

JESSE POLAND

Wheat Genetics Resource Center
Applied Wheat Genomics Innovation Lab
Kansas State University

4702 Throckmorton Plant Science Center
Kansas State University
Manhattan, KS 66506
phone: +1.785.532.2709
email: jpoland@ksu.edu

www.wheatgenetics.org

EDUCATION

- Ph.D. (2010) - Cornell University, Plant Breeding and Genetics
Thesis: Genetic Architecture of Quantitative Disease Resistance in Maize
- M.S. (2004) - Kansas State University, Plant Pathology
Thesis: Structure and Recombination of Complex Resistance Gene Loci in Maize
- B.S. (2003) - Kansas State University, Agronomy

APPOINTMENTS

Associate Professor, Department of Plant Pathology, Kansas State University, *2017 – present*
Director, Feed the Future Innovation Lab for Applied Wheat Genomics, *2013 - present*
Associate Director, Wheat Genetics Resource Center, Kansas State University, *2014 – present*
Affiliate Faculty, Dept. of Soil and Crop Science, Colorado State University, *2011 - present*

Previous:

Assistant Professor, Department of Plant Pathology, Kansas State University, *2014 – 2017*
Research Geneticist, USDA-ARS, Manhattan, KS, *2010 – 2014*
Adjunct Assistant Professor, Kansas State University, Manhattan, KS, *2010 - 2014*
Research Geneticist (Postdoctoral Scholar), USDA-ARS, Ithaca, NY, *2010*

RESEARCH

- Wheat genetics and germplasm improvement
- Genetic diversity and genomics of wheat and its wild-relatives
- Genomics of wheat and wild relatives, barley, *Thinopyrum intermedium*
- Genomic selection in wheat breeding
- Field-based high-throughput phenotyping
- phenoApps and bioinformatics

TEACHING

Courses: Advanced Plant Genetics – PLPTH 915 (Fall 2015, Fall 2017)
Plant Genetics - AGRON 770 (Fall 2014)

KSU Graduate Faculty in Plant Pathology, Agronomy and Genetics

Advisor, KSU Plant Breeding and Genetics Graduate Student Club, *Sept, 2012 – present*

Major Advisor: 12 Ph.D. students (5 current) in Genetics at Kansas State University and with highly recognized and awarded students including Monsanto Beachell-Borlaug International Scholars (3); Fulbright International Scholars (2)

Graduate Committee Member for 17 students: 11 Ph.D. and three M.S. student at Kansas State University; two Ph.D. students at Colorado State University; Ph.D. student at Univ. of Chicago, Ph.D. student at Universidad de la Republica, Uruguay

Mentor: 13 Post-Doctoral Research Fellows (9 current); awarded USDA-NIFA Postdoctoral Fellows (2)

EDUCATION EXPERIENCE

Graduate Research Assistant, Dept. of Plant Breeding & Genetics, Cornell University, *2005-2009*
Advisor: Dr. Rebecca Nelson, Department of Plant Breeding & Genetics
Mapping and genetic dissection of quantitative trait loci conditioning resistance to northern leaf blight in maize

Graduate Research Assistant, Dept. of Plant Pathology, Kansas State University, *2003-2004*
Advisor: Dr. Scot Hulbert, Department of Plant Pathology, KSU
Molecular genetics studies of complex host plant resistance gene loci

Undergraduate Research Assistant, Wheat Genomics, USDA-ARS, Manhattan, KS *2000-2002*
Advisor: Dr. Gina Brown-Guedira, Department of Agronomy, KSU
Wheat germplasm improvement and genetic mapping of leaf rust resistance

Family Farming Operation, Poland Farms, Junction City, KS
Crop production: Wheat, Corn, Soybeans, Sorghum, Sunflowers, and Alfalfa

HONORS, AWARDS & MEMBERSHIP

National Association of Plant Breeders (NAPB) Early Career Scientist Award, *Sept 2016*

Crop Science Society of America, *Member*

Munger/Murphy Award, Dept. of Plant Breeding & Genetics, Cornell University, *Sept 2009*

Barbara McClintock Graduate Student Award, College of Agriculture and Life Sciences, Cornell University, *May 2008*

National Council of Commercial Plant Breeders Graduate Student Award, *Dec. 2007*

EDITORIAL

Associate Editor – The Plant Genome, *June 2015 - present*

Associate Editor – Crop Science, *Jan 2013 – present*

Reviewer: Crop Science; Agronomy Journal; BMC Genomics; BMC Genetics; Crop Science; Genetics; G3:Gene,Genomics,Genetics; Genetics Research; Heredity; Molecular Breeding; Molecular Biology and Evolution; Nature; Nature Genetics; Phytopathology; PLoS ONE; The Plant Genome; Theoretical Applied Genetics

Grant Reviewer: NSF Plant Genome Research Program (panel); Icelandic Research Fund; U.S.-Egypt Joint Science and Technology Program; AgreenSkills Fellowship, NSF Plant Genome Research Program

PUBLICATIONS

103 publications with over 9450 total citations including 15 publications with over 100 citations

h-index: 33

i10-index: 63

- Singh, N., S. Wu, J. Raupp, S. Sehgal, S. Arora, V. Tiwari, P. Vikram, S. Singh, P. Chhuneja and B. Gill (2018) Efficient curation of genebanks using next-generation sequencing reveals substantial duplication of germplasm accessions. *bioRxiv*: 410779.
- Wang, X., Singh, D., Marla, S., Morris, G., & Poland, J. (2018). Field-based high-throughput phenotyping of plant height in sorghum using different sensing technologies. *Plant Methods*, 14(1), 53. <https://doi.org/10.1186/s13007-018-0324-5>
- International Wheat Genome Sequencing Consortium (2018) Shifting the limits in wheat research and breeding using a fully annotated reference genome. *Science*. 2018;361(6403).
- Belamkar, V., Guttieri, M. J., Hussain, W., Jarquín, D., El-Basyoni, I., Poland, J., Lorenz, A. J., & Baenziger, P. S. (2018). Genomic Selection in Preliminary Yield Trials in a Winter Wheat Breeding Program. *G3 (Bethesda, Md.)*, g3.200415.2018. <https://doi.org/10.1534/g3.118.200415>
- Shao, M., Bai, G., Rife, T. W., Poland, J., Lin, M., Liu, S., Chen, H., Kumssa, T., Fritz, A., Trick, H., Li, Y., & Zhang, G. (2018). QTL mapping of pre-harvest sprouting resistance in a white wheat cultivar Danby. *Theoretical and Applied Genetics*, 1–15. <https://doi.org/10.1007/s00122-018-3107-5>
- Hussain, W., Guttieri, M. J., Belamkar, V., Poland, J., Sallam, A., & Baenziger, P. S. (2018). Registration of a Bread Wheat Recombinant Inbred Line Mapping Population Derived from a Cross Between ‘Harry’ and ‘Wesley.’ *Journal of Plant Registrations*, 0(0), 0. <https://doi.org/10.3198/jpr2017.11.0085crmp>
- DeHaan, L., Christians, M., Crain, J., & Poland, J. (2018). Development and Evolution of an Intermediate Wheatgrass Domestication Program. *Sustainability*, 10(5), 1499. <https://doi.org/10.3390/su10051499>
- Brunazzi, A., Scaglione, D., Talini, R. F., Miculan, M., Magni, F., Poland, J., Enrico Pè, M., Brandolini, A., & Dell’Acqua, M. (2018). Molecular diversity and landscape genomics of the crop wild relative *Triticum urartu* across the Fertile Crescent. *The Plant Journal*, 94(4), 670–684. <https://doi.org/10.1111/tpj.13888>
- Elbasyoni, I. S., A. J. Lorenz, M. Guttieri, K. Frels, P. S. Baenziger, J. Poland and E. Akhunov (2018) A comparison between genotyping-by-sequencing and array-based scoring of snps for genomic prediction accuracy in winter wheat. *Plant Science* 270: 123-130. DOI: <https://doi.org/10.1016/j.plantsci.2018.02.019>
- Mourad, A. M. I., Sallam, A., Belamkar, V., Wegulo, S., Bowden, R., Jin, Y., Mahdy, E., Bakheit, B., El-Wafaa, A. A., Poland, J., & Baenziger, P. S. (2018). Genome-Wide Association Study for Identification and Validation of Novel SNP Markers for Sr6 Stem Rust Resistance Gene in Bread Wheat. *Frontiers in Plant Science*, 9, 380. <https://doi.org/10.3389/fpls.2018.00380>
- Eltaher, S., Sallam, A., Belamkar, V., Emara, H. A., Nower, A. A., Salem, K. F. M., Poland, J., & Baenziger, P. S. (2018). Genetic Diversity and Population Structure of F3:6 Nebraska Winter Wheat

Genotypes Using Genotyping-By-Sequencing. *Frontiers in Genetics*, 9, 76.
<https://doi.org/10.3389/fgene.2018.00076>

- Crain, J., S. Mondal, J. Rutkoski, R. P. Singh and J. Poland (2018) Combining high-throughput phenotyping and genomic information to increase prediction and selection accuracy in wheat breeding. *The Plant Genome* 11(1). DOI: 10.3835/plantgenome2017.05.0043
- Danilova, T. V., Friebe, B., Gill, B. S., Poland, J., & Jackson, E. (2018). Development of a complete set of wheat–barley group-7 Robertsonian translocation chromosomes conferring an increased content of β -glucan. *Theoretical and Applied Genetics*, 131(2), 377–388. <https://doi.org/10.1007/s00122-017-3008-z>
- Krause, M. R., L. G. Pérez, J. Crossa, P. Pérez-Rodríguez, O. A. Montesinos-López, R. Singh, S. Dreisigacker, J. Poland, J. Rutkoski and M. E. Sorrells (2018) Use of hyperspectral reflectance-derived relationship matrices for genomic prediction of grain yield in wheat. bioRxiv: 389825.
- Juliana, P., Singh, R. P., Singh, P. K., Poland, J. A., Bergstrom, G. C., Huerta-espino, J., Bhavani, S., Crossa, J., & Sorrells, M. E. (2018). Genome-wide association mapping for resistance to leaf rust, stripe rust and tan spot in wheat reveals potential candidate genes. *Theoretical and Applied Genetics*, 131, 1405–1422. <https://doi.org/10.1007/s00122-018-3086-6>
- Danilova, T. V., Friebe, B., Gill, B. S., Poland, J., & Jackson, E. (2018). Chromosome Rearrangements Caused by Double Monosomy in Wheat-Barley Group-7 Substitution Lines. *Cytogenetic and Genome Research*, (0). <https://doi.org/10.1159/000487183>
- Wiersma, A. T., Whetten, R. B., Zhang, G., Sehgal, S. K., Kolb, F. L., Poland, J. A., Mason, R. E., Carter, A. H., Cowger, C., & Olson, E. L. (2018). Registration of Two Wheat Germplasm Lines Fixed for. *Journal of Plant Registrations*, 12(2), 270. <https://doi.org/10.3198/jpr2017.06.0036crg>
- Arora, S., Steuernagel, B., Chandramohan, S., Long, Y., Matny, O., Johnson, R., Enk, J., Periyannan, S., Hatta, M. A. M., Athiyannan, N., Cheema, J., Yu, G., Kangara, N., Ghosh, S., Szabo, L. J., Poland, J., Bariana, H., Jones, J. D. G., Bentley, A. R., Ayliffe, M., Olson, E., Xu, S. S., Steffenson, B. J., Lagudah, E., & Wulff, B. B. H. (2018). Resistance gene discovery and cloning by sequence capture and association genetics. *BioRxiv*, 248146. <https://doi.org/10.1101/248146>
- Neilsen, M., C. Courtney, S. Amaravadi, Z. Xiong, J. Poland and T. Rife (2017) A dynamic, real-time algorithm for seed counting. *26th International Conference on Software Engineering and Data Engineering*
- Mideros, S. X., C.-L. Chung, T. Wiesner-Hanks, J. Poland, D. Wu, A. A. Fialko, G. Turgeon and R. Nelson (2017) Determinants of virulence and in-vitro development colocalize on a genetic map of *Setosphaeria turcica*. *Phytopathology*. DOI: 10.1094/PHTO-01-17-0021-R
- Hussain, W., P. S. Baenziger, V. Belamkar, M. J. Guttieri, J. P. Venegas, A. Easterly, A. Sallam and J. Poland (2017) Genotyping-by-sequencing derived high-density linkage map and its application to qtl mapping of flag leaf traits in bread wheat. *Scientific Reports* 7(1): 16394. DOI: 10.1038/s41598-017-16006-z
- Zhang, X., S. R. Larson, L. Gao, S. L. Teh, L. R. DeHaan, M. Fraser, A. Sallam, T. Kantarski, K. Frels, J. Poland, D. Wyse and J. A. Anderson (2017) Uncovering the genetic architecture of seed weight and size in intermediate wheatgrass through linkage and association mapping. *The Plant Genome*. DOI: 10.3835/plantgenome2017.03.0022

- Lado, B., S. Battenfield, C. Guzmán, M. Quincke, R. P. Singh, S. Dreisigacker, R. J. Peña, A. Fritz, P. Silva, J. Poland and L. Gutiérrez (2017) Strategies for selecting crosses using genomic prediction in two wheat breeding programs. *The Plant Genome* 10(2). DOI: 10.3835/plantgenome2016.12.0128
- Haghighattalab, A., J. Crain, S. Mondal, J. Rutkoski, R. P. Singh and J. Poland (2017) Application of geographically weighted regression to improve grain yield prediction from unmanned aerial system imagery. *Crop Science*. DOI: 10.2135/cropsci2016.12.1016
- Jarquín, D., C. Lemes da Silva, R. C. Gaynor, J. Poland, A. Fritz, R. Howard, S. Battenfield and J. Crossa (2017) Increasing genomic-enabled prediction accuracy by modeling genotype × environment interactions in Kansas wheat. *The Plant Genome* 10(2). DOI: 10.3835/plantgenome2016.12.0130
- Sun, J., J. E. Rutkoski, J. A. Poland, J. Crossa, J.-L. Jannink and M. E. Sorrells (2017) Multitrait, random regression, or simple repeatability model in high-throughput phenotyping data improve genomic prediction for wheat grain yield. *The Plant Genome* 10(2). DOI: 10.3835/plantgenome2016.11.0111
- Arora, S., N. Singh, S. Kaur, N. S. Bains, C. Uauy, J. Poland and P. Chhuneja (2017) Genome-wide association study of grain architecture in wild wheat *Aegilops tauschii*. *Frontiers in Plant Science* 8: 886. DOI: 10.3389/fpls.2017.00886
- Mascher, M., H. Gundlach, A. Himmelbach, S. Beier, S. O. Twardziok, T. Wicker, V. Radchuk, C. Dockter, P. E. Hedley, J. Russell, M. Bayer, L. Ramsay, H. Liu, G. Haberer, X.-Q. Zhang, Q. Zhang, R. A. Barrero, L. Li, S. Taudien, M. Groth, M. Felder, A. Hastie, H. Šimková, H. Staňková, J. Vrána, S. Chan, M. Muñoz-Amatriaín, R. Ounit, S. Wanamaker, D. Bolser, C. Colmsee, T. Schmutzer, L. Aliyeva-Schnorr, S. Grasso, J. Tanskanen, A. Chailyan, D. Sampath, D. Heavens, L. Clissold, S. Cao, B. Chapman, F. Dai, Y. Han, H. Li, X. Li, C. Lin, J. K. McCooke, C. Tan, P. Wang, S. Wang, S. Yin, G. Zhou, J. A. Poland, M. I. Bellgard, L. Borisjuk, A. Houben, J. Doležel, S. Ayling, S. Lonardi, P. Kersey, P. Langridge, G. J. Muehlbauer, M. D. Clark, M. Caccamo, A. H. Schulman, K. F. X. Mayer, M. Platzer, T. J. Close, U. Scholz, M. Hansson, G. Zhang, I. Braumann, M. Spannagl, C. Li, R. Waugh and N. Stein (2017) A chromosome conformation capture ordered sequence of the barley genome. *Nature* 544(7651): 427-433.
- Pérez-Rodríguez, P., J. Crossa, J. Rutkoski, J. Poland, R. Singh, A. Legarra, E. Autrique, G. d. I. Campos, J. Burgueño and S. Dreisigacker (2017) Single-step genomic and pedigree genotype × environment interaction models for predicting wheat lines in international environments. *The Plant Genome*. DOI: doi:10.3835/plantgenome2016.09.0089
- Moore, J., H. Manmathan, V. Anderson, J. Poland, C. Morris and S. Haley (2017) Improving genomic prediction for pre-harvest sprouting tolerance in wheat by weighting large-effect quantitative trait loci. *Crop Science*. 10.2135/cropsci2016.06.0453
- Juliana, P., R. Singh, P. Singh, J. Crossa, J. Rutkoski, J. Poland, G. Bergstrom and M. Sorrells (2017) Comparison of models and whole-genome profiling approaches for genomic-enabled prediction of *Septoria tritici* blotch, *Stagonospora Nodorum* Blotch, and Tan Spot resistance in wheat. *The Plant Genome*. DOI: 10.3835/plantgenome2016.08.0082
- Tanger, P., S. Klassen, J. Mojica, J. Lovell, B. Moyers, M. Baraoidan, M. E. B. Naredo, K. McNally, J. Poland, D. Bush, H. Leung, J. Leach and J. McKay (2017) Field-based high throughput phenotyping rapidly identifies genomic regions controlling yield components in rice. *Scientific Reports* 7: 42839.
- Dunckel, S., J. Crossa, S. Wu, D. Bonnett and J. Poland (2017) Genomic selection for increased yield in synthetic-derived wheat. *Crop Science* 57(2): 713-725.
- Rutkoski, J. E., J. Crain, J. Poland and M. E. Sorrells (2017). Genomic selection for small grain improvement. In *Genomic selection for crop improvement: New molecular breeding strategies for*

- crop improvement*. R. K. Varshney, M. Rorkiwal and M. E. Sorrells. Cham, Springer International Publishing: 99-130.
- Beier, S., A. Himmelbach, C. Colmsee, X.-Q. Zhang, R. A. Barrero, Q. Zhang, L. Li, M. Bayer, D. Bolser, S. Taudien, M. Groth, M. Felder, A. Hastie, H. Šimková, H. Staňková, J. Vrána, S. Chan, M. Muñoz-Amatriain, R. Ounit, S. Wanamaker, T. Schmutzer, L. Aliyeva-Schnorr, S. Grasso, J. Tanskanen, D. Sampath, D. Heavens, S. Cao, B. Chapman, F. Dai, Y. Han, H. Li, X. Li, C. Lin, J. K. McCooke, C. Tan, S. Wang, S. Yin, G. Zhou, J. A. Poland, M. I. Bellgard, A. Houben, J. Doležel, S. Ayling, S. Lonardi, P. Langridge, G. J. Muehlbauer, P. Kersey, M. D. Clark, M. Caccamo, A. H. Schulman, M. Platzer, T. J. Close, M. Hansson, G. Zhang, I. Braumann, C. Li, R. Waugh, U. Scholz, N. Stein and M. Mascher (2017) Construction of a map-based reference genome sequence for barley, *hordeum vulgare* L. *Scientific Data* 4: 170044. DOI: 10.1038/sdata.2017.44
- Juliana, P., R. P. Singh, P. K. Singh, J. Crossa, J. Huerta-Espino, C. Lan, S. Bhavani, J. E. Rutkoski, J. A. Poland, G. C. Bergstrom and M. E. Sorrells (2017) Genomic and pedigree-based prediction for leaf, stem, and stripe rust resistance in wheat. *Theoretical and Applied Genetics*: 1-16. DOI: 10.1007/s00122-017-2897-1
- Crain, J., M. Reynolds and J. Poland (2017) Utilizing high-throughput phenotypic data for improved phenotypic selection of stress-adaptive traits in wheat. *Crop Science*. DOI: 10.2135/cropsci2016.02.0135
- Kantarski, T., S. Larson, X. Zhang, L. DeHaan, J. Borevitz, J. Anderson and J. Poland (2017) Development of the first consensus genetic map of intermediate wheatgrass (*Thinopyrum intermedium*) using genotyping-by-sequencing. *Theoretical and Applied Genetics* 130(1): 137-150. DOI: 10.1007/s00122-016-2799-7
- Edae, E., P. Olivera, Y. Jin, J. Poland and M. Rouse (2016) Genotype-by-sequencing facilitates genetic mapping of a stem rust resistance locus in *Aegilops umbellulata*, a wild relative of cultivated wheat. *BMC Genomics* 17(1):1039. DOI: 10.1186/s12864-016-3370-2
- Wiersma, A., L. Brown, E. Brisco, T. Liu, K. Childs, J. Poland, S. Sehgal and E. Olson (2016) Fine mapping of the stem rust resistance gene SrTA10187. *Theoretical and Applied Genetics*, 1–10. DOI: 10.1007/s00122-016-2776-1
- Wang, X., K. Thorp, J. White, A. French and J. Poland (2016) Approaches for geospatial processing of field-based high-throughput plant phenomics data from ground vehicle platforms. *Transactions of the ASABE*, 59(5), 1053–1067. DOI: 10.13031/trans.59.11502
- Guzman, C., Peña, R. J., Singh, R., Autrique, E., Dreisigacker, S., Crossa, J., Rutkoski, J., Poland, J., and S. Battenfield (2016) Wheat quality improvement at CIMMYT and the use of genomic selection on it. *Applied & Translational Genomics*. DOI: 10.1016/j.atg.2016.10.004
- Pauli, D., S. Chapman, R. Bart, C. Topp, C. Lawrence-Dill, J. Poland and M. Gore (2016) The quest for understanding phenotypic variation via integrated approaches in the field environment. *Plant Physiology*. DOI: 10.1104/pp.16.00592
- Cohnstaedt, L. W. and J. Poland (2016) Review Articles: The black-market of scientific currency. *Annals of the Entomological Society of America*: saw061. DOI: 10.1093/aesa/saw061
- Rutkoski, J., J. Poland, S. Mondal, E. Autrique, L. G. Pérez, J. Crossa, M. Reynolds and R. Singh (2016) Canopy temperature and vegetation indices from high-throughput phenotyping improve accuracy of pedigree and genomic selection for grain yield in wheat. *G3: Genes | Genomes | Genetics*. DOI: 10.1534/g3.116.032888
- Poland, J. and J. Rutkoski (2016) Advances and challenges in genomic selection for disease resistance. *Annual Review of Phytopathology* 54(1): DOI: doi:10.1146/annurev-phyto-080615-100056

- Kono, T., S. Kiran, J. Poland and P. Morrell (2016) Barley genotyping SNPs annotated using SNPMeta. *Data Repository for U of M*. DOI: 10.13020/D63K53
- Chaffin, A. S., Y.-F. Huang, S. Smith, W. A. Bekele, E. Babiker, B. N. Gnanesh, B. J. Foresman, S. G. Blanchard, J. J. Jay, R. W. Reid, C. P. Wight, S. Chao, R. E. Oliver, E. Islamovic, F. L. Kolb, C. McCartney, J. W. Mitchell Fetch, A. D. Beattie, Å. Bjørnstad, J. M. Bonman, T. Langdon, C. J. Howarth, C. R. Brouwer, E. N. Jellen, K. E. Klos, J. A. Poland, T.-F. Hsieh, R. Brown, E. W. Jackson, J. A. Schlueter and N. A. Tinker (2016) A consensus map in cultivated hexaploid oat reveals conserved grass synteny with substantial subgenome rearrangement. *The Plant Genome*. DOI: doi:10.3835/plantgenome2015.10.0102
- Battenfield, S. D., C. Guzmán, R. C. Gaynor, R. P. Singh, R. J. Peña, S. Dreisigacker, A.K. Fritz and J. Poland (2016). Genomic selection for processing and end-use quality traits in the CIMMYT spring bread wheat breeding program. *The Plant Genome*. DOI: 10.3835/plantgenome2016.01.0005
- Haghighattalab, A., L. González Pérez, S. Mondal, D. Singh, D. Schinstock, J. Rutkoski, I. Ortiz-Monasterio, R. P. Singh, D. Goodin and J. Poland (2016) Application of unmanned aerial systems for high throughput phenotyping of large wheat breeding nurseries. *Plant Methods* 12(1): 1-15. DOI: 10.1186/s13007-016-0134-6
- Baenziger, P., R. Graybosch, T. Regassa, R. Klein, G. Kruger, D. Santra, L. Xu, D. Rose, S. Wegulo, Y. Jin, J. Kolmer, G. Hein, M.-S. Chen, G. Bai, R. Bowden and J. Poland (2016) Registration of 'NE05548' (Husker Genetics Brand Panhandle) Hard Red Winter Wheat. *Journal of Plant Registrations*. DOI: doi:10.3198/jpr2016.01.0006crc
- Xiao, X., H. W. Ohm, G. J. Hunt, J. A. Poland, L. Kong, J. A. Nemacheck and C. E. Williams (2016) Genotyping-by-sequencing to remap QTL for Type II Fusarium head blight and leaf rust resistance in a wheat–tall wheatgrass introgression recombinant inbred population. *Molecular Breeding* 36(4): 1-11.
- McCallum, S., J. Graham, L. Jorgensen, L. J. Rowland, N. V. Bassil, J. F. Hancock, E. J. Wheeler, K. Vining, J. A. Poland, J. W. Olmstead, E. Buck, C. Wiedow, E. Jackson, A. Brown and C. A. Hackett (2016) Construction of a SNP and SSR linkage map in autotetraploid blueberry using genotyping by sequencing. *Molecular Breeding* 36(4): 1-24. DOI: 10.1007/s11032-016-0443-5
- Barker, J., N. Zhang, J. Sharon, R. Steeves, X. Wang, Y. Wei and J. Poland (2016) Development of a field-based high-throughput mobile phenotyping platform. *Computers and Electronics in Agriculture* 122: 74-85.
- Tiwari, V. K., A. Heesacker, O. Riera-Lizarazu, H. Gunn, S. Wang, Y. Wang, Y. Q. Gu, E. Paux, D.-H. Koo, A. Kumar, M.-C. Luo, G. Lazo, R. Zemetra, E. Akhunov, B. Friebe, J. Poland, B.S. Gill, S. Kianian and J. Leonard (2016) A whole-genome, radiation hybrid mapping resource of hexaploid wheat. *The Plant Journal* 86(2): 195-207. DOI: 10.1111/tpj.13153
- Zhang, X., A. Sallam, L. Gao, T. Kantarski, J. Poland, L. DeHaan, D. Wyse and J. Anderson (2016) Establishment and optimization of genomic selection to accelerate the domestication and improvement of Intermediate Wheatgrass. *The Plant Genome* 9(1). DOI: 10.3835/plantgenome2015.07.0059
- Sun, J., H. Ohm, J. Poland and C. Williams (2016) Mapping four quantitative trait loci associated with Type I Fusarium Head Blight resistance in winter wheat 'INW0412'. *Crop Science* 56(3): 1163-1172. DOI: 10.2135/cropsci2015.06.0390
- Crain, J., Y. Wei, J. Barker, S. Thompson, P. Alderman, M. Reynolds, N. Zhang and J. Poland (2016) Development and deployment of a portable field phenotyping platform. *Crop Science* 56(3): 965-975. DOI: 10.2135/cropsci2015.05.0290

- DeHaan, L., D. Van Tassel, J. Anderson, S. Asselin, R. Barnes, G. Baute, D. Cattani, S. Culman, K. Dorn, B. Hulke, M. Kantar, S. Larson, M. Marks, A. Miller, J. Poland, D. Ravetta, E. Rude, M. Ryan, D. Wyse and X. Zhang (2016) A pipeline strategy for grain crop domestication. *Crop Science* 56(3): 917-930. DOI: 10.2135/cropsci2015.06.0356
- Tack, J., A. Barkley, T. Rife, J. Poland and L.L. Nalley (2016) Quantifying variety-specific heat resistance and the potential for adaptation to climate change. *Global Change Biology* 22(8): 2904-2912. DOI: 10.1111/gcb.13163
- Edae, E., R. Bowden, and J. Poland (2015) Application of population sequencing (PopSeq) for ordering and imputing genotyping-by-sequencing markers in hexaploid wheat. *G3: Genes/Genomics/Genetics* 5(12): 2547-2553.
- Zhang, X., A. Sallam, L. Gao, T. Kantarski, J. Poland, L. DeHaan, D. Wyse, J. Anderson (2015) Establishment and optimization of genomic selection to accelerate the domestication and improvement of intermediate wheatgrass (*Thinopyrum intermedium*) using recurrent selection. *The Plant Genome* DOI: 10.3835/plantgenome2015.07.0059
- Tiwari, V., Wang, T. Danilova, D-H. Koo, J. Vrána, M. Kubaláková, E. Hribova, N. Rawat, B. Kalia, N. Singh, B. Friebe, J. Dolezel, E. Akhunov, J. Poland, J. Sabir, B.S. Gill (2015) Exploring the tertiary gene pool of bread wheat: Sequence assembly and analysis of chromosome 5Mg of *Aegilops geniculata*. *The Plant Journal* DOI: 10.1111/tpj.13036
- Dunckel, S., M. Rouse, R Bowden, and J. Poland (2015) Genetic mapping of race-specific stem rust resistance in the synthetic hexaploid W7984 x Opata M85 mapping population. *Crop Sci.* 55:1-9. DOI: 10.2135/cropsci2014.11.0755
- Talukder, S., P. V. Vara Prasad, T. Todd, M. Babar, J. Poland, R. Bowden and A. Fritz (2015) Effect of cytoplasmic diversity on post anthesis heat tolerance in wheat. *Euphytica* 204(2): 383-394. DOI: 10.1007/s10681-014-1350-7
- Juliana, P., J. Rutkoski, J. Poland, R.P. Singh, S. Murugasamy, S. Natesan, H. Barbier and M. Sorrells (2015) Genome-wide association mapping for leaf tip necrosis and pseudo-black chaff in relation to durable rust resistance in wheat. *The Plant Genome* DOI: 10.3835/plantgenome2015.01.0002
- Poland, J. (2015) Breeding assisted genomics. *Current Opinion in Plant Biology*: 24,119-124
- Hulse-Kemp, A. M., J. Lemm, J. Plieske, H. Ashrafi, R. Buyyarapu, D. D. Fang, J. Frelichowski, M. Giband, S. Hague, L. L. Hinze, K. J. Kochan, P. K. Riggs, J. A. Scheffler, J. A. Udall, M. Ulloa, S. S. Wang, Q.-H. Zhu, S. K. Bag, A. Bhardwaj, J. J. Burke, R. L. Byers, M. Claverie, M. A. Gore, D. B. Harker, M. S. Islam, J. N. Jenkins, D. C. Jones, J.-M. Lacape, D. J. Llewellyn, R. G. Percy, A. E. Pepper, J. A. Poland, K. Mohan Rai, S. V. Sawant, S. Kumar Singh, A. Spriggs, J. M. Taylor, F. Wang, S. M. Yourstone, X. Zheng, C. T. Lawley, M. W. Ganal, A. Van Deynze, I. W. Wilson and D. M. Stelly (2015) Development of a 63K SNP array for cotton and high-density mapping of intra- and inter-specific populations of *Gossypium* spp. *G3: Genes/Genomes/Genetics*. DOI: 10.1534/g3.115.018416
- Rife, T., S. Wu, R. Bowden and J. Poland (2015) Spiked GBS: a unified, open platform for single marker genotyping and whole-genome profiling. *BMC Genomics* 16(1): 248
- Rutkoski, J., R. P. Singh, J. Huerta-Espino, S. Bhavani, J. Poland, J. L. Jannink and M. E. Sorrells (2015). Genetic gain from phenotypic and genomic selection for quantitative resistance to stem rust of wheat. *The Plant Genome* 8(2). DOI: 10.3835/plantgenome2014.10.0074
- Benson, J. M., J. A. Poland, B. M. Benson, E. L. Stromberg and R. J. Nelson (2015). Resistance to gray leaf spot of maize: Genetic architecture and mechanisms elucidated through nested association mapping and near-isogenic line analysis. *PLoS Genet* 11(3): e1005045. DOI: 10.1371/journal.pgen.1005045

- Rutkoski, J., R. P. Singh, J. Huerta-Espino, S. Bhavani, J. Poland, J. L. Jannink and M. E. Sorrells (2015). Efficient use of historical data for genomic selection: A case study of stem rust resistance in wheat. *The Plant Genome* 8(1). DOI: 10.3835/plantgenome2014.09.0046
- Li, G., Y. Wang, M.-S. Chen, E. Edae, J. Poland, E. Akhunov, S. Chao, G. Bai, B. F. Carver and L. Yan (2015) Precisely mapping a major gene conferring resistance to Hessian Fly in bread wheat using genotyping-by-sequencing. *BMC Genomics* 16(1): 108.
- Lopez-Cruz, M., J. Crossa, D. Bonnett, S. Dreisigacker, J. Poland, J.-L. Jannink, R. P. Singh, E. Auriague and G. de los Campos (2015) Increased prediction accuracy in wheat breeding trials using a marker \times environment interaction genomic selection model. *G3: Genes/Genomes/Genetics*.
- Mora, F., D. Castillo, B. Lado, I. Matus, J. Poland, F.J. Belzile, J. von Zitzewitz and A. del Pozo (2015) Genome-wide association mapping of agronomic traits and carbon isotope discrimination in a worldwide germplasm collection of spring wheat using SNP markers. *Molecular Breeding* 35, 1-12
- Chapman, J., M. Mascher, A. Buluc, K. Barry, E. Georganas, A. Session, V. Strnadova, J. Jenkins, S. Sehgal, L. Olikier, J. Schmutz, K. Yelick, U. Scholz, R. Waugh, J. Poland, G. Muehlbauer, N. Stein and D. Rokhsar (2015). A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. *Genome Biology* 16(1): 26
- Isidro, J., J.-L. Jannink, D. Akdemir, J. Poland, N. Heslot and M. E. Sorrells (2015) Training set optimization under population structure in genomic selection. *Theoretical and Applied Genetics* 128(1): 145-158.
- Kumssa, T.T., P.S. Baenziger, M.N. Rouse, M. Guttieri, I. Dweikat, G. Brown-Guedira, S. Williamson, R.A. Graybosch, S.N. Wegulo, A.J. Lorenz, and J. Poland (2015) Characterization of stem rust resistance in wheat cultivar gage. *Crop Science* 55, 229-239 DOI: 10.2135/cropsci2014.05.0348
- Talukder, S. K., M. A. Babar, K. Vijayalakshmi, J. Poland, P. V. Prasad, R. Bowden and A. Fritz (2014) Mapping QTL for the traits associated with heat tolerance in wheat (*Triticum aestivum* L.). *BMC Genetics* 15(1): 97.
- Tinker, N. A., S. Chao, G. R. Lazo, R. E. Oliver, Y.-F. Huang, J. A. Poland, E. N. Jellen, P. J. Maughan, A. Kilian and E. W. Jackson (2014) A SNP genotyping array for hexaploid oat. *The Plant Genome* 7(3).
- Jamann, T., J. Poland, J.M. Kolkman, L.G. Smith, R.J. Nelson (2014) Unraveling genomic complexity at a quantitative disease resistance locus in maize. *Genetics* DOI: 10.1534/genetics.114.167486
- Huang, Y.-F., J. A. Poland, C. P. Wight, E. W. Jackson and N. A. Tinker (2014) Using genotyping-by-sequencing (GBS) for genomic discovery in cultivated oat. *PLoS ONE* 9(7): e102448.
- The International Wheat Genome Sequencing Consortium (2014) Ancient hybridizations among the ancestral genomes of bread wheat. *Science* 345:6194 DOI: 10.1126/science.1250092
- The International Wheat Genome Sequencing Consortium (2014) A chromosome-based draft sequence of the hexaploid bread wheat (*Triticum aestivum*) genome. *Science* 345:6194 DOI: 10.1126/science.1250092
- Baenziger, P.S., R.A. Graybosch, T. Regassa, R.N. Klein, G.R. Kruger, D.K. Santra, L. Xu, D.J. Rose, S.N. Wegulo, Y. Jin, J. Kolmer, G.L. Hein, M.-S. Chen, G. Bai, R.L. Bowden, J. Poland (2014) Registration of 'NE06545' (Husker Genetics brand 'Freeman') hard red winter wheat. *Journal of Plant Registrations* doi:10.3198/jpr2014.02.0009crc
- Rife, T., J. Poland (2014) Field Book: An open-source application for field data collection on Android. *Crop Science* DOI: 10.2135/cropsci2013.08.0579
- Gore, M., D. Fang, J. Poland, J. Zhang, R. Percy, R. Cantrell, G. Thyssen, A. Lipka (2014) Linkage map construction and quantitative trait locus analysis of agronomic and fiber quality traits in cotton. *The Plant Genome* 7:1 DOI:10.3835/plantgenome2013.07.0023

- Liu, H., M. Bayer, A. Druka, J.R. Russell, C.A. Hackett, J. Poland, L. Ramsay, P.E. Hedley, and R. Waugh (2014) An evaluation of genotyping by sequencing (GBS) to map the Breviaristatum-e (ari-e) locus in cultivated barley. *BMC Genomics* 15:104 DOI:10.1186/1471-2164-15-104
- Kono, T. J. Y., K. Seth, J. A. Poland and P. L. Morrell (2014). SNPMeta: SNP annotation and SNP metadata collection without a reference genome. *Molecular Ecology Resources* 14(2): 419-425.
- Mascher, M., S. Wu, P. St Amand, N. Stein, and J. Poland (2013) Application of genotyping-by-sequencing on semiconductor sequencing platforms: A comparison of genetic and reference-based marker ordering in barley. *PLoS ONE* 8(10): e76925. doi:10.1371/journal.pone.0076925
- Lado, B., I. Matus, A. Rodriguez, L. Inostroza, J. Poland, F. Belzile, A. del Pozo, M. Quincke, and J. von Zitzewitz (2013) Increased genomic prediction accuracy through spatial adjustment of field trial data. *G3* 3:12, 2105-2114 DOI: 10.1534/g3.113.007807
- Mascher, M., G. J. Muehlbauer, D. S. Rokhsar, J. Chapman, J. Schmutz, K. Barry, M. Muñoz-Amatriáin, T. J. Close, R. P. Wise, A. H. Schulman, A. Himmelbach, K. F. X. Mayer, U. Scholz, J. A. Poland, N. Stein and R. Waugh (2013) Anchoring and ordering NGS contig assemblies by population sequencing (POPSEQ). *The Plant Journal* DOI: 10.1111/tpj.12319
- Dawson, J. C., J. B. Endelman, N. Heslot, J. Crossa, J. Poland, S. Dreisigacker, Y. Manès, M. E. Sorrells and J.-L. Jannink (2013) The use of unbalanced historical data for genomic selection in an international wheat breeding program. *Field Crops Research* dx.doi.org/10.1016/j.fcr.2013.07.020
- Heslot, N., J. Rutkoski, J. Poland, J.-L. Jannink and M. E. Sorrells (2013) Impact of marker ascertainment bias on genomic selection accuracy and estimates of genetic diversity. *PLoS ONE* 8(9): e74612.
- Rutkoski, J.E., J. Poland, J.-L. Jannink and M. E. Sorrells (2013) Imputation of unordered markers and the impact on genomic selection accuracy. *G3: Genes Genomes Genetics* 3(3): 427-439.
- Olson, E., M. Rouse, M. Pumphrey, R. Bowden, B.S. Gill, J. Poland. (2013) Introgression of stem rust resistance genes SrTA10187 and SrTA10171 from *Aegilops tauschii* to wheat, *Theor. Appl. Genetics*, DOI 10.1007/s00122-013-2148-z
- Olson, E., M. Rouse, R. Bowden, M. Pumphrey, B.S. Gill, J. Poland. (2013) Simultaneous transfer, introgression, and genomic localization of genes for resistance to stem rust race TTKSK (Ug99) from *Aegilops tauschii* to wheat, *Theor. Appl. Genetics* 126: 1179-1188
- Poland, J., T. Rife. (2012) Genotyping-by-sequencing for plant breeding and genetics. *The Plant Genome* 5(3): 92-102. (invited review)
- Poland, J., J. Endelman, J. Dawson, J. Rutkoski, S. Wu, Y. Manes, S. Dreisigacker, J. Crossa, H. Sanchez-Villeda, M. Sorrells, J.-L. Jannink. (2012) Genomic selection in wheat breeding using genotyping-by-sequencing. *The Plant Genome* 5(3): 103-113.
- International Barley Sequencing Consortium (2012) A physical, genetic and functional sequence assembly of the barley genome. *Nature* 491,711–716
- Chia, J.-M., C. Song, P. J. Bradbury, D. Costich, N. de Leon, J. Doebley, R. J. Elshire, B. Gaut, L. Geller, J. C. Glaubitz, M. Gore, K. E. Guill, J. Holland, M. B. Hufford, J. Lai, M. Li, X. Liu, Y. Lu, R. McCombie, R. Nelson, J. Poland, B. M. Prasanna, T. Pyhajarvi, T. Rong, R. S. Sekhon, Q. Sun, M. I. Tenailon, F. Tian, J. Wang, X. Xu, Z. Zhang, S. M. Kaeppler, J. Ross-Ibarra, M. D. McMullen, E. S. Buckler, G. Zhang, Y. Xu and D. Ware (2012). Maize HapMap2 identifies extant variation from a genome in flux. *Nature Genetics* 44(7): 803-807.
- Poland J., Brown P., Sorrells M., & Jannink J-L (2012) Development of high-density genetic maps for barley and wheat using a novel two-enzyme genotyping-by-sequencing approach. *PLoS ONE* 7(2):e32253.

- Poland, J., P. Bradbury, E. Buckler, and R. Nelson (2011), Genome-wide nested association mapping of quantitative resistance to northern leaf blight in maize. *PNAS* 108: 17,6893–6898
- Veturi, Y., K. Kump, E. Walsh, O. Ott, J. Poland, J. M. Kolkman, P. J. Balint-Kurti, J. B. Holland and R. J. Wisser (2012) Multivariate mixed linear model analysis of longitudinal data: An information-rich statistical technique for analyzing plant disease resistance. *Phytopathology* 102 (11): 1016-1025.
- Elshire, R., J. Glaubitz, Q. Sun, J. Poland, K. Kawamoto, E. Buckler, and S. Mitchell (2011) A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. *PLoS ONE* 6(5): e19379. doi:10.1371/journal.pone.0019379
- Chung, C., J. Poland, K. Kump, J. Benson, J. Longfellow, E. Walsh, P. Balint-Kurti and R. Nelson (2011) Targeted discovery of quantitative trait loci for resistance to Northern Leaf Blight and other diseases in maize, *Theor Appl Genet* 123:307–326
- Poland, J. and R. Nelson (2011) In the eye of the beholder: The effects of rater variability and different rating scales on QTL mapping. *Phytopathology* 101:290-298.
- Zeid, M., G. Belay, S. Mulkey, J. Poland, M. E. Sorrells (2010) QTL mapping for yield and lodging resistance in an enhanced SSR-based map for tef. *Theor Appl Genet* (2011) 122:77–93
- Poland, J., P. Balint-Kurti, R. Wisser, R. Pratt and R. Nelson (2009) Shades of gray: the world of quantitative disease resistance. *Trends in Plant Science* 14(1): 21-29
- Zhao, B., X. Lin, J. Poland, H. Trick, J. Leach, and S. Hulbert (2005) A maize resistance gene functions against bacterial streak disease in rice. *PNAS* 102:43, 15383–15388
- Poland, J (2003) Mapping of *Aegilops tauschii* derived leaf rust resistance genes in common wheat. *J. Nat. Resour. Life Sci. Educ.* 32: 2003
-

INVITED PRESENTATIONS

62 invited presentations including Plant and Animal Genome, ASA-CSSA-SSSA Annual Meetings, keynote at MONOGRAM, UK; CIMMYT, Mexico; IRRI, Philippines; departmental and special seminars at Cornell University, Univ. of Minnesota, Brigham Young Univ., Cold Spring Harbor, Univ. of Georgia Athens, Univ. Illinois, Univ. Nebraska Lincoln, Bangladesh Agriculture Research Institute, Indian Council Agriculture Research, Pakistan National Agriculture Research Council

Artificial neural networks for high throughput phenotyping in wheat. New Frontiers in Genetic Evaluation Conference, Corteva Agriscience (DuPont Pioneer), Johnston IA, July 2018

High-throughput Phenotyping to Accelerate Wheat Breeding, Wheat Research Institute, Faisalabad, Pakistan, April 2018

Artificial neural networks for high throughput phenotyping of heading date in wheat. Cornell University, Department of Plant Breeding and Genetics Seminar (Graduate Student Invited Seminar), Cornell University, Ithaca NY, Nov 2017

Artificial neural networks for high throughput phenotyping of heading date in wheat. The Plant Phenome Journal 2017 Webinar Series, Oct 2017

Leveraging ‘Big Data’ for Wheat Improvement in Kansas and Around the World, Cutting Edge Science in Development Session, BIFAD Public Meeting, Washington D.C. Sept 2017

Application of UAVs to Increase Genetic Gain, National Association of Plant Breeders, Davis CA, Aug 2017

Accelerating Wheat Breeding with Genomic Selection and High Throughput Phenotyping, National Agriculture Research Council - Pakistan, Islamabad, Pakistan, April 2017

Accelerating Wheat Breeding with Genomic Selection, Wheat Research Institute, Faisalabad, Pakistan, April 2017

Accelerating Wheat Breeding with Genomic Selection and High Throughput Phenotyping, University of Maryland, Department of Plant Science, Feb 2017

Increasing Yield Prediction Accuracy for Wheat Breeding Through Combined Genomic Selection and Field-based High Throughput Phenotyping, PHENOME 2017, Tuscon AZ, Feb 2017

Application of Artificial Neural Networks and Real Neural Networks to Field-based High Throughput Phenotyping, Plant and Animal Genome - National Plant Genome Initiative Workshop, San Diego CA, Jan 2017

Genomic Selection and High Throughput Phenotyping for Wheat Improvement, Bangladesh Agriculture Research Institute, Jamalapur Bangladesh, Jan 2017

Deep learning for high-throughput phenotyping of “complex” trait in wheat. ASA-CSSA International Annual Meetings, Phoenix AZ, Nov 2016

Field-based high throughput phenotyping with breeder trained artificial neural networks, NSF-National Science Foundation – Plant Genome Research Program Principle Investigator Annual Meeting, Arlington VA, Sept 2016

The Future of Wheat: Genomics to Accelerate Wheat Breeding. WheatU, Wichita, KS, Aug 2016

Field-based high-throughput phenotyping for evaluation of barely yellow dwarf resistance in wheat breeding. American Phytopathological Society Annual Meeting, Tampa, FL, Aug 2016

Accelerating Wheat Breeding with Genomic Selection. University of Nebraska (UNL) Plant Breeding Symposium, Lincoln, NE, March 2016

Advances in High Throughput Phenotyping. Bangladesh Agriculture Research Institute (BARI), Jamalpur, Bangladesh, March 2016

Android Apps for Plant Breeding and Genetics #phenoApps. Bangladesh Agriculture Research Institute (BARI), Jamalpur, Bangladesh, March 2016

Application of Unmanned Aerial Systems for High-throughput Phenotyping in Wheat. ASA-CSSA International Annual Meetings, Minneapolis, MN, Nov 2015

Advances in Phenomics. GK-12 Insight Workshop, Kansas State University, May 2015

Intersection of whole-genome prediction and high-throughput phenotyping for wheat breeding. CROPS 2015, HudsonAlpha, Huntsville AL, May 2015

Phenomics is the new genomics: Accelerating genetic gain in wheat breeding. MONOGRAM, Rothamsted Research Institute, Harpenden UK, April 2015

Overview of US wheat research. MONOGRAM, Rothamsted Research Institute, Harpenden UK, April 2015

Phenomics is the new genomics: Integration of physiological breeding and genomic selection for wheat improvement. College of Life Science seminar, Brigham Young University, Provo, UT, April 2015

Genomic selection for wheat improvement, Special Seminar, Directorate of Wheat Research, Karnal India, Feb 2015

Integration of physiological breeding and genomic selection for wheat improvement, 5th International Workshop on Next Generation Genomics and Integrated Breeding for Crop Improvement. ICRISAT, Patancheru, India, Feb 2015

A Tale of Two Accessions: Rapid Curation of Germplasm Collections Using Genotyping-by-Sequencing, Gene Introgression Workshop, Plant and Animal Genome, San Diego CA, Jan 2015

Enabling Applied Wheat Genomics with Next-Generation Sequencing, Illumina User-group Workshop, St. Louis, MO, Nov 2014

High Throughput Genotype and Phenotype Analysis of Agricultural Ecosystems, Ecological Genomics Symposium, Kansas City, MO, Nov 2014

Genomic Resources and Trait Mapping in Intermediate Wheatgrass, New Roots for Ecological Intensification, Estes Park, CO, Oct 2014

Advancements in Phenomics, Kansas State Research and Extension Symposium, Manhattan, KS, Oct 2014

Genomics Assisted Breeding and Field-based High Throughput Phenotyping, DOE ARPA-E Advanced Plant Phenotyping Workshop, Chicago, IL, June 2014

Connecting High-throughput Phenotype to High-throughput Genotype in Wheat, UGA Plant Center Spring Symposium, University Georgia Athens, May 2014

Genomic Selection and Precision Phenotyping, Borlaug Summit on Wheat for Food Security, Cd. Obregon, Mexico, Mar 2014

Integrating Genomic Selection and Selection for Large Effect QTL, Trait Pipeline Workshop hosted by The Bill and Melinda Gates Foundation, ICRISAT, Patancheru, India, Feb 2014

Applications of genotyping-by-sequencing for wheat breeding and genetics, 4th International Workshop on Next Generation Genomics and Integrated Breeding for Crop Improvement. ICRISAT, Patancheru, India, Feb 2014

Applied Genomics to Address Food Security, Plant Genomes & Biotechnology, Cold Spring Harbor Laboratories, NY, Dec 2013

Genotyping-by-Sequencing for Plant Breeding and Genetics, ASA-CSSA-SSSA Annual Meetings, Tampa FL, Nov 2013

A Field-based High Throughput Phenotyping Platform for Plant Breeding and Genetics. Donald Danforth Plant Science Center Fall Symposium/PhenoDays, Sept 2013

Computational Challenges in Next-Generation Food Security. Department of Bioinformatics and Genomics, University of North Carolina Charlotte, Charlotte NC, Sept 2013

Applications of Genotyping-by-Sequencing for Wheat Breeding and Genetics. Borlaug Global Rust Initiative Technical Workshop, New Delhi, India, Aug 2013

Field-based High-throughput Phenotyping for Plant Breeding and Genetics. Triticeae Coordinated Agriculture Project Webinar Series, May 2013

Genotyping-by-Sequencing for Plant Breeding and Genetics. Plant Breeding, Genetics and Biotechnology Seminar, International Rice Research Institute, Los Banos, Philippines, April 2013

Genotyping-by-Sequencing for Plant Breeding and Genetics. Kansas State University Plant Breeding Symposium, Manhattan, KS, April 2013

Connecting High-Throughput Phenotype to High-Throughput Genotype. University of Minnesota Plant Breeding Symposium, St. Paul MN, March 2013

Genomic Selection for Oat Breeding. Collaborative Oat Research Enterprise Technical Workshop, Ottawa Canada, March 2013

Applications of Precision Ag. in Wheat Breeding. Kansas Agriculture Research and Technology Association, Salina, KS, Jan 2013

Making Whole Genome Predictions In The World Of Cheap Genotyping and Difficult Phenotyping: Implications For Plant Breeding In The Developing World. USAID - Strategies For Leveraging Bioinformatics and Genomic Data to Advance Food Security Workshop, Plant and Animal Genome, San Diego, CA, Jan 2013

Genomic Selection In Wheat Breeding Using Genotyping-By-Sequencing. Genomics Assisted Breeding Workshop, Plant and Animal Genome, San Diego, CA, Jan 2013

High-Density Molecular Marker Discovery in Barley using Genotyping by Sequencing (GBS). Life Technologies - Genetic Analysis Approaches in Agriculture Biotechnology Workshop, Plant and Animal Genome, San Diego, CA, Jan 2013

High Throughput Phenotyping For Wheat Breeding and Genetics. CSSA: Translational Genomics Workshop, Plant and Animal Genome, San Diego, CA, Jan 2013

Genomic Selection in Wheat Breeding Using Genotyping-by-Sequencing. American Seed Trade Association: CSS 2012; 67th Corn and Sorghum Seed Research conference; 42nd Soybean Seed Research Conference; Seed Expo 2012, Chicago, IL, Dec 2012

Accelerating wheat breeding with high-throughput genotyping and phenotyping. The Donald Danforth Plant Science Center, Nov 2012

Applying 'Next-Generation' Sequencing and Phenotyping to Accelerate Wheat Breeding. Pioneer Hybrid International, Johnston IA, Nov 2012

Understanding and Utilizing Genetic Diversity in Wheat Breeding. Symposium--Using Genotypic Data to Strategically Develop Core Collections, Mini-Cores, and Trait-Specific Subsets, ASA-CSSA-SSSA Annual Meetings, Cincinnati, OH, Oct. 2012

Accelerating Wheat Breeding with Next-Generation Sequencing and High-Throughput Phenotyping. Symposium--Tools for Enhancing Genetic Progress: Genomics and Phenomics, ASA-CSSA-SSSA Annual Meetings, Cincinnati, OH, Oct 2012

Genotyping-by-Sequencing for Polyploid Species and Application in Wheat and Oat Breeding. Progress and Applications of Next Generation Sequencing Workshop, Saskatoon, Canada, May 2012

Genotyping-by-sequencing to Enable Genomics Assisted Breeding in Wheat. Plant and Animal Genome, San Diego, CA, Jan 2012

Genotyping-by-Sequencing Approaches for Your Favorite Large Polyploid Genome (Avena sativa), Plant and Animal Genome, San Diego, CA, Jan 2012

Genotyping-by-sequencing for Genomic Selection in Wheat, Department of Plant Molecular Biology, University of Illinois, Urbana-Champaign, Nov. 2011

Next Generation Plant Breeding, Department of Soil and Crop Science Cargill Sponsored Lecture, Colorado State University, Oct. 2011

Genotyping-by-Sequencing for Barley and Wheat Breeding and Genetics. International Triticeae Mapping Initiative, Mexico City, Mexico, Sept 2011

Genotyping-by-Sequencing in Barley and Wheat. Barley Improvement Conference, San Diego, CA, Jan 2011

GRANT FUNDING

Awarded over \$20M in competitive grant funding through NSF Plant Genome Research Program, Kansas Wheat Alliance, Kansas Wheat Commission, Kansas Crop Improvement Association, The Bill and Melinda Gates Foundation, The McKnight Foundation, USDA-NIFA, USDA-ARS, and USAID.

Development of a Genomic Selection Training Population for KSU Wheat Germplasm

Kansas Wheat Alliance | PI - \$39,100 | 2011–2012

Genomic Selection: The Next Frontier for Rapid Genetic Gains in Maize and Wheat
The Bill and Melinda Gates Foundation | coPI - \$355,000 (\$2,862,515) | 2011–2014

Genome-wide Characterization and Capture of Exotic Alleles for Increased Yield from Primary Synthetic Bread Wheat
Monsanto Beachell-Borlaug Intl Scholars Program | PI (Grad Advisor) - \$187,743 | 2011–2015

Improving Barley and Wheat Germplasm for Changing Environments
USDA – NIFA | co-PI - \$114,580 (\$25,000,000) | 2011– 2015

Applying Genomic Selection in KSU Wheat Breeding Programs
Kansas Wheat Alliance | PI - \$166,000 | 2012 – 2016

High-throughput Phenotypic Characterization and QTL Analysis of Stress Adaptive Traits in Wheat
Monsanto Beachell-Borlaug Intl Scholars Program | PI (Grad Advisor) - \$199,977 | 2012–2016

Characterization Of Allelic Variation Introduced Into Cultivated Hexaploid Wheat From The D-Genome Progenitor Species Aegilops Tauschii
USDA-NIFA | PI (Postdoctoral Advisor) - \$130,000 | 2012–2014

Pilot Project of One Handheld per Breeder (OHPB)
The McKnight Foundation | PI - \$70,000 | 2013–2015

A Field-Based High-Throughput Phenotyping Platform for Plant Genetics
NSF - PGRP | PI - \$1,639,615 | 2013–2018

Development of Genomic Selection Predictions Models for Yield and Important Agronomic Traits in Hard Winter Wheat
USDA-ARS | PI - \$100,000 | 2013– 2015

Feed the Future Innovation Lab for Applied Wheat Genomics
US Agency for International Development | PI - \$9,449,308 (\$4,450,322) | 2013–2023

Confirmation of Genetic Identity and Purity of Certified Wheat Seed Lots
Kansas Crop Improvement Association | PI - \$20,000 | 2013–2015

Development of Wheat Varieties with High Beta-glucan
General Mills Inc. | PI - \$513,505 | 2013–2016

NSF - I/UCRC: Collaborative Research: Wheat Genetics Resource Center: A Public-Private Consortium
National Science Foundation | \$367,500 | 2013–2018

Screening and Improvement of Barley Yellow Dwarf Resistance
Kansas Wheat Commission | PI - \$57,662 | 2014 - 2015

Wheat Genetics Research at Kansas State
Kansas Wheat Commission and Kansas Wheat Alliance | PI - \$300,000 | 2014 - 2016

Development of Heat Tolerant Wheat for Bangladesh
Borlaug Higher Education Agricultural Research and Development (BHEARD)
USAID Program: Bangladesh | PI (Graduate Advisor) – \$179,465 | 2014 – 2018

MRI: Acquisition of an Adaptive Data Cluster for Data-intensive Applications in Science and Engineering
NSF-MRI | co-PI (\$300,000) | 2014

KGEM: Next-generation Networking Environments for Biological and Agricultural Data-driven Research at Kansas State University
CC-IIE Networking Infrastructure | coPI – \$34,500 (\$231,500) | 2014

Genotyping-by-sequencing Training, Support and Sequencing

USDA-ARS SCA | PI - \$20,000 | 2014

GPF-PG: Genome Structure and Diversity of Wheat and Its Wild Relatives

NSF-PGRP | PI - \$1,585,420 | 2015 - 2018

Improving Genomic Prediction Models for End-use Quality in CIMMYT Wheat Breeding

Monsanto Beachell-Borlaug Intl Scholars Program | PI (Graduate Advisor) - \$160,000 | 2015–2019

Applied Genomics for Functional Foods in Wheat: Connecting Wheat Variety Development with Targeted, Novel Consumer Quality

General Mills, Inc. and Kansas Dept. of Commerce | PI - \$408,000 | 2015 - 2018

Integrative and Innovative Approaches to Diminish Barley Yellow Dwarf Epidemics in Kansas Wheat

Kansas Wheat Commission | coPI - \$42,000 (\$150,000) | 2015 – 2016

A Reference Phenotyping System for Energy Sorghum

DoE TERRA | coPI - \$363,518 (\$1,101,570 KSU; \$7,999,989) | 2015-2019

Developing Massively-Parallel Phenotyping Systems for Winter Wheat

Kansas Wheat Alliance | coPI (\$38,776) | 2015-2016

*Development of Genomics and Phenomics Tools to Accelerate *Thinopyrum intermedium* Improvement*

The Malone Family Foundation and The Land Institute | PI – \$233,141 | 2015-2017

BREAD PHENO: High-Throughput Phenotyping with Smart Phones. #phenoApp

NSF-BREAD | PI \$714,804 (\$859,221 KSU) (\$1,696,435) | 2016–2019

Delivering Genetic Gain in Wheat

BMGF | coPI \$414,915 (\$24,000,000) | 2016–2020

Development of Field Book and PhenoApps for Use in Specialty Crops

USDA / WSU | PI - \$118,800 | 2016–2019

Wheat Yield Prediction and Advanced Selection Methodologies through Field-Based High-Throughput Phenotyping with UAVs

USDA-NIFA | PI - \$975,000 | 2016–2019

An integrated 'omics Approach to Wheat Quality Improvement

USDA-NIFA | PI - \$980,000 | 2017 – 2020

Exploring the Genomic Landscape of Perenniality within the Triticeae

USDA-NIFA | coPI (Postdoctoral Advisor) - \$151,660 | 2016-2018