

**CURRICULUM VITAE for  
WILLIAM D. BEAVIS, Ph.D.**

**Citizenship:** USA.

**Birthplace:** Ypsilanti, Michigan.

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**Positions Held:**

*Professor, and GF Sprague Chair, Department of Agronomy, Iowa State University, (Sept 2007 to present)*

*Director of Graduate Education in Plant Breeding, Department of Agronomy, Iowa State University, (Sept 2014 to present)*

*Interim Director, Plant Sciences Institute. Iowa State University (Sept 2009 to April 2014)*

*Chief Science Officer, National Center for Genome Resources (NCGR), Santa Fe, NM (October 2000 to Sept., 2007).*

*Adjunct Professor, Department of Mathematics and Statistics, University of New Mexico (November, 2002 – Sept. 2007)*

*Adjunct Assistant Professor, Department of Biochemistry and Molecular Biology, School of Medicine, University of New Mexico (January 2003 – December 2006).*

*Adjunct Research Scientist, Lovelace Respiratory Research Institute, Albuquerque, New Mexico (January 2004 –2009)*

*Director of Science Programs, NCGR, Santa Fe, NM (June 1999 to October 2000)*

*Program Leader for Complex Traits, NCGR, Santa Fe, NM (September 1998-June 1999)*

*Research Statistician, Pioneer Hi-Bred, Int'l, Johnston, IA (1987-1998)*

*Data Manager and Population Breeder, Sorghum Breeding Department, Pioneer Hi-Bred, Int'l, Plainview, TX (1986-1987)*

**Education:**

Ph.D., 1986, Plant Breeding Major, Statistics Minor, Iowa State University, Ames, IA

M.S., 1981, Interdisciplinary Biology-Statistics, New Mexico State University, Las Cruces, NM

B.S., 1978, Range Management, Humboldt State University, Arcata, CA.

## Extramural Research Support:

### Current:

NSF Engineering Directorate 9/1/18-8/30/23 (\$1,999,000 \$480,770)  
Title: Engineering Crops for Genetic Adaptation to Changing Environments  
Role: Co-PI

NCSRP 10/1/16 - 9/31/19 (\$3,125,564 \$236,250)  
Title: Increasing the rate of genetic gain for yield in soybean breeding programs  
Role: Co PI

### Completed:

NCSRP 9/1/14 - 8/31/16 (\$991,374 \$178,191)  
Title: Acceleration of Soybean Yield and Composition Improvement through Genomic Selection  
Role: Co PI

Syngenta 8/15/2015 – 12/30/2015 (\$80,000)  
Title: FPDA Transforming Plant Breeding into an Engineering Discipline  
Role: PI

Bill and Melinda Gates Foundation 12/5/13– 11/30/16 (\$1,750,000 \$150,000)  
Title: Plant Breeding MS Program for Africa  
Role: Co-PI

USDA-ARS 3/1/2012 - 6/1/2015 (\$212,188)  
Title: Nested Association Mapping to Identify Yield QTL in High Yielding Elite Soy Lines  
Role Co PI

Syngenta 9/1/2012 – 6/30/2014 (\$176,740)  
Title: Backcross Breeding Optimization  
Role: PI

USDA-ARS (58-1275-2-343) 4/1/2011-3/31/2012 (\$25,000)  
Title: Design and Analysis of Nested Association mapping Populations in Soybean  
Role PI

United Soybean Board (20110565308) 2/28/2011-3/31/2012 ( \$16,572)  
Title: Nested Association Mapping of Genes Controlling Soybean Yield and Other Key Traits  
Role: Co PI

United Soybean Board (2241; 2011-05907-03) 4/12/2012-3/13/2013 (\$25,043)  
Title: Nested Association Mapping to Identify Yield QTL in Diverse High Yielding Elite Soybean  
Role: Co PI

North Central Soybean Research Program (PHASEII2010-2013) 3/1/2011-2/28/2013 (\$22,200)  
Title: The Sudden Death Syndrome Research Alliance  
Role: Co PI

USDA-AFRI 06/01/08-12/31/10 (\$500,000)  
Title: Training Maize Breeders for Sustainable Bioenergy Maize Production  
Role: Co-PI

PIONEER Hi-Bred 01/01/08 – 12/31/10 (\$50,000)  
Title: Combinatorial Partitioning Methods for identifying functional markers.  
Role: PI

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| USDA-NRI   | 02/27/08 – 11/30/11 (\$305,040)                            |
| Title: Enhancement of Oat and Barley Germplasm   |  |
| Role Co-PI   |  |
| NIH-NIAID  | 10/01/04 – 9/31/09 (NCGR - \$2,620,000)                    |
| Title: Immunity to Infections and Vaccines   |  |
| Role: Co-PI  |  |
| NSF-MGI 05-512   | 10/1/05 – 9/30/07 (\$1,760,000)                            |
| Title: Population Resource and Genome Sequence of the Vegetable Pathogen <i>Phytophthora capsici</i>                           |  |
| Role: Co-PI  |  |
| NSF-BDI  | 9/1/05 – 8/31/07 (\$1,700,000)                             |
| Title: Virtual Plant Information Network   |  |
| Role: Co-PI  |  |
| NIH-NIAID  | 3/01/05 – 2/28/07 (\$100,000)                              |
| Title: Genetic Analysis of Murine Pulmonary Immunity.  |  |
| Role: Co – PI  |  |
| USDA-ARS   | 01/01/02-12/31/07 (\$6,540,000)                            |
| Title: Model Plant Initiative, Legume Information System   |  |
| <u>Role:PI</u>   |  |
| NSF-PGRP   | 5/1/05 – 4/30/08 (\$3,000,000)                             |
| Title: Soymap, an Integrated Map of Soybean  |  |
| Role: Co-PI  |  |
| USDA-ARS   | 10/1/06 – 12/31/06 (\$225,000)                             |
| Title: A Legume Information Network  |  |
| Role: PI   |  |
| NSF-BDI  | 04/01/01–09/31/04 (\$500,000)                              |
| Title: GeneX: An Internet Accessible Gene Expression Database  |  |
| Role: PI   |  |
| NSF-BDI  | 09/01/99-08/31/2004 (total-\$5,429,525 / NCGR-\$1,931,527) |
| Title: AtIR-An Arabidopsis thaliana Information Resource   |  |
| Role: Institutional representative and Co-PI   |  |
| USAID  | 02/01/03–12/31/2003 (\$100,000)                            |
| Title: Comparative Map Viewer: an integrated bioinformatic tool to display and compare genetic information on a consensus map. |  |
| Role: PI   |  |
| European Union 5 <sup>th</sup> Framework.  | 11/01/00 – 10/31/03 (total-\$1,292,814 / NCGR-\$83,649)    |
| Title: Gene-Mine   |  |
| Role: Co-PI  |  |
| Consultative Group for International Agricultural Research   | 07/01/01-06/31/02 (\$148,000)                              |
| Title: Comparative Map and Trait Viewer  |  |
| Role: Principle Investigator   |  |
| International Maize and Wheat Improvement Center   | 03/01/02-02/29/03 (\$18,000)                               |
| Title: Comparative Map and Trait Viewer.   |  |
| Role:Principle Investigator  |  |
| Rockefeller Foundation   | 12/31/00-12/31/01 (\$35,000)                               |

Title: International Bioinformatics Workshop.

Role: Institutional Representative

USDA-NRI

10/01/99-9/30/01 (\$35,000)

Title: Development of Resources for Functional Genomics in Pig

Role: Co-PI

USDA-NRI

06/01/99-06/01/01 (\$60,000)

Title: Development of a Comparative Map Viewer

Role: PI

## Publications:

### Peer Reviewed:

Kim, B., X. Dai, W. Zhang, Z. Zhuang, D.L. Sanchez, T. Lübberstedt, Y. Kang, M. Udvardi, **W.D. Beavis**, S. Xu, P. Zhao (2018) GWASpro: A High-Performance Genome-Wide Association Analysis Server. *Bioinformatics* [https://doi: 10.1093/bioinformatics/bty989](https://doi.org/10.1093/bioinformatics/bty989)

Akdemir, D., **W.D. Beavis**, R. Fritsche-Neto, A. K. Singh, J. Isidro-Sánchez (2018) Multi-objective optimized genomic breeding strategies for sustainable food improvement. *Heredity* (online 27 August 2018) <https://doi.org/10.1038/s41437-018-0147-1>

Diers, Brian W., J. Specht, K. Martin Rainey, P. Cregan, Q. Song, V. Ramasubramanian, G. Graef, R. Nelson, W. Schapaugh, D. Wang, G. Shannon, L. McHale, S. Kantartzi, A. Xavier, R. Mian, R. M. Stupar, J-M. Michno, Y-Q. C. An, W. Goettel, R. Ward, C. Fox, A. E.Lipka, D. Hyten, T. Cary, **W. D. Beavis** (2018). Genetic Architecture of Soybean Yield and Agronomic Traits. *G3: Genes|Genomes|Genetics* 8:3367-3375.

Xavier, A, D. Jarquin, R. Howard, V. Ramasubramanian, J. Specht, G. Graef, **W.D. Beavis**, B. Diers, Q. Song, P. Cregan, R. Nelson, R. Mian, G. Shannon, L. McHale, D. Wang, W. Schapaugh, A. Lorenz, S. Xu, W. Muir, K. Rainey, (2018). Genome-wide analysis of grain yield stability and environmental interactions in a multi-parental soybean population. *G3: Genes|Genomes|Genetics* 8: 519-529 <https://doi.org/10.1534/g3.117.300300>

Byrum, J, **WD Beavis**, C Davis, G Doonan, T Doubler, V Kaster, R Mowers and S Parry, (2017). Genetic Gain Performance Metric Accelerates Agricultural Productivity. *Interfaces* 47: 47:442-453. <https://doi.org/10.1287/inte.2017.0909> (finalist for the Daniel H Wagner Prize for Excellence in Operations Research)

Cameron, J.N., Y. Han; L. Wang; **W.D. Beavis** (2017). Systematic Design for Trait Introgression Projects. *Theor. Apl Gen.* 130: 1993-2004 doi: 10.1007/s00122-017-2938-9.

Howard, R, AL Carriquiry, **W.D. Beavis** (2017). Response Surface Methodology in Genomic Selection. *G3: Genes, Genomes, Genetics* 7:3103-3113. doi.org/10.1534/g3.117.044453.

Peixoto, L.deA., T.C Moellers, J Zhang, A.J. Lorenz, LL Bhering, **W.D. Beavis**, A.K. Singh. (2017). Leveraging genomic prediction to scan germplasm collection for crop improvement. *PLoS1*: doi.org/10.1371/journal.pone.0179191

Song, Q., L. Yan, C. Quigley, B.D. Jordan, E. Fickus, S. Schroeder, B-H Song, Y-Q.C. An, D. Hyten, R. Nelson, K. Rainey, **W.D. Beavis**, J. Specht, B. Diers, and P. Cregan. (2017). Genetic characterization of Soybean Nested Association Mapping population. *The Plant Genome*:10:1-14 doi: 10.3835/plantgenome2016.10.0109

- Han, Y, JN Cameron, L Wang, **WD Beavis** (2017). The predicted cross value for genetic introgression of multiple alleles. *Genetics* 205:1409-1423, doi: 10.1534/genetics.116.197095)
- Kim, B and **WD Beavis** (2017). Numericware-i: Identity by state calculator. *Evolutionary Bioinformatics* 13: doi: [10.1177/1176934316688663](https://doi.org/10.1177/1176934316688663)
- Xu, Z., J Yu, RJ Kohel, RG Percy, **WD Beavis**, D Main, ZY John (2015). Distribution and evolution of cotton fiber development genes in the fiberless *Gossypium raimondii* genome. *Genomics* 106:61-69. doi: 10.1016/j.ygeno.2015.03.002. Epub 2015 Mar 18
- Howard, R, AL Carriquiry, **WD Beavis** (2014). Parametric and Nonparametric Statistical Methods for Genomic Selection of Traits with Additive and Epistatic Genetic Architectures. *G3: Genes, Genomes, Genetics* 1:1027-46. doi: 10.1534/g3.114.010298.
- Meade, K.A., M. Cooper, **WD Beavis** (2013). Modeling biomass accumulation in maize kernels. *Field Crops Research* 151: 92–100
- Guo, B, D Wang, Z Guo, **WD Beavis** (2013). Family-based association mapping in crop species. *Theor Appl Genet* 126:1419-1430
- Asoro, FD, MA Newell, **WD Beavis**, MP Scott, NA. Tinker, and J-L Jannink (2013) Comparison of Genomic, Marker-Assisted, and Pedigree-BLUP Selection Methods to Increase  $\beta$ -Glucan Concentration in Elite Oat Germplasm. *Crop Science* 53:1894-1906.
- Asoro, FG, M Newell, P Scott, **WD Beavis**, JL Jannink,(2013) Genomewide Association Study for Beta-glucan Content in North American Elite Oat *Crop Science* 53:542-553  
doi:10.2135/cropsci2012.01.0039
- Woody, J.L., **Beavis, WD**, Shoemaker, R.C. (2012) Large homogeneous genome regions (isochors) in soybean [*Glycine max* (L.) Merr]. *Frontiers of Genetics and Genomics* 3:98  
doi:10.3389/fgene.2012.00098.
- Newell, MA, FG Asoro, MP Scott, PJ White, **WD Beavis**, and JL Jannink (2012) Genome-Wide association study for oat (*Avena sativa* L.) beta-glucan using germplasm of worldwide origin. *Theor Appl Genet* 125:1687-1696 doi :10.1007/s00122-012-1945-0.
- Asoro F.G., M.A. Newell, **W.D. Beavis**, M.P. Scott and J.-L. Jannink. (2011) Accuracy and training population design for genomic selection in elite North American oats. *Plant Genome* 4:132-144
- Xu, P, L Wang, and **WD Beavis** (2011) An optimization approach to gene stacking. *European Journal of Operational Research* 214: 168–178 doi:10.1016/j.ejor.2011.04.012
- Guo, B and **WD Beavis** (2010) *In silico* Genotyping of the Maize Nested Association Mapping Population. *Molecular Breeding* 27: 107–113 DOI 10.1007/s11032-010-9503-4
- Guo, B, SA Sleper, **WD Beavis** (2010) Nested Association Mapping for Identification of Functional Markers *Genetics* 186, 373-383
- Brock, GN, **WD Beavis**, LS Kubatko (2008) Fuzzy logic and related methods as a screening tool for detecting gene regulatory networks. *Informat.Fusion* 10:250–259 doi:10.1016/j.inffus.2008.11.008
- Mudge,J, NA Miller, I Khrebtukova, IE Lindquist, GD May, JJ Huntley, S Lu, L Zhang, JC van Velkinburgh, AD Farmer, S Lewis, **WD Beavis**, FD Schilkey, SM Virk, CF Black, MK Myers, LC Mader, RJ Langley, JP Utsey, RW Kim, RC Roberts, SK Khalsa, M Garcia, V Ambriz-Griffith, R Harlan, WCzika, S Martin, RD Wolfinger, NI Perrone-Bizzozero, GP Schroth, SF Kingsmore. (2008) Genomic Convergence Analysis of Schizophrenia. 1. mRNA Sequencing

Reveals Altered Synaptic Vesicular Transport in Post-Mortem Cerebellum. *PLoS ONE* 3(11): e3625. doi:10.1371/journal.pone.0003625

- Kingsmore, SF, N Kennedy, HL Halliday, JC VanVelkinburgh, S Zhong, V Gabriel, J Grant, **WD Beavis**, VT Tcherney, L Perlee, S Lejnine, B Grimwade, M Sorette, JM Edga (2008) Identification of Diagnostic Biomarkers for Infection in Premature Neonates. *Mol Cell Proteomics* 7(10): 1863–1875. doi: 10.1074/mcp.M800175-MCP200
- Kingsmore, SF, IE Lindquist, J Mudge, DD Gesler, **WD Beavis** (2008) Genome-wide association studies: progress and potential for drug discovery and development. *Nature Reviews Drug Discovery* 7:221-230 doi:10.1038/nrd2519
- Beavis, WD**, FD Schilkey, SM Baxter (2007). Translational Bioinformatics: At the Interface of Genomics and Quantitative Genetics. *Crop Science* 47(s3): 32-43
- Kingsmore, SF, IE Lindquist, J Mudge **WD Beavis** (2007) Genome-Wide Association Studies: Progress in Identifying Genetic Biomarkers in Common, Complex Diseases. *Biomarker Insights* 2007:2 1–10.
- Stein, L, DD Gessler, D Rokshar, D Main, L Mueller, E Huala, C Lawrence, S Rhee, **WD Beavis** (2006) Save our Data. *The Scientist* April 24-25.
- Munneke, B., K.A. Schlauch, **WD Beavis**, and R.W. Doerge (2005). Adding Confidence to Gene Expression Clustering. *Genetics* 170:2003-2011.
- Gonzales, M, E Archuleta, A Farmer, K Gajendran, D Grant, R Shoemaker, **WD Beavis**, ME Waugh (2005). THE LEGUME INFORMATION RESOURCE (LIS): An Integrated Information Resource for Comparative Legume Biology. *Nucleic Acids Research* 33: D660-D665
- Thro, AM, W Parrott, JA. Udall, **WD Beavis**. (2004). Genomics and Plant Breeding: The Experience of the Initiative for Future Agricultural and Food Systems. *Crop Science* 44:1836.
- Huala, E., A Dickerman, M Garcia-Hernandez, D Weems, L Reiser, F LaFond, D Hanley, D Kiphart, M Zhuang, W Huang, L Mueller, D Bhattacharyya, D Bhaya, BW Sobral, **WD Beavis**, DW Meinke, CD Town, C Somerville, SY Rhee, (2001) The Arabidopsis Information Resource (TAIR): a comprehensive database and web-based information retrieval, analysis, and visualization system for a model plant. *Nucleic Acids Research* 29:102-5.
- Churchill, GA and The Complex Traits Consortium (2004). The Collaborative Cross: A Community Resource for the Genetic Analysis of Complex Traits. *Nature Genetics* 36:1133-7
- Jansen, RC, JL Jannink and **WD Beavis**. (2003) Mapping quantitative trait loci in plant breeding populations: use of parental haplotype sharing. *Crop Science* 43: 829-834.
- Tuggle, CK, JA Green, C Fitzsimmons, R Woods, RS Prather, S Malchenko, M Bento-Soares, T Kucaba, K Crouch, C Smith, D Tack, N Robinson, B O’Leary, T Scheetz, T Casavant, D Pomp, JB Edeal, Y Zhang, MF Rothschild, K Garwood, **WD Beavis**. (2003) EST-Based Discovery in Pig: Virtual Expression Patterns and Comparative Mapping to Human. *Mammalian Genome* 14: 565-579.
- Vigouroux, Y., JS Jaqueth, Y Matsuoka, OS Smith, **WD Beavis**, JSC Smith and J Doebley. (2002). Rate and pattern of mutation at microsatellite loci in maize. *Mol Biol Evol* 19:1251-1260.
- Lee, M., Sharopova, N., **Beavis, WD.**, Grant, D., Katt, M., Blair, D., Hallauer, A. (2002) Expanding the genetic map of maize with the intermated B73 x Mo17 (IBM) population. *Plant Molecular Biology*. 48:453-61.

- Mangalam, H, Stewart, J, Zhou, J, Schlauch, K, Waugh, M, Chen, G, Farmer, A, Colello, G, Weller, J, and **Beavis, WD** (2001) GeneX: an Open Source Gene Expression Database and Integrated Tool Set. *IBM Systems Journal*. 552-570.
- Siepel, A, Tolopko, A, Farmer, A, Steadman, P, Schilkey, F, Perry, BD, and **Beavis, WD**. (2001) A development platform for the integration of heterogeneous bioinformatics software components. *IBM Systems Journal*. 540-592.
- Siepel, A., Farmer, A, Tolopko, A, Zhuang, M, Mendes, P, **Beavis, WD**, and Sobral, BWS (2001) ISYS: A decentralized, component-based approach to the integration of heterogeneous bioinformatics resources. *Bioinformatics*. 17:83-94.
- Beavis, WD**, OS Smith, D Grant, R Fincher (1994). Identification of quantitative trait loci using a small sample of topcrossed and F4 progeny from Maize. *Crop Science* 34:882-895.
- Keim P, **WD Beavis**, JM Schupp BM Baltazar L Mansur RE Freestone M Vahedian DM Webb (1994) RFLP analysis of Soybean breeding populations: I Genetic structure difference due to inbreeding methods. *Crop Science* 34:55-61.
- Bubeck, DM. MM Goodman, **WD Beavis**, D Grant (1993) Quantitative trait loci controlling resistance to Gray Leaf Spot in Maize. *Crop Science* 33:838-847.
- Keim P, **WD Beavis**, J Schupp, R Freestone (1992) Evaluation of Soybean RFLP marker diversity in adapted Germplasm. *Theor Appl Genet* 85:205-212.
- Beavis WD**, D Grant, M Albertsen, R Fincher (1991) Quantitative trait loci for plant height in four maize populations and their associations with qualitative genetic loci. *Theor Appl Genet* 83:141-145.
- Beavis WD** and D Grant (1991) A linkage map based on information from four F2 populations of maize. *Theor Appl Genet* 82:636-644.
- Beavis WD** and KJ Frey (1987) Expression of nuclear-cytoplasmic interactions and heterosis in quantitative traits of oats. *Euphytica* 36:877-886.
- Beavis WD**, E Pollak, KJ Frey (1987) A theoretical model for quantitatively inherited traits influenced by nuclear-cytoplasmic interactions. *Theor Appl Genet* 74: 571-578
- Beavis WD**, JC Owens, JA Ludwig and EW Huddleston (1982) Grassland Communities of East-Central New Mexico and density of range caterpillar, *Hemileuca oliviae*, Cockerell. *Southwestern Naturalist* 27:335-343.
- Beavis WD**, JC Owens, M Ortiz (1981) Density and developmental stage of range caterpillar, *Hemileuca oliviae*, Cockerell, as affected by topographic position. *Journal of Range Management* 34:389-392.

#### Patents

- Beavis, WD** (2002) QTL Mapping in Plant Breeding Populations. US Patent (US 6399855 B1).

#### Refereed Proceedings

- Gepts, P. **WD Beavis**, EC Brummer, RC Shoemaker, HT Stalker, NF Weeden, ND Young. (2005) Legumes as a Model Plant Family: Genomics for Food and Feed. Report of the Cross Legume Advances through Genomics Conference. *Plant Physiology* 137: 1228-1235.
- Beavis, WD**. (2005) Architectures for Integration of Data and Applications: Lessons from Integration Projects. In *Genome Exploration: Data Mining and the Genome. The Stadler Genetics Symposia XXII*..Springer (eds. P. Gustafson, R. Shoemaker and J.W. Snape) pp. 31-46

Tuggle, CK, RS Prather, MS Soares, T Casavant, D Pomp, MF Rothschild, **WD Beavis**. (2001) Gene Discovery and Functional Genomics in the Pig. In *The Proceedings of the National Swine Improvement Federation*.

**Beavis, WD** (1996) QTL mapping in plant breeding populations. In *1996 Proceedings of the Biometric Section of the American Statistical Association*. Am Statistical Assoc.13-20.

Lindsey DL and **WD Beavis** (1985) Vesicular Arbuscular Mycorrhizal Associations in *Atriplex canescens* and *Ceratoides lanata*. In *Wildland Shrub Symposium*. BYU Press, Provo, Utah

**Beavis, WD** (1985) An electronic hand-held notebook. pp.89-109 IN: *Proceedings NCCI Data Acquisition Workshop*. NCCI. Madison, Wisconsin.

#### Invited and Refereed Book Chapters:

Huntley, JA, SJ Maleki, MD Gonzales, **WD Beavis** (2008) Bioinformatic tools, resources and strategies for comparative structural studies for food allergens. In Eds. Siantar, DP, MW Trucksess, PM Scott, WM Herman. *Food Contaminants: Mycotoxins and Food Allergens*. American Chemical Society, Washington DC pp 322-356.

Gonzales, MD, K Gajendran, AD Farmer, E Archuleta, **WD Beavis** (2007) Leveraging model legume information to find candidate genes for soybean Sudden Death Syndrome using the Legume Information System (LIS). In Ed. Edwards D. *Methods in Molecular Biology*, Humana Press (USA), pp. 245-260

Sobral, BWS and **WD Beavis** (2001) Information System Approaches to Support Discovery in Agricultural Genomics. In *DNA-Based Markers in Plants*. Kluwer Academic Publishers. RL Philips (ed).

**Beavis, WD** (1998) QTL Analyses: Power, Precision and Accuracy. In *Molecular Analysis of Complex Traits*. AH Paterson (ed). CRC Press.145-161.

Smith, S, **WD Beavis** (1996) Molecular marker assisted breeding in a company environment. In *The Impact of Plant Molecular Genetics*. BWS Sobral (ed), Birkhauser. 260-272.

**Beavis, WD**, P Keim (1996) Identification of QTL that are affected by environment. In *Genotype by Environment Interactions: New Perspectives*. MS Kang and H Gauch (eds), CRC press.123-150.

**Beavis, WD** (1994) The power and deceit of QTL experiments: Lessons from comparative QTL studies. *Proceedings of the forty-ninth annual corn and sorghum industry research conference* 49:250-266.

Briggs SP, **WD Beavis** (1992) How RFLP loci can be used to assist transposon-tagging efforts. pp. 653-659 In *The Maize Handbook*. M Freeling and V Walbot (eds.) Springer Verlag, New York.

**Beavis, WD**, M Lee, D. Grant, AR Hallauer, T. Owens, M Katt, D Blair (1992) The influence of random mating on recombination among RFLP loci. *Maize Genetic Cooperation Newsletter* 66:52-53.

**Beavis WD**, OS Smith, D Grant, R Fincher, JSC Smith (1989) Identification and genetic localization of loci affecting yield and other agronomic traits in maize. Vortrage fur Pflanzenzuchteng 29-7 Eucarpia Congress, Gottingen, FDR

#### Invited Presentations:

**Beavis, WD** (2017) Operations Research for Genetic Improvement. *Crops*. 7 June. Hudson Alpha Institute. Huntsville, AL.



- Beavis, WD** (2016) Transforming Breeding into an Engineering Discipline. *Graduate Plant Science Seminar Series*. 22 October. Athens, GA.
- Beavis, WD** (2015) Transforming Breeding into an Engineering Discipline. *Plant Science Seminar Series*. 20 April. Columbia, MO.
- Beavis, WD** (2015) Transforming Breeding to an Engineering Discipline. *Animal Science Seminar Series*. 17 February. Ames, IA.
- Beavis, WD** (2015) Optimal Use of Genomic Prediction in Plant Breeding. *Soybean Breeders and Physiologists Workshop*. St Louis. 16 February. St. Louis, MO.
- Beavis, WD** (2014) Using next-gen sequencing technologies for predicting the best parents for the next generation. *Second Plant Genomics Congress*. St. Louis, MO.
- Beavis, WD.** (2014) Transforming Plant Breeding into an Engineering Discipline Workshop. *Annual Meeting of North American Plant Breeders*. Minneapolis, MN
- Beavis, WD.** (2014). Transforming plant breeding from art to an engineering discipline. *Sustainability Genetics and Future Cultivars Workshop. Phytopath Soc Meetings*. Minneapolis, MN.
- Beavis, WD.** and L Wang (2014) Opportunity for Emergent Disciplines at the Interface of Engineering and Plant Science. *International Workshop on Computationally Engineered Plants*. Des Moines, Iowa
- Beavis, WD.** (2012) Transforming Biology from a Descriptive to a Predictive Science. *Interdisciplinary Program in Predictive Biology Seminar Series at University of Nebraska, Lincoln*. Lincoln Ne. October 17, 2012.
- Beavis, WD** (2012). Plant Breeding: Art, Science or Engineering?. *Winfield U, a short course*. Ankeny, Ia March 7, 2012
- Beavis, WD** and L Wang (2011). Translating Discoveries for soybean breeding. *Soybean Breeders and Physiologists Workshop*. St Louis. 22 February.
- Beavis, WD** and L Wang (2011) Vision for soybean Research: Translating Discoveries. St. Louis. July 27.
- Beavis, WD** and L Wang (2009). Optimization and Marker Assisted Breeding. *Proceedings of the American Seed Trade Association*. Chicago Ill. 9 December
- Beavis WD** (2009) Translational Research – Realizing the Promises of Genomics. *Graduate Seminar Series, Kansas State University, Manhattan, Kansas*. 22 September.
- Beavis WD** (2009) To Realize the Promises of Genomics Are New Quantitative Genetic Models Needed? *Gordon Research Conference on Quantitative Genetics and Genomics*. 22, Febraury.
- Beavis WD** (2008). Realizing Impacts from Knowledge of Fundamental Biological Processes. *Translational Biology Workshop*. USDA-ARS Ames, Iowa. 27 October.
- Beavis WD** (2008) Utilizing the Tools of Genomics and Bioinformatics for Plant Breeding. *Workshop on Integrating Genomics and Quantitative Genetics Syngenta Biotechnology*. 9 July.
- Beavis WD** (2008). Decision Support Systems for Plant Breeding. *U Wisconsin*. Madison, Wisc. 10 May.
- Beavis WD** (2008). Translational Research for Applied Plant Breeding. *Plant Breeding Symposium. U Minnesota*, St. Paul, MN. 17 March.
- Beavis WD** (2008). Maize-TREC. *Illinois Corn Breeders School*. Champaign, Ill. 4 March.

- Beavis WD** (2008). Is Applied Genomics an Oxymoron? *NCCI67 Maryland Feb 2*
- Beavis WD** (2007). Is Applied Genomics an Oxymoron? *Proceedings of the American Seed Trade Association*. Chicago Ill. 7 December
- Beavis, WD** (2007). Genomics and Quantitative Genetics. *Conference on Genomics and the Land Grant Mission: Emerging Trends in Application of Genomics to Agricultural Research*. Purdue University.
- Beavis, WD** (2007). Bayesian Inference for Predicting Response to Infection. *Statistical Genomics Workshop of the Plant and Animal Genome XV*. San Diego, Ca.
- Beavis, WD** (2006). Genomics? Bioinformatics? Translation Please! *National Coalition for Food and Agricultural Research*. Washington DC, 10 July.
- Beavis WD** and DD Gessler (2005) Tuberculosis as a Worldwide Model System for Systems Biology. *New Mexico Consortium for BioResearch, Research Task Group Strategy Workshop*, Las Cruces, NM
- Beavis, WD** (2005) At the Interface of Systems Biology and Quantitative Genetics. *Workshop on Biocomputing/Biostatistics@UNM*. Albuquerque, NM
- Beavis, WD** (2005) Bioinformatics for Translational Crop Genomics. *A Presentation to the Stakeholder Assessment of NPI 301 (Plant, Microbial and Insect Genetic Resources, Genomics and Genetic Improvement)*, Baltimore, Md.
- Beavis WD** and SM Baxter (2005) Associative Genomics and Bioinformatic Resources. *A Conference on Establishing a Center for Theoretical and Computational Pathomics at Los Alamos National Laboratory*. Los Alamos, NM
- Beavis, WD** (2005) At the Interface Between Quantitative Genetics and Systems Biology. *Gordon Research Conference on Quantitative Genetics and Genomics*. Ventura, Ca.
- Beavis, WD, L. Salter, G. Brock.** (2004) Fuzzy Logic for Fuzzy Data? *Plant and Animal Genome XII*. San Diego, Ca.
- Beavis, WD, M Waugh, D Grant, RS Shoemaker** (2004). The Legume Information System: Whatever Happened to Soybase? *The 10th Biennial Conference on the Cellular and Molecular Biology of the Soybean*, St Louis Mo.
- Beavis, WD** (2004). The Power and Deceit of Inferential Statistics to Associate Genotypes with Phenotypes. *Division of Mathematics and Computing, Oak Ridge National Laboratory*. Oak Ridge, Tn.
- Beavis, WD** (2003) Loose Coupling Architectures for Integrating Data and Applications. *22<sup>nd</sup> Stadler Genetics Symposium*. Columbia, Missouri.
- Beavis, WD** 2002. Can we breathe in a flood of biological data? *Lovelace Respiratory Research Institute Fifth Symposium on Molecular Approaches for Early Diagnosis and Treatment of Respiratory Diseases*. Santa Fe, NM.
- Beavis, WD** 2002, Enabling Biology to Become a Predictive Science, *Department of Energy, Genomes to Life Symposia*, Germantown, MD
- Beavis, WD** 1999. Integrating the Central Dogma with Plant Breeding. *Plant and Animal Genome VII*. San Diego, Ca.
- Beavis, WD.** 1995. Influence of inbreeding and outcrossing on QTL identification. *Annual meeting of the Society for the Study of Evolution*. Montreal, Canada.

- Beavis, WD.** 1994. Lessons from comparative yield QTL experiments. *Keystone Symposia on Molecular and Cellular Biology, Improved Crop and Plant Products Through Biotechnology*. Keystone, Co.
- Smith, S and **WD Beavis.** 1993. Molecular marker assisted selection of quantitative characters and finger-printing of maize genotypes. "*The impact of genetic engineering in Plant Breeding*". Aristotelian University of Thessaloniki, Thessaloniki, Greece.
- Grant, D and **WD Beavis.** 1993. The Power to identify QTL. *Third International Congress of Genetics*. Birmingham, England.
- Beavis, WD.** 1993. Power and Deceit of QTL experiments. *Gordon Research Conference on Quantitative Genetics and Biotechnology*. Ventura, Ca.
- Beavis, WD.** 1992. Identification of QTL among and within maize populations. *Univ Minn lecture series*, St Paul, Mn.
- Keim P, **WD Beavis**, J Schupp, R Freestone. 1991. RFLP Analysis of Soybean Breeding Populations: Genetic mapping of markers and QTL's *3rd Int'l Congress on Molecular Biology of Plant Growth and Development*. Tucson, AZ.
- Keim P, RC Shoemaker, **WD Beavis.** 1991. Coupling traditional breeding with new technologies towards improving soybean. *Int'l Congress on Soybean Improvement*. Sao Paulo, Brazil.
- Beavis, WD**, D Grant, R Fincher, and OS Smith. 1989. Associations between RFLP's and the expression of agronomic traits in Maize. *ASA meetings*, Las Vegas, NV.

#### Volunteered Oral Presentations and Posters:

- Kim, Bongsong, **WD Beavis** (2015) Trait-associated markers increase the prediction accuracy in ridge regression best linear unbiased prediction. *Soybean Breeders' Workshop*, St. Louis, MO.
- Diers, BW, C Bonin, R Nelson, T Cary, J Meharry, D Gibson, R Howard, K Martin Rainy, B Muir, A Xavier, J Specht, G Graef, P Cregan, W Schapaugh, S Kantartzi, D Wang, G Shannon, L Mchale, R Mian, **WD Beavis** (2014) Nested association mapping of agronomic traits in soybean" *Molecular and Cellular Biology of the Soybean 15<sup>th</sup> Biennial Conference*, Minneapolis, MN.
- Diers, BW, C Bonin, R Nelson, T Cary, J Meharry, D Gibson, R Howard, K Martin Rainy, B Muir, A Xavier, J Specht, G Graef, P Cregan, W Schapaugh, S Kantartzi, D Wang, G Shannon, L Mchale, R Mian, **WD Beavis** (2014) SoyNAM project update: preliminary results. *Soybean Breeders' Workshop*, St. Louis, MO.
- Mukherjee S, GR Johnson, MP Scott, AD Farmer, GD May, KR Lamkey and **WD Beavis** (2014) spliceR: Detection and quantification of splice variants in maize inbreds and hybrids from RNA-seq data. *PAG XXII* San Diego, CA.
- Howard, R., A. Carriquiry, **WD Beavis.** (2012) Implementation of parametric and nonparametric models for genomic assisted prediction in plant breeding. *Plant Breeding for Future Generation. Proceedings of the 19<sup>th</sup> EUCARPIA General Congress*. Budapest, Hungary.
- Mukherjee S, GR Johnson, MP Scott, AD Farmer, GD May, KR Lamkey and **WD Beavis** (2012) spliceR: A novel method to investigate Allele-Specific Expression from RNA-seq data *VI International Conference on Legume Genetics and Genomics*, Hyderabad, India.
- Suza W, W Fehr, **WD Beavis** (2012) An online Master of Science in Plant Breeding. *2nd National Association of Plant Breeders Meeting*, Indianapolis, IN

- Mukherjee S, MP Scott, and **WD Beavis** (2012) A novel method to read level genomic statistics from RNA-seq data *8th International Purdue Symposium on Statistics* West Lafayette, In.
- Cannon, S , D. Sandhu, , S MacMil, , G. Wiley , **WD Beavis** , B. Roe , M.K. Bhattacharyya (2012). Transcript Profiles of the Soybean-Phytophthora sojae Interaction using 454 Pyrosequencing. *Soybean Breeders and Physiologists Workshop*. St Louis..
- Meade, KA., M Cooper, **WD Beavis**, (2011) Phenotypic and genotypic analysis of biomass and moisture contents in testcrossed double-haploids of maize. *ASA, CSSA, SSSA International Annual Meetings*, San Antonio, TX, USA.
- Meade, K, M Cooper., **WD Beavis** (2011) Phenotypic and genotypic analysis of biomass and moisture content in testcrossed double-haploids of Maize. Poster Presentation at *the Quantitative Genetics and Genomics Gordon Research Conference*, Galveston, TX, USA.
- Diers, BW, JS Specht, D Hyten, P Cregan, R Nelson, **WD Beavis** (2011) Soybean nested association mapping. *Soybean Breeders' Workshop*, St. Louis, MO. February 21.
- Merrick, L, T Lubberstedt, KR Lamkey, K Moore, **WD Beavis** (2010) Toward a master of Science in Plant Breeding via Distance Education. *4<sup>th</sup> Plant Breeding Conference*, Johnston Iowa.
- Meade, KA and **WD Beavis** (2010). Phenotypic analysis of kernel biomass and moisture content in testcrossed double haploids. *52nd Annual Maize Genetics Conference*, Riva del Garda, Trento, Italy.
- Meade, K, **WD Beavis** (2009). Phenotypic analysis of kernel biomass and moisture contents in testcrossed double-haploids. *American Seed Trade Association Seed Expo 2010*, Chicago, IL, USA.
- Wang, L and **WD Beavis** (2009) An integer programming approach to a biological system *IERC Conference* Miami, FL.
- Kingsmore, SF, **WD Beavis**, GD May, K Gajendran, KH Lamour, S Kamoun, P Richardson (2006) A Population Resource and Genome Sequence of the Vegetable Pathogen *Phytophthora capsici*. *NSF-MGI and USDA-NRI New Awardees Conference*. San Diego, Ca.
- Huntley, JM, MD Gonzales, **WD Beavis** (2006) Tools, Resources and Strategies for Characterizing and Comparing Legume Seed-storage Protein Structures. *Plant Genome XIV* , San Diego, CA.
- Gonzales, MD, E Archuleta, AD Farmer, K Gajendran, D Grant, R Shoemaker, **WD Beavis** (2006) THE LEGUME INFORMATION SYSTEM (LIS): Using comparative analysis to determine a set of candidate genes for a complex trait. *Plant Genome XIV*, San Diego, CA.
- Grant, D, AD Farmer, MD Gonzales, E Archuleta, K Gajendran, RC Shoemaker, ME Waugh, **WD Beavis** (2005) Genetic And Physical Maps In The Legume Information System. . *Plant Genome XIII*, San Diego, CA.
- Gonzales, MD, **WD Beavis**, K Gajendran, AD Farmer, E Archuleta, D Grant, R Nelson, RS Shoemaker, ME Waugh, The Legume Information Resource (LIS): An Integrated Information Resource For Comparative Legume Biology. *Plant Genome XIII*, San Diego, CA.
- Gonzales, MD, K Gajendran , E Archuleta, A Farmer, J Sullivan, S Li, D Grant, R Shoemaker, **WD Beavis**, ME Waugh. (2004) The Legume Information System (LIS): A Next Generation Legume Resource. *Plant Genome XII*, San Diego, CA.

- Waugh, ME, W Anderson, MD Gonzales, S Li, L Montoya, GL Nell, AN Tolopko, JP Sullivan, D Grant, RS Shoemaker, **WD Beavis** (2003). The Legume Information System: Leveraging Model Plants to Fill Knowledge Gaps in Crop Species. *Plant Genome XI*, San Diego, CA.
- Dixon, DS, G Davenport, TJJ van Hintum, D Weems, J Dicks, **WD Beavis** (2003) A Generic Model for an Object Oriented Interface to a Relational Database and its Application to Genebank Data. *Plant Genome XI*, San Diego, CA.
- Davenport, G., **WD Beavis**, MCAM Bink, KJ Dehmer, J Dicks, DS Dixon, V Fens, M Frisch, G Gort, E Křístová, A Lebeda, T Metz, AE Melchinger, J Peleman, D Pink, J Reif, JR van der Voort, R van Treuren, T JL van Hintum (2003). GENE-MINEing Agronomically Important Traits in Germplasm. *Plant Genome XI*, San Diego, CA
- Zhang, Y, K Garwood, **WD Beavis**, CT Tuggle, MF Rothschild (2002). Porcine Expressed Sequence Tags (ESTs): Comparative Analysis and Database Development. *Plant Genome X*, San Diego, CA.
- Harger, CA, JW Weller, HJ Mangalam, JE Stewart, ME Waugh, J Zhou, GD Colello, **WD Beavis** (2001). GENEX: A Flexible Data Management and Analysis System for Gene Expression Data. *Plant Genome IX*, San Diego, CA.
- Munneke, B, **WD Beavis**, RW Doerge (2001) Permutation Based Confidence Measures Applied to mRNA Cluster Groupings *Plant Genome IX*, San Diego, CA.
- Pecherer, RM, M Polacco, HB Zhang, **WD Beavis**, T Cartner, S Shroeder (2000) A Comparison of Maize and Rice Genome Maps. *Plant Genome VIII*, San Diego, CA.
- Pecherer, RM, T Cartner, JJ Zhuang, **WD Beavis** (2000) A Comparative Genome Mapping Tool. *Plant Genome VIII*, San Diego, CA.
- Pecherer, RM, **WD Beavis**, BWS Sobral (1999). Comparative Genomic Mapping Toolset and Database. *Plant Genome VII*, San Diego, CA.
- Beavis, WD** and SJ Openshaw. (1999). Integrating the Central Dogma With Plant Breeding. *Plant Genome VII*, San Diego, CA.
- Beavis, WD**, RW Doerge, TK Blake, PL Wargo (1999) Evolution of JQTL to JAG. *Plant Genome VII*, San Diego, CA.
- Lee, M, , J Vogel, W Woodman, S Tingey, MJ Long, M Krakowsky, A Hallauer, D Austin, D Ritland, **WD Beavis** (1999) Tools for High Resolution Genetic Mapping in Maize-Status Report. *Plant Genome VII*, San Diego, CA.
- Webb, DM, BM Baltzar, AP Rao-Arelli, S. Schupp, P Keim, K Clayton, A Fercia, T Owens, **WD Beavis** (1994) QTL affecting soybean cyst-nematode resistance. *Plant Genome II*, San Diego, CA.
- Jarboe, SG, **WD Beavis**, SJ Openshaw, BE Zehr (1994) Computer-simulated study of factors affecting marker-assisted backcross conversion. *Plant Genome II*, San Diego, CA.
- Jarboe, SG, **WD Beavis**, SJ Openshaw, BE Zehr (1993). Computer simulated study of factors affecting marker assisted backcross conversion. *Am Soc Agron*, Cincinnati, OH.
- Owens T, **WD Beavis**, DE Blair (1992) An expert system for detection and identification of errors in genetic segregation data. *Plant Genome I*, San Diego, CA.
- Blair DE, **WD Beavis**, T Owens, (1992) Impact of errors in segregation scores on linkage maps and QTL identification. *Plant Genome I*. San Diego, CA.

- Keim P, **WD Beavis**, J Schupp, R Freestone, M Vahedian, DM Webb, and T Gocken (1992) RFLP Analysis of a Soybean Breeding Population: Genetic Structure and Trait Variation. *Am Soc Agron* Minneapolis, MN.
- Grant D, **WD Beavis**, ML Katt, T Owens, A Hallauer, M Lee, KR Lamkey (1991) Comparison of QTL of Plant Height Between Two Samples of B73xMO17. *Maize Genetics*, Delavan WN.
- Keim P, **WD Beavis**, J Schupp, R Freestone (1990) Evaluation of Public RFLP Markers in Cultivated Soybean. *Am Soc Agron*. San Antonio, TX.
- Bubeck DM, MM Goodman, **WD Beavis**, D Grant (1990) Quantitative Trait Loci Controlling Resistance to Gray Leaf Spot in Maize. *Am Soc Agron*. San Antonio, TX.
- Fincher R, **WD Beavis**, D Grant (1990) Genotype by Environment Interactions Associated with molecular marker identified QTL effects. *Am Soc Agron*. San Antonio, TX.
- Grant D, **WD Beavis**, R Fincher, M Albertsen (1990) Correspondence between qualitative genes and QTL in maize. *Am Soc Agron*. San Antonio, TX.
- Grant D, **WD Beavis**, ML Katt, R Feazel, R Meier, R Fincher (1989) Comparison of QTLs form maturity related traits among different crosses of maize. *Am Soc Agron*. Las Vegas, NV.
- Beavis WD** and KJ Frey (1985) Genetic modelling of nuclear-cytoplasmic heterosis in oats. *Am Soc Agron*. Chicago, IL.
- Beavis WD** and KJ Frey (1984) The influence of cytoplasmic inheritance on quantitative traits. *Am Soc Agron*. Las Vegas, NV.
- Beavis WD** (1982) Economical computerized data collection and management for field use. *Am Soc Agron* Anaheim, CA.
- Beavis WD** and JC Owens (1979) The ecology of oviposition exhibited by the range caterpillar, *Hemileuca oliviae*, Cockerell. *Ent Soc Am* Denver, CO.
- Beavis WD** and NL Green (1979) The effect of Vesicular Arbuscular Mycorrhizae on growth and nodulation of roots of sub-clover, *Trifolium subterraneum*. *Am Soc Rge Mgmt*, Caspar, WY.

## **Outreach Activities:**

### Workshops, Short-courses and Conferences:

**Beavis, WD**, (2017). Convener of Translational Genomics: Redesigning Genetic Improvement Projects. *Plant and Animal Genome Conference XXVI* January 17, San Diego, Ca.

**Beavis, WD**, and J Byrum (2017). Convener of Optimal Designs for Genetic Improvement. *10th World Soybean Congress* September 9-13, Savannah, Georgia.

**Beavis, WD**, L Wang and J Byrum (2017). Operations Research in Plant Breeding. *Summer Institute for Advanced Topics in Plant Breeding* May 22-26. Iowa State University, Ames, Iowa.

**Beavis, WD**, L Wang and J Byrum (2016). Operations Research in Plant Breeding. *Summer Institute for Advanced Topics in Plant Breeding*. June 20-24. Iowa State University, Ames, Iowa.

**Beavis, WD**, T Doubler and L Wang. *Workshop on Optimization in Agriculture* (2016 ). Designing optimal genetic improvement and agronomic systems. Nov. 29. Iowa State University, Ames, Iowa.

**Beavis, WD** and L Wang. *Summer Institute for Advanced Topics in Plant Breeding* (2015). Transforming Plant Breeding Into an Engineering Discipline. July 1-2. Iowa State University, Ames, Iowa.

**Beavis, WD**, J Colletti, KR Lamkey. *Workshop on Optimization in Agriculture* (2015) Operations Research and Advanced Analytics at Syngenta – Franz Edelman Prize from INFORMS. Nov. 13. Iowa State University, Ames, Iowa.

## **Education Activities:**

### e-Modules for Gates Foundation

**Beavis, WD**, JN Cameron, D Dykema, R Howard. *Biometry*. Completely randomized designs for single factors.

**Beavis, WD**, JN Cameron, D Dykema, R Howard. *Biometry*. Completely randomized designs for two factors.

**Beavis, WD**, JN Cameron, D Dykema, R Howard. *Biometry*. ANOVA and multiple comparisons.

**Beavis, WD**, JN Cameron, D Dykema, R Howard. *Biometry*. Randomized complete block designs.

**Beavis, WD**, JN Cameron, D Dykema, R Howard. *Biometry*. Multiple regression.

**Beavis, WD**, JN Cameron, D Dykema, R Howard. *Biometry*. Non-linear regression.

**Beavis, WD**, R Howard. *Quantitative Genetics*. Review of metrics, models and plant breeding.

**Beavis, WD**. *Quantitative Genetics*. Multi-environment trials and GxE.

**Beavis, WD** and KR Lamkey. *Quantitative Genetics*. Population genetics.

**Beavis, WD** and KR Lamkey. *Quantitative Genetics*. Quantitative genetic models.

**Beavis, WD** and KR Lamkey. *Quantitative Genetics*. Covariance among relatives, variance components and heritability.

**Beavis, WD** and KR Lamkey. *Quantitative Genetics*. Mating designs and genetic gain.

**Beavis, WD**. *Quantitative Genetics*. Covariance among relatives, BLUP and genetic gain.

**Beavis, WD.** *Quantitative Genetics*. Resource allocation and genetic gain.

Graduate Student advisees (degree, program, year completed):

Vishnu Ramasubramnian, ISU (Bioinformatics Computational Biology)  
Andreomar Kurek, ISU (PhD, Plant Breeding)  
Danielle Dykema, ISU (PhD, Plant Breeding)  
Zhanyou Xu, ISU (PhD, Bioinformatics Computational Biology)  
Haley Trumpy, ISU (PhD, Plant Breeding)  
John Cameron, ISU (PhD, Plant Breeding, 2017)  
Tracy Doubler, ISU (PhD, Plant Breeding, 2016)  
Reka Howard, ISU (PhD, Statistics and Plant Breeding, 2016)  
Shreyartha Mukherjee, ISU (PhD, Bioinformatics Computational Biology, 2013)  
Jenna Woody, ISU (PhD, Interdepartmental Genetics, 2012)  
Kendra Meade, ISU (PhD, Plant Breeding, 2012)  
Franco Asoro, ISU (PhD, Plant Breeding, 2012)  
Mark Newell, ISU (PhD, Plant Breeding, 2011)  
Heather Mannion, ISU (MS, Plant Breeding, 2016)  
Carla Gho, ISU (MS, Plant Breeding, 2015)  
Joseph Strottman, ISU (MS, Plant Breeding, 2015)  
Justin Morrison, ISU (MS, Plant Breeding)  
Erin Jones, ISU (MS, Plant Breeding, 2014)  
Dawn Gibson, ISU (MS, Plant Breeding, 2014)

Graduate Student committees (degree, program, year completed) :

Henrique Uliana Trentin (PhD, Plant Breeding)  
Anderson Versegnazzi (PhD, Plant Breeding)  
Longui Ren, ISU (PhD, Plant Breeding)  
Ye Han, ISU (PhD, Industrial and Manufacturing Systems Engineering)  
Kara Lind (PhD, Materials Science and Engineering)  
Brian Hughs (MS, Plant Breeding, 2016)  
Jennifer Robinson, (MS, BBMB, 2016)  
Ignacio Trucillo (PhD, Plant Breeding, 2015)  
Ye Han, ISU (MS Industrial and Manufacturing Systems Engineering, 2014)  
Yong Sheng, Chen, ISU (PhD Plant Breeding 2013)  
Naser Alkalifah, ISU (MS Plant Breeding 2013)  
Trent Moore, ISU (MS Plant Breeding withdrawal)  
Bryce Lemke, ISU (PhD Plant Breeding withdrawal)  
Pan Xu, ISU (PhD Industrial and Manufacturing Systems Engineering 2012)  
Katie Strand, ISU (MS Plant Breeding 2012)  
Massiel Orellana, ISU (PhD Plant Breeding 2012)  
Karen Grote, ISU (PhD Plant Breeding 2011)  
Carla Vogel, ISU (MS Plant Breeding 2010)  
Jonathon Jenkinson, ISU (PhD Plant Breeding 2009)  
Kristina Strandberg, University of New Mexico (MS, Statistics, 2005)



Guy Brock, University of New Mexico (PhD Statistics 2003)

Brian Munneke, Purdue University (PhD Statistics 2001)

Lance Veldboom, ISU (PhD Plant Breeding 1994)

Post Doctoral Fellows (Employer):

Dr. Bongsong Kim (Noble Foundation)

Dr. Kendra Meade (Nature Source Genetics)

Dr. Baohong Guo (Syngenta Int'l)

Dr. Lisa Astuto (Sandia National Laboratories)

Dr. Karen Schlauch (University of Nevada, Reno)

Dr. Brian Shiloff (Exagen Corp)

Classes taught:

Agronomy 528 Introduction to Quantitative Genetics 2014 Iowa State University

Agronomy 513 Quantitative Methods 2008, 2009 Iowa State University

Agronomy 523x Molecular Plant Breeding 2009, 2010 Iowa State University

Agronomy 621 Advanced Plant Breeding 2009, 2011, 2013 Iowa State University

Short Courses:

Operations Research in Plant Breeding

2015 Iowa State University

2014

Techniques for identification of QTL:

1995 Cold Spring Harbor

1994 Cold Spring Harbor

1993 Cold Spring Harbor

1993 Iowa State University

1992 University of Minnesota

1991 Iowa State University

1991 Pioneer Hi-Bred soybean breeders

1990 Pioneer Hi-Bred corn breeders

1990 Pioneer Hi-Bred research directors

Techniques for generating linkage maps:

1994 Cold Spring Harbor

1993 Cold Spring Harbor

1991 Pioneer Hi-Bred soybean breeders

1990 Pioneer Hi-Bred corn breeders

1990 Pioneer Hi-Bred research directors

Introductory Statistics for Laboratory Experiments:

1993 Pioneer Hi-Bred, AMB labs

1993 Pioneer Hi-Bred, Disease Resistance and Insect Bioassay labs

1989 Pioneer Hi-Bred, Biotech Research Assoc

## Professional Service Activities:

- 2016-2017 Panelist for Syngenta crop challenge administered by the Institute for Operations Research and Management Sciences. Panelists review over 40 proposed solutions to complex agricultural system challenges using advanced analytics and ‘Big Data’ by interdisciplinary teams composed of applied mathematicians and domain experts.
- 2014-present Plant Breeding Director of Graduate Education
- 2014-present Coordinator Hatch project IOW04314
- 1990-present Referee 5-10 manuscripts per year for *Genetics*, *Theoretical and Applied Genetics*, *Crop Science*, *Trends in Genetics*, *Trends in Plant Science*, *PlosOne*, *Molecular Breeding*.
- 2014 North Central Soybean Research Program Review Panel. Increasing Soybean yields by 50 % by 2025.
- 2012 BioRenewables BEACON Blue Ribbon Panel
- 2008-2014 Coordinator Hatch project IOW0316
- 2005-2007 Science advisory board to NSF funded CREST (Centers for Research Excellence in Science & Technology) award to the New Mexico Center for Bioinformatics & Computational Biology
- 2004 Lead review of the USDA-ARS Soybean Genomics and Improvement Laboratory, Beltsville, Md.
- 2003-2013 *Board of Directors*, National Center for Genome Resources (NCGR), Santa Fe, NM
- 2003-2008 Science advisory board to NSF-PGI funded project on structural genomics and association genetics of maize evolution.
- 2003-2005 *Board of Directors*, New Mexico Technology Research Collaborative
- 2002-2005 Science Advisory Board to NSF-PGI funded project on functional genomics of root growth and root signaling under drought.
- 2002-2004 *Board of Directors*, New Mexico Biomedical and Biotechnology Association
- 2001-2004 Advisory Board to USDA-IFAFS funded project on Compositae Genomics Project.
- 2000-2002 Advisory Board to NSF-PGRI funded project on the Cotton Genome Project.
- 1999-2002 Advisory Board to NSF-PGRI funded project on soybean functional genomics.
- 1998 Panel Manager for the Plant Genome Panel of the National Research Initiative Competitive Grants Program, CSRS, USDA.
- 1997 Member of the Genome Panel for the National Research Initiative Competitive Grants Program, CSRS, USDA.
- 1997 Chair of the Gordon Research Conference on Quantitative Genetics and Biotechnology.
- 1996-2007 Associate Editor of *Genetical Research*, Cambridge.
- 1995-1996 Review panel for MILQTL program at the University of Liege, Belgium.
- 1994 Member of the Genome Panel for the National Research Initiative Competitive Grants Program, CSRS, USDA.
- 1992-1994 Member of the genetic nomenclature and database committees of the Maize Genome
- 1990-1995 Review competitive grant proposals submitted to PHI.
- 1993-1994 Chair of maize genetic mapping team at PHI.
- 1992-1994 Heterosis committee member at PHI.

## Honors and Awards:

- 2008 GFS Sprague Endowed Chair
- 2005-2007 Dream Catcher Science Program, Sandia National Laboratory
- 2002 Elected to the Board of Directors for the New Mexico Biomed Biotech Association
- 2001 Elected to the Board of Directors for the National Center for Genome Resources.
- 1998 Development of a *Useful Maize Map* by Pioneer Hi-Bred.
- 1991 Development of a *Comprehensive Research Information System* by Pioneer Hi-Bred
- 1993 Elected to Chair the Gordon Research Conference on Quantitative Genetics
- 1985 Iowa State University Research Excellence Award.
- 1983 Gamma Sigma Delta.
- 1980 Sigma XI.