 sequences). This pig gene index remains central to comparative map development, efforts to sequence the pig genome, and development of microarrays for the analysis of porcine gene expression.

Fahrenkrug, S.C., G.A. Rohrer, B.A. Freking, T.P.L. Smith, K. Osoegawa, C.L. Shu, J. Cantonese, and P. de Jong. 2001. A porcine BAC library with tenfold genome coverage: A resource for physical and genetic map integration. *Mamm. Genome*. 2001 12(6):472-474.

A porcine BAC library was prepared and characterized as a resource for pig genome mapping. This resource continues to be an important resource as preparations are made for sequencing of the pig genome. In addition, this resource has provided reagents for manipulation of the pig genome using recombinering methods currently being pursued in Dr. Fahrenkrug's laboratory.

Fahrenkrug, S.C., B.A. Freking, C.E. Rexroad, K.A. Leymaster, S.M. Kappes, and T.P.L. Smith. 2000. Comparative mapping of the ovine *clpg* locus. *Mamm. Genome*. 2000 11(10):871-876.

The Callipyge mutation is polar overdominant, with only animals inheriting a mutant allele from their sire and a normal allele from their mother displaying a phenotype. All other genotypic combinations are normal. For this paper physical and genetic mapping approaches were used to localize the sheep callipyge mutation from a previous resolution of 15 cM, to within 165 kB (a single BAC). Based on these results, dysregulation in either of two candidate genes; PREF-1 (aka DLK) and MEG3 (aka Glt2) were proposed to underlie the callipyge phenotype. The mutation has since been identified in an imprinting control region that indeed involves alteration of the expression of these genes in a parent-of-origin specific manner, a potential mechanism explored in the discussion of this paper. The Callipyge locus represents the best characterized example of imprinting in livestock and continues to contribute to our understanding of imprinting in all animals. In addition, the candidate genes are now active targets in other labs as potential regulators of muscle growth and meat tenderness.

Refereed Journal Publications and Book Chapters (Last Five Years)

Authored or co-authored 35 papers in peer-reviewed journals; 18 are listed below.

- Klee, E.W., D.F. Carlson, **S.C. Fahrenkrug**, S.C. Ekker, and L.B. Ellis. 2004. Identifying secretomes in people, pufferfish and pigs. *Nucleic Acids Res.* 2004 32(4):1414-21.
- Nadershahi, A., **S.C. Fahrenkrug**, and L.B. Ellis. 2004. Comparison of computational methods for identifying translation initiation sites in EST data. *BMC Bioinformatics*. 2004 5(1):14.
- Robalino, J., B. Joshi, **S.C. Fahrenkrug**, and R. Jagus. 2004. Two zebrafish eIF4E family members are differentially expressed and functionally divergent. *J. Biol. Chem.* 2004 279(11):10532-41.
- Boland, L.M., M. Jiang, S.Y. Lee, **S.C. Fahrenkrug**, M.C. Harnett, and S.M. O'Grady. 2003. Functional properties of a brain-specific NH₂-terminally spliced modulator of Kv4 channels. *Am. J. Physiol. [Cell Physiology]* 285(1):C161-C171, 2003.
- Fahrenkrug, S.C.**, B.A. Freking, T.P.L. Smith, G.A. Rohrer, and J.W. Keele. 2002. Single nucleotide polymorphism (SNP) discovery in porcine expressed genes. *Anim. Genet.* 33(3). p. 186-195.
- Fahrenkrug, S.C.**, T.P. Smith, B.A. Freking, J. Cho, J. White, J. Vallet, T. Wise, G. Rohrer, G. Perte, R. Sultana, J. Quackenbush, and J.W. Keele. 2002. Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly. *Mamm. Genome*. 13(8) 475-478.
- McCoard, S.A., **S.C. Fahrenkrug**, L.J. Alexander, B.A. Freking, G.A. Rohrer, T.H. Wise, and J.J. Ford. 2002. An integrated comparative map of the porcine X chromosome. *Anim. Genet.* 33(3). p. 178-185.
- Rohrer, G.A., **S.C. Fahrenkrug**, D. Nonneman, N. Tao, and W.C. Warren. 2002. Mapping microsatellite markers identified in porcine EST sequences. *Animal Genet.* 33(5) 372-6.
- Wilson, M.E., **S.C. Fahrenkrug**, G.A. Rohrer, T.P.L. Smith, and S.P. Ford. 2002. Differential expression of cyclooxygenase-2 around the time of elongation in the pig conceptus. *Anim. Repro. Sci.* 2002. 71(3-4):229-37.
- Campbell, E.M., **S.C. Fahrenkrug**, J.L. Vallet, T.P. Smith, and G.A. Rohrer. 2001. An updated linkage and comparative map of porcine chromosome 18. *Anim. Genet.* 32(6):375-9.

- Fahrenkrug, S.C.**, G.A. Rohrer, B.A. Freking, T.P.L. Smith, K. Osoegawa, C.L. Shu, J. Cantonese, and P. de Jong. 2001. A porcine BAC library with 10-fold genome coverage: A resource for physical and genetic map integration. *Mamm. Genome*. 12(6):472-4.
- Keele, J.W. and **S.C. Fahrenkrug**. 2001. Optimum mating systems for the myostatin locus in cattle. *J. Anim. Sci.* 79(8):2016-22.
- McCoard, S., T. Wise, **S.C. Fahrenkrug**, and J. Ford. 2001. Temporal and spatial localization patterns of Gata4 during porcine gonadogenesis. *Biology of Reproduction* Aug;65(2):366-74.
- Rexroad, C.E. 3rd, G.L. Bennett, J.W. Keele, **S.C. Fahrenkrug**, B.A. Freking, S.M. Kappes, R.T. Stone, and T.P.L. Smith. 2001. Comparative mapping of BTA15 and HSA11 including a region containing a QTL for meat tenderness. *J. Anim. Sci.* 12(7):561-5. 2001
- Smith, T.P.L., **S.C. Fahrenkrug**, G.A. Rohrer, F.A. Simmen, C.E. Rexroad, and J.W. Keele. 2001. Mapping of expressed sequence tags from a porcine early embryonic cDNA library. *Anim. Genet.* 32(2):66-72.
- Smith, T.P., W.M. Grosse, B.A. Freking, A.J. Roberts, R.T. Stone, E. Casas, J.E. Wray, J. White, J. Cho, **S.C. Fahrenkrug**, G.L. Bennett, M.P. Heaton, W.W. Laegreid, G.A. Rohrer, C.G. Chitko-McKown, G. Perlea, I. Holt, S. Karamycheva, F. Liang, J. Quackenbush, and J.W. Keele. 2001. Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle. *Genome Res.* 2001 11(4):626-30.
- Smith, T.P., A.D. Showalter, K.W. Sloop, G.A. Rohrer, **S.C. Fahrenkrug**, B.C. Meier, and S.J. Rhodes. 2001. Identification of porcine Lhx3 and SF1 as candidate genes for QTL affecting growth and reproduction traits in swine. *Anim. Genet.* 32(6):344-50.
- Vallet, J.L., T.P. Smith, T.S. Sonstegard, M. Heaton, and **S.C. Fahrenkrug**. 2001. Structure of the genes for porcine endometrial secreted and membrane folate binding proteins. *Domest. Anim. Endocrinol.* 21(1):55-72.

Proceedings and Invited Lectures

- “Resources for Bovine Functional Genomics”. (Aug, 2004) The Environmental Impact of Agriculture and Energy Use: How New Technologies, Including Biotechnology, can Provide Sustainable Solutions. GENOMICS and BIOMASS/BIOENERGY, Staur Gjestegård, Stange, Norway
- “Interface between molecular genetics and swine nutrition”. (Sept, 2004) Minnesota Nutrition Conference. Saint Paul, MN
- "Bioinformatics in Livestock Comparative and Functional Genomics". (2002) Health Informatics Seminar, co-sponsored by the Supercomputing Institute, the Digital Technology Center, and the BioTechnology Institute, 2002.
- Rohrer, G., B. Freking, **S. Fahrenkrug**, D. Nonneman. 2002. Genetic Mapping of Porcine EST Sequences Using Length Polymorphisms. In: *Proc. of the 28th International Conference on Animal Genetics*, August. Goettingen, Germany.

Funding (Last Five Years) – \$90,565

- USDA**. Genetic linkage map for the turkey. K. Reed (PI). 2003-06. \$382,028.
- UMN AHC**. Development of a transgenic cystic fibrosis pig. C. Steer (PI). 2004-05. \$249,921.
- Babcock Swine**. Locus specific amplification and comparative resequencing of the porcine 5'-AMP'activated protein kinase, gamma-3 subunit gene. 2003. \$20,798.
- USDA**. Porcine Peyer's Patch expressed sequences associated with disease resistance. M. Murtaugh (PI). 2002-04. \$240,000.
- UMN Grad School Grant in Aid**. Calcineurin signaling in zebrafish muscle-cell specification and differentiation. 2002-03. \$27,266.
- USDA**. Generation and mapping of genetic markers for swine. 1999-2003. \$42,501.

Graduate Student and Post-doctoral Supervision - Current Advisees

Hehuang Xie, Ph.D. Postdoctoral Research Associate
 Daniel Carlson M.S.

Courses Taught (Last Five Years)

Designator	Name	Cr	% Effort	Term	Years
AnSc 5200	Statistical Genetics and Genomics	4	5%	Spring	2002, '03
Agri 1910	Freshman Seminar – Genomics	2	33%	Spring	2002
AnSc 3509	Animal Biotechnology	3	100%	Spring	2004

Service

Reviewer, *Animal Genetics, Mammalian Genome, Gene, J. for Brain Research*

Reviewed Grants for USDA NRI, BARD

USDA Animal Bioinformatics Panel

Animal Biotechnology Center - Steering Committee Member

Development of Bioinformatics core for AB Center

Service to National and Regional Research Committees

NC 1004 Representative, member NRSP8