BIOGRAPHICAL SKETCH

NAME	Womack, James E.	POSITION TITLE	Distinguished Professor

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	YEAR CONFERRED	FIELD OF STUDY
Abilene Christian College	B.S.	1964	Mathematics Ed.
Oregon State University	Ph.D.	1968	Genetics

A. Positions and Honors

Positions and Employment

1968-1971 Assistant Professor, Abilene Christian College
1971-1973 Associate Professor, Abilene Christian College
1973-1975 Visiting Scientist, The Jackson Laboratory
1975-1977 Staff Scientist, The Jackson Laboratory
1977-1983 Associate Professor, Texas A&M University
1983- Present Professor, Veterinary Pathology, Texas A&M University
1987-Present W.P. Luse Professor, Texas A&M University
1989-1996 Director, Center for Animal Genetics, Institute of Biosciences & Technology
1990-1993 Interim Asst. Department Head, Veterinary Pathobiology, Texas A&M University
2001-Present Distinguished Professor, Texas A&M University
Director, Center for Animal Biotechnology and Genomics, Texas A&M University

Other Experience and Professional Memberships

1978-Present Texas Genetics Society (President, 1989)
1981-Present American Genetic Association (President, 1985; Executive V.P. 1996-2003)
1993-Present Coordinator, USDA-NRSP8 Bovine Genome Program
1988-Present International Society for Animal Genetics (President, 2000-Present)
1993-Present Human Genome Organization (HUGO)
2001 Nominating Committee, National Academy of Sciences USA

Editorial Boards (past and present)

Genomics, Journal of Heredity, Biochemical Genetics, Animal Genetics, Mammalian Genome, Genome Research, Animal Biotechnology

Honors

Alumni Citation Award, Abilene Christian University, 1983
Faculty Distinguished Achievement Award for Research, Texas A&M University, 1987
Carrington Award for Research in Cell Biology, 1990
McMaster Fellow, CSIRO, Australia, 1990
CIBA Prize for Research in Animal Health, 1993
Outstanding Texas Geneticist, Texas Genetics Society, 1996
Fellow, American Association for the Advancement of Science, 1999
National Academy of Sciences, USA, 1999
Wolf Prize in Agriculture, 2001
Distinguished Service Award, Texas Genetics Society, 2006
Outstanding Alumnus of the Year, Abilene Christian University, 2006
Dean's Impact Award, CVM, Texas A&M University, 2007
Bush Excellence Award for Faculty in International Research, Texas A&M University, 2008

B. Selected peer-reviewed publications (from total of 300+)

Ozawa, A., Band, M.R., Larson, J.H., Donovan, J., Green, C.A., Womack, J.E., and Lewin, H.A.: Comparative organization of cattle chromosome 5 revealed by comparative mapping by annotation and sequence similarity and radiation hybrid mapping. Proc. Natl. Acac. Sci. USA 97:4150-4155, 2000.

Band, M.R., Larson, J.H., Rebeiz, M., Green, C.A., Heyen, D.W., Donovan, J., Windish, R., Steining, C., Mahyuddin, P., Womack, J.E., and Lewin, H.A.: An ordered comparative map of the cattle and human genomes. Genome Research 1359-1368, 2000.

Rexroad, C.E.III, Owens, E.K., Johnson, J.S. and Womack, J.E.: A 12000 rad whole genome radiation hybrid panel for high resolution mapping in cattle: characterization of the centromeric end of chromosome 1. Animal Genetics 31:262-265, 2000.

Goldammer, T., Kata, S.R., Brunner, R.M., Dorroch, U., Sanftleben, H., Schwerin, M., and Womack, J.E.: A comparative radiation hybrid map of bovine chromosome 18 and homologous chromosomes in human and mice. Proc. Natl. Acad. Sci. USA, 99:2106-2111, 2002.

Takeda, H., Takami, M., Oguni, T., Tsuji, T., Yoneda, K., Sato, H., Ihara, N., Itoh, T., Kata, S.R., Mishina, Y., Womack, J.E., Moritomo, Y., Sugimoto, Y. and Kunieda, T.: Positional cloning of the gene LIMBIN responsible for bovine chondrodysplastic dwarfism. Proc. Natl. Acad. Sci. USA, 99:10549-10554, 2002.

Winter, A., Krämer, W., Werner, F.A., Kollers, S., Kata, S., Durstewitz, G., Buitkamp, J., Womack, J.E., Thaller, G., and Fries, R.: Association of a lysine-232/alanine polymorphism in a bovine gene encoding acyl-CoA:diacylglycerol acyltransferase (*DGAT1*) with variation at a quantitative trait locus for milk fat content. Proc. Natl. Acad. Sci. USA 97:9300-9305, 2002.

Brunner, R.M., Sanftleben, H., Goldammer, T., Kühn, C., Weikard, R., Kata, S.R., Womack, J.E., and Schwerin, M.: The telomeric region of BTA18 containing a potential QTL region for health in cattle exhibits high similarity to the HSA19q region in humans. Genomics 81:270-278, 2003.

White, S.N., Kata, S.R., and Womack, J.E.: Comparative fine maps of bovine toll-like receptor 4 and toll-like receptor 2 regions. Mammalian Genome 14:149-155, 2003.

White, S.N., Taylor, K.H., Abbey, C.A., and Gill, C.A., and Womack, J.E.: Haploytype variation in bovine Toll-like receptor 4 and computational predication of a positively selected ligand-binding domain. Proc. Natl. Acad. Sci. USA 100:10364-10369, 2003.

Larkin, D.M., der Wind, A.E., Rebeiz, M., Schweitzer, P.A., Bachman, S., Green, C., Wright, C.L., Campos, E.J., Benson, L.D., Edwards, J., Liu, L., Osoegawa, K., Womack, J.E., de Jong, P., and Harris, A.L.: A cattle-human comparative map built with cattle BAC-ends and human genome sequence. Genome Research 13:1966-1973, 2003.

Raudsepp T., Lee, E.-J., Kata, S.R. Brinkmeyer, C., Mickelson, J.R., Skow, L.C., Womack, J.E. and Chowdhary, B.P.: Exceptional conservation of horse-human gene order on X chromosome revealed by high-resolution radiation hybrid mapping. Proc. Natl. Acad. Sci. USA 2386-2391, 2004.

Raudsepp, T., Santani, A., Wallner, B., Kata, S.R., Ren, C., Zhang, H.-B., Womack, J.E., Skow, L.C., and Chowdhary, B.P.: A detailed physical map of the horse Y chromosome. Proc. Natl. Acad. Sci. USA 101:9321-9326, 2004.

Everts-van der Wind, A., Kata, S.R., Band, M.R., Rebeiz, M., Larkin, D.M., Everts, R., Green, C.A., Liu, L., Natarajan, S., Goldammer, T., Lee, J.H., McKay, S., Womack, J.E. and Lewin, H.A.: A 1463 gene cattle-human comparative map with anchor points defined by human genome sequence coordinates. Genome Research 14:1424-1437, 2004.

Murphy, W.J,. Larkin D.M., Everts-van der Wind A., Gurque G., Tesler G., Auvil L., Beever J.E., Chowdhary B.P., Galibert F., Gatzke L., Hitte C., Meyers S.N., Mlan D., Ostrander E.A., Pape G., Parker G.H., Raudseep T., Rogatcheva M.B., Schook L.B., Skow L.C., Welge M., Womack J.E., O'Brien S.J., Pevzner P.A., and Lewin H.A.: Dynamics of mammalian chromosome evolution inferred from multispecies comparative maps. Science 309, 613-617, 2005.

Everts-van der Wind , A., Larkin, D.M., Green, C.A., Elliott, J.S., Olmstead, C., Chiu, R., Schein, J.E., Marra, MA, Womack, J.E., Lewin, H.A.: A high-resolution whole-genome cattle-human comparative map reveals details of mammalian chromosome evolution. Proc Natl Acad Sci USA;102:18526-18531, 2005.

Childers, C.P., Newkirk, H.L., Honeycutt, D.A., Ramlachan N., Muzney D.M., Sodergren E., Gibbs, R.A, Weinstock, G.M., Womack, J.E. and Skow, L.C.: Comparative analysis of the bovine MHC class *IIb* sequence identified inversion breakpoints and three unexpected genes. Animal Genetics 37:121-129, 2005.

Womack, J.E.: Advances in livestock genomics: Opening the barn door. Genome Research 15:1699-1705, 2005.

Sugimoto, M., Fujikawa A., Womack, J.E., Sugimoto Y.: Evidence that bovine forebrain embryonic zinc finger-like gene influences immune response associated with mastitis resistance. Proc Natl Acad Sci USA 103:6454-6459, 2006.

Womack, J.E.: The impact of sequencing the bovine genome. Australian Journal of Experimental Agriculture 46:151-153, 2006.

Callicott, R. and Womack, J.E.: Real-time PCR assay for measurement of mouse telomeres. Comp Med, 56:17-22, 2006.

Weikard R., Goldammer T., Laurent P., Womack, J.E. and Kuehn C.: A gene-based high-resolultion comparative radiation hybrid map as a framework for genome sequence assembly of a bovine chromosome 6 region associated with QTL for growth, body composition, and mild performance traits. BMC Genomics 7:53-(1-15), 2006.

Ghebranious N, Burmester JK, Glurich I, McPherson E, Ivacic L, Kislow J, Rasmussen K, Kumar V, Raggio CL, Blank RD, Jacobsen FS, Faciszewski T, Womack J, Giampietro PF: Evaluation of SLC35A3 as a candidate gene for human vertebral malformations. Am J Med Genet Part A 140A:1346-1348, 2006.

Taylor, K.H., Taylor, J.F., White, S.N. and Womack, J.E.: Identification of genetic variation and putative regulatory regions in bovine CARD15. Mammalian Genome 17:892-901, 2006

Cargill, E.J., Paetzold, L., and Womack, J.E.: Radiation hybrid mapping and comparative sequence analysis of bovine RIG-I and MAVS genes. DNA Sequence 17:314-318, 2006.

Van Stijn, T.C., French, M.C., Dodds, K.G., McEwan, J.C., Broad, T.E., Womack, J.E., Tisdall, D.J. and Galloway, S.M.: Comparative mapping of sheep chromosome 2q. Cytogenet and Genome Res 116-85-92, 2007.

Cargill, E.J. and Womack, J.E.: Detection of polymorphisms in bovine toll-like receptors 3, 7, 8, and 9. Genomics 89:745-755, 2007.

Snelling, W.M. and 54 others including Womack, J.E.: A physical map of the bovine genome. Genome Biology 8:R165, 2007.

Marques, E., de Givry, S., Stothard, P., Murdoch, B., Wang, Z., Womack, J., and Moore, S.M.: A high resolution radiation hybrid map of bovine chromosome 14 identifies scaffold rearrangement in the latest bovine assembly. BMC Genomics, 8:254,

2007.

Callicott, R.J., Ballard, S.T., and Womack, J.E.: Genomic comparison of Lewis and Wistar-Furth rat substrains by use of microsatellite markers. J Am Assoc Lab Anim Sci 46:25-29, 2007.

Schlapffer, J., Stahlberger-Saitbekova, N., Comincini, S., Gaillard, C., Hills, D., Meyer, R.K., Williams, J.L., Womack, J.E., Zurbriggen, A., and Dolf G.: A higher resolution radiation hybrid map of bovine chromosome 13. Genet. Sel. Evol. 34:255-267, 2007.

Seabury, C.M., Cargill, E.J., and Womack, J.E.: Sequence variability and protein domain architectures for bovine Toll-like receptors 1, 5 and 10. *Genomics* 90:502-515, 2007.

Stafuzza, N.B., Ianella, P., Miziara, M.N., Schäffer, A.A., Agarwala, R., Riggs, P.K., Womack, J.E., and Amaral, M.E.J.: Preliminary comparative RH mapping between river buffalo chromosome 6 (BBU6) and bovine chromosome 3 (BTA3). Animal Genetics 38:406-409, 2007.

Miziara, M.N., Goldammer, T., Stafuzza, N.B., Ianella, P., Agarwala, R., Schaffer, A.A., Elliott, J.S., Riggs, P.K., Womack, J.E., and Amaral, M.E.J.: A radiation hybrid map of river buffalo (Bubalus bubalis) chromosome 1 (BBU 1). Cytogenetics and Genome Res 119:100-104, 2007.

Van Stijn, T.C., French, M.C., Dodds, K.G., McEwan, J.C., Broad, T.E., Womack, J.E., Tisdall, D.J. and Galloway, S.M.: Comparative mapping of sheep chromosome 2q. Cytogenet and Genome Res 116-85-92, 2007.

Hansen, G.R., Abbey, C.A., Gaile, D.P., Raudsepp, T., Chowdhary, B.P., Womack, J.E. and Gill, C.A.: Assignment of six genes to bovine chromosomes 5 and 16 by fluorescence in situ hybridization, radiation hybrid mapping and genetic linkage analysis. Cytogenet. Genome Res. 116:194-197, 2007.

Prasad, A., Schiex, T., McKay, S., Murdoch, B., Wang, Z., Womack, J.E., Stothard, P., and Moore, SS.: High resolution radiation hybrid maps of bovine chromosomes 19 and 29: comparison with the bovine genome sequence assembly. BMC Genomics. 8:310, 2007.

Amaral, M.E.J., Owens, K.E., Elliott, Fickey, C., Schaffer, A.A., Agarwala, R., and Womack, J.E.: Construction of a river buffalo (Bubalus bubalis) whole-genome radiation hybrid panel and preliminary RH mapping of chromosomes 3 and 10. Animal Genetics 38:311-314, 2007.

Goldammer, T., Weikard R., Miziara, M.N., Brunner, R.M., Agarwala, R., Schaffer, A.A., Womack, J.E., and Amaral, M.E.: A radiation hybrid map of river buffalo (Bubalus bubalis) chromosome 7 and comparative mapping to the cattle and human genomes. Cytogenet. Genome Res. 119:235-241, 2007.

Snelling, W.M., Chiu, R., Schein, J.E., Hobbs, M., Abbey, C.A., Adelson, D.L., Aerts, J., Bennett, G.L., Bosdet, I.E., Boussaha, M., Brauning, R., Caetano, A.R., Costa, M.M., Crawford, A.M., Dalrymple, B.P., Eggen, A., Everts-van der Wind, A., Floriot, S., Gautier, M., Gill, C.A., Green, R.D., Holt, R., Jann, O., Jones, S.J.M., Kappes, S.M., Keele, J.W., de Jong, P.J., Larkin, D.M., Lewin, H.A., McEwan, J.C., McKay, S., Marra, M.A., Mathewson, C.A., Matukumalli, L.K, Moore, S.S., Murdock, B., Nicholas, F.W., Osoegawa, K., Roy, A., Salih, H., Schibler, L., Schnabel R.D., Silveri, L., Skow, L.C., Smith, T.P.L., Sonstegard, T.S., Taylor, J.F., Tellam, R., Van Tassell, C.P., Williams, J.L., Womack, J.E., Wye, N.H, Yang, G., and Zhao, S.: A physical map of the bovine genome. Genome Biology. 8:RI65, 2007.

Ianella, P., Stafuzza, N.B., Miziara, M.N., Agarwala R., Schäffer A.A., Riggs, P.K., Womack, J.E., and Amaral, M.E.J. First radiation hybrid map of the river buffalo X chromosome (BBUX) and comparison with BTAX. Anim. Genet. 39:196-200, 2008.

C. Research Support

Ongoing Research Support

N02 CM-87014 Womack (P.I.) 1/15/03-1/14/08
NIH/NCI
Biochemical Genetic Monitoring of Rodents
This is a contract with NCI for genotypic testing of inbred, congenic, and coisogenic strains of mice distributed to the research community for cancer research.
Role: P.I.

USDA CREES/RRF Womack (P.I.) 9/1/03-8/31/08
NAGRP Coordinator for Cattle Genome Research
This funding is to coordinate the use of bovine genome resources among laboratories supported by the USDA to conduct research on the bovine genome.
Role: P.I.

Kleberg Foundation Womack (P.I.) 1/1/05 – 12/31/09
Bovine genomics and disease resistance.
This funding is to support the application of emerging bovine genome sequence data to the identification of genomic diversity underlying differential susceptibility to disease.
Role: P.I.

Completed Research Support (past 3 years)

USDA CREES/NRI Lewin (P.I.) 9/1/03-8/31/06
Radiation Hybrid Mapping of 3000 Cattle BAC-end Sequences: A Comparative Genomics Resource
This study is designed to build a high resolution comparative map of the bovine genome relative to both mouse and human by radiation hybrid mapping bovine BAC end sequences that have significant BLAST hits to unique human and mouse sequence at 1 Mbp intervals on the human sequence.
Role: Co P.I.

USDA CREES/NRI Cockett (P.I.) 9/1/02-8/31/05
Development of a Whole Genome Radiation Hybrid Map for Sheep
This funding is to develop and characterize a radiation hybrid panel for sheep. The map will be used for comparative mapping relative to the human and other animal genomes and as a tool for mining genes responsible for biologically interesting traits.
Role: Co P.I.

USDA-NRI 1999-2002
Production of a 25,000 cattle ESTs and development of a high resolution radiation hybrid map
This study produced a second generation, high resolution comparative map of the human and bovine genomes
Role: Co P.I.

NSF OISE – 0405743 Womack (P.I.) 9/1/04-8/31/06
Development of radiation hybrid map of river buffalo.
Role: P.I.