Dr. David L. Hyten Jr.

University of Nebraska-Lincoln
Agronomy & Horticulture
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Education

Ph D, University of Maryland, College Park, MD, 2002-2005

- Ph.D. Natural Resource Sciences, specializing in Crop Genetics
- Outstanding Graduate Student in Natural Resource Sciences, 2005
- James R. Miller/Maryland Crop Improvement Association Award, 2004

MS, University of Tennessee, Knoxville, TN, 2000-2002

- M. S. Plant and Soil Science specializing in Plant Breeding and Genetics
- Provosts' Award for Extraordinary Professional Promise, 2002
- Outstanding Technical Paper Award, Biotechnology Division, American Oil Chemists Society, 2002
- Gamma Sigma Delta Agricultural Honor Society, 2002

BA, Southern Illinois University, Carbondale, IL, 1995-1999

- B.A. Microbiology
- Minor Chemistry

Professional Positions

Associate Professor, University of Nebraska – Lincoln. (August 17, 2015 - Present)

Haskins Professor of Plant Genetics, University of Nebraska – Lincoln. (December 1, 2015 – Present)

Graduate Committee Chair, University of Nebraska – Lincoln. (2023 - Present)

Faculty Associate, Center for Plant Science Innovation, University of Nebraska – Lincoln. (August 17, 2015 – Present)

Faculty Associate, Nebraska Food for Health Center, University of Nebraska – Lincoln. (September 1, 2016 – Present)

Associate Department Chair, University of Nebraska – Lincoln. (January 1, 2019 – December 31, 2020)

Senior Research Manager, DuPont Pioneer. (September 1, 2013 - July 31, 2015)

Research Scientist, DuPont Pioneer. (April 23, 2011 - September 1, 2013)

Research Geneticist, U.S. Dept. of Agriculture, Agricultural Research Service. (November 1, 2007 - April 15, 2011)

Postdoctoral Fellow, U.S. Dept. of Agriculture, Agricultural Research Service. (April 1, 2005 - November 1, 2007)

Graduate Research Assistant, University of Maryland. (June 1, 2002 - April 1, 2005)

Graduate Research Assistant, University of Tennessee. (June 1, 2000 - June 1, 2002)

Researcher I, Southern Illinois University. (September 1, 1998 - June 1, 2000)

Professional Memberships

Crop Science Society of America. (April 30, 2004 - Present).

American Association for the Advancement of Science. (February 5, 2012 - Present).

American Society of Agronomy. (April 30, 2007 - 2021).

Genetics Society of America. (April 6, 2016 - 2021).

Genetics Society of America. (March 1, 2007 - March 1, 2011).

TEACHING

Teaching Experience

University of Nebraska-Lincoln

AGRO 919, Advanced Crop Genetics and Genomics, instructor, 2019, 2021, 2023, 2025.

AGRO 833, Molecular Plant Breeding, instructor, 2024.

AGRO 896-009, Independent Study; Molecular Plant Breeding, developed course and instructor, 2016, 2018, 2020, 2022.

AGRO 896-004, Independent Study; Advanced Crop Genomics, developed course and instructor, 2017.

AGRO 201, Agronomic Internship and Career Preparation, co-instructor, 2016.

University of Maryland, College Park

NRSC 601, Plant Genomics (Applied), Teaching Assistant, 2004.

Southern Illinois University, Carbondale

PLSS 305, Plant Genetics, Teaching Assistant, 1999-2000.

Marker Assisted Selection Workshop, Instructor, 1999-2000.

Mentoring

Graduate Students

Jennifer Derkits, PhD (committee chair/supervisor), Agronomy & Horticulture, 2022-present.

Ben Harms, Masters (committee chair/supervisor), Agronomy & Horticulture, 2019-2023.

Sarah Johnson, Doctorate (committee chair/supervisor), Complex Biosystems, 2017-2023.

Érika Sánchez-Betancourt, Doctorate (committee co-chair), Agronomy & Horticulture, 2017-2022.

Mary Happ, Doctorate (committee chair/supervisor), Agronomy & Horticulture, 2016- 2023.

Samantha McConaughy, Doctorate (committee chair/supervisor), Agronomy & Horticulture, 2015-2022.

Postdocs

Jacqui Siqueira, (supervisor), Agronomy & Horticulture, 2020-2022.

Committee member

Felipe Krause, Doctorate (committee member), Agronomy & Horticulture, 2024-present.

Arthur Bernardeli, Doctorate (committee member), Agronomy & Horticulture, 2022-present.

Hafith Furqoni, Doctorate (committee member), Agronomy & Horticulture, 2022-2024.

Kyle Linders, Masters (committee member), Agronomy & Horticulture, 2022-2023.

Herbert Sserunkuma, Doctorate (committee member), Agronomy & Horticulture, 2020-2022.

Mackenzie Zwienter, Masters (committee member), Agronomy & Horticulture, 2019-2020.

Fang Wang, Doctorate (committee member), Agronomy & Horticulture, 2018-2022.

Shawn Jenkins, Doctorate (committee member), Agronomy & Horticulture, 2017-2020.

Preston Hurst, Masters, (committee member), Agronomy & Hokyrticulture, 2017-2019.

Mallory Suhr, Doctorate (committee member), Food Science & Technology, 2016-2021.

Jake Ziggafoos, Masters, incomplete, (committee member), Agronomy & Horticulture, 2016-2018.

Ravi Mural, Doctorate (committee member), Agronomy & Horticulture, 2015-2019.

RESEARCH

Published Intellectual Contributions

Overall: h-index=51, i10-index=70, total citations 17,052.

Book Chapters

1. **Hyten, D.L.** (2022). Genotyping Platforms for Genome-Wide Association Studies: Options and Practical Considerations. In: Torkamaneh, D., Belzile, F. (eds) Genome-Wide Association Studies. Methods in Molecular Biology, vol 2481. Humana, New York, NY. https://doi.org/10.1007/978-1-0716-2237-7_3
2. Anderson, E. J., Ali, M. L., Beavis, W. D., Chen, P., Clemente, T. E., Diers, B. W., Graef, G., Grassini, P., **Hyten Jr, D.**, McHale, L. K., Nelson, R. L., Parrott, W. A., Patil, G. B., Stupar, R. M., Tilmon, K. J. (2019). Soybean [*Glycine max* (L.) Merr.] Breeding: History, Improvement, Production and Future Opportunities. In Advances in Plant Breeding Strategies: Legumes., J.M. Al-Khayri, S.M. Jain and D.V. Johnson (Ed.), (pp. 431-516). New York City, NY:. Springer.
3. **Hyten Jr, D.** (2012). Advances in genome sequencing and genotyping technology for soybean diversity analysis. In Rich Wilson (Ed.), *Designing Soybeans for 21st Century Markets* (pp. 45-52). Urbana, IL: AOCS Press/Academic.

Refereed Journal Articles

1. Wartha, C.A., Campbell, B.W., Ramasubramanian, V., Nice, L., Brock, A., Cai, G., Eskandari, M.M., Graef, G., Hudson, M.E., Hyten, D., Mahan, A.L., Martin, N.F., McHale, L., Miranda, C., Dominguez, E.M., Nelson, R., Rainey, K., Rajcan, I., Scaboo, A., Schapaugh, W., Singh, A.K., Gomes, J.P., Wang, D., and Lorenz, A.J., (2025), Genomic Analysis and Predictive Modeling in the Northern Uniform Soybean Tests. Crop Science, in press.
2. Johnson, S., Hyten, D. (2025), Genomic markers associated with soybean resistance to the stem borer, Dectes texanus (Coleoptera: Cerambycidae). Plant Direct, 9(3), e70040. DOI: 10.1002/pld3.70040.

3. McConaughy, S., Amundsen, K. and Hyten, D. (2024), Effects of demographic history on recombination hotspots in soybean. The Plant Journal, 119: 1030-1038. https://doi.org/10.1111/tpj.16814

4. Stupar, R. M., Locke, A. M., Allen, D. K., Stacey, M. G., Ma, J., Weiss, J., Nelson, R. T., Hudson, M. E., Joshi, T., Li, Z., Song, Q., Jedlicka, J. R., MacIntosh, G. C., Grant, D., Parrott, W. A., Clemente, T. E., Stacey, G., An, Y.-C., Aponte-Rivera, J., Bhattacharyya, M.K., Baxter, I., Bilyeu, K.D., Campbell, J.D., Cannon, S.B., Clough, S.J., Curtin, S.J., Diers, B.W., Dorrance, A.E., Gillman, J.D., Graef, G.L., Hancock, N., Hudson, K.A., Hyten, D.L., ….O'Rourke, J. A. (2024). Soybean genomics research community strategic plan: A vision for 2024–2028. The Plant Genome, 17(4), e20516. https://doi.org/10.1002/tpg2.20516

5. Wang H., Zhao X., Tan L., Zhu J., Hyten D. (2024) Crop DNA extraction with lab-made magnetic nanoparticles. PLoS ONE 19(1): e0296847.

6. McConaughy, S., Amundsen, K., Song, Q., Pantalone, V., Hyten Jr, D. (2023) Recombination Hotspots in Soybean [Glycine max (L.) Merr.]. G3: Genes, Genomes, Genetics. 13(6), jkad075. https://doi.org/10.1093/g3journal/jkad075

7. Fields, J., Saxton, A., Beyl, C., Kopsell, D., Cregan, P., **Hyten Jr, D.**, Cuvuca, I., Pantalone, V. (2023) Seed Protein and Oil QTL in a Prominent Glycine max Genetic Pedigree: Enhancing stability for Marker Assisted Selection. *Agronomy*. 13(2), 567.

8. Wang, H., Campbell, B., Happ, M., McConaughy, S., Lorenz, A., Amundsen, K., Pantalone, V., **Hyten Jr, D.** (2023). Development of Molecular Inversion Probes for Soybean Progeny Genomic Selection Genotyping. The Plant Genome. e20270. https://doi.org/10.1002/tpg2.2027

9. Dietz, N., Chan, Y. O., Scaboo, A., Graef, G., **Hyten Jr, D.**, Happ, B., Lorenz, A., Wang, Joshi, T., Bilyeu, K. (2022). Candidate genes modulating reproductive timing in elite US soybean lines identified in soybean alleles of Arabidopsis flowering orthologues with divergent latitude distribution. Frontiers in Plant Science, 13, 889066.

10. Happ, M., Graef, G., Wang, H., Howard, R., Posadas, L., and **Hyten, D.** (2021) Comparing a Mixed Model Approach to Traditional Stability Estimators for Mapping Genotype by Environment Interactions and Yield Stability in Soybean [*Glycine max* (L.) Merr.]. *Frontiers in Plant Science* 12:542.

11. Torkamaneh, D., Laroche, J., Boyle, B., **Hyten, D.**, and Belzile, F. (2021). A bumper crop of SNPs in soybean through high-density genotyping-by-sequencing (HD-GBS). *Plant Biotechnology Journal* 19(5):860.

12. Song, Q., Yan, L., Quigley, C., Fickus, E., Wei, H., Chen, L., Dong, F., Araya, S., Liu, J., **Hyten D.**, Pantalone, V., Nelson, R. (2020). Soybean BARCSoySNP6K: An assay for soybean genetics and breeding research. *The Plant Journal* 104(3):800-811.

13. Happ, M., Wang, H., Graef, G., **Hyten Jr, D.** (2019). Generating High Density, Low Cost Genotype Data in Soybean [*Glycine max* (L.) Merr.]. *G3: Genes, Genomes, Genetics*, 9(7), 2153-2160.

14. Smallwood, C. J., Saxton, A. M., Gillman, J. D., Bhandari, H. S., Wadl, P. A., Fallen, B., **Hyten, D.L.**, Song, Q. J., Pantalone, V. R. (2019). Context specific genomic selection strategies outperform phenotypic selection for soybean quantitative traits in the progeny row stage. *Crop Science* 59:54-67.

15. Diers, B. W., Specht, J., Rainey, K. M., Cregan, P., Song, Q., Ramasubramanian, V., Graef, G., Nelson, R., Schapaugh, W., Wang, D., Shannon, G., McHale, L., Kantartzi, S. K., Xavier, A., Mian, R., Stupar, R., Michno, J.-M., Charles An, Y.-Q., Goettel, W., Ward, R., Fox, C., Lipka, A. E., **Hyten, D.L.**, Cary, T., Beavis, W. D. (2018). Genetic architecture of soybean

yield and agronomic traits. *G3: Genes, Genomes, Genetics*, 8: 3367-3375. doi:10.1534/g3.118.200332.

16. Smallwood, C. J., Gillman, J. D., Saxton, A. M., Bhandari, H. S., Wadl, P. A., Fallen, B., **Hyten, D.L.**, Song, Q. J., Pantalone, V. R. (2017). Identifying and Exploring Significant Genomic Regions Associated with Soybean Yield and Seed Fatty Acids, Protein and Oil. Springer *Journal of Crop Science and Biotechnology*, 20(4), 243-253.
17. Song, Q., Yan, L., Quigley, C., Jordan, B. D., Fickus, E., Schroeder, S., Song, B., An, C. Y.-Q., **Hyten, D.L.**, Rainey, K., Beavis, B., Specht, J., Diers, B., Cregan, P. (2017). Genotyping recombinant inbred lines and parents of the Nested Association Mapping (NAM) population of soybean. *The Plant Genome*, 10(2), 1-14.
18. Bandillo, N. B., Lorenz, A. J., Graef, G., Hernandez Jarquin, J. D., **Hyten, D.L.**, Nelson, R. L., Specht, J. (2017). Genome-wide association mapping of qualitatively inherited traits in a germplasm collection. *The Plant Genome*, 10(2), 1-18.
19. Vuong, T. D., Walker, D. R., Nguyen, B. T., Nguyen, T. T., Dinh, H. X., **Hyten, D.L.**, Cregan, P. B., Sleper, D. A., Lee, J. D., Shannon, J. G., Nguyen, H. T. (2016). Molecular characterization of resistance to soybean rust (Phakopsora pachyrhizi Syd. & Syd.) in soybean cultivar DT 2000 (PI 635999). *PLoS One*, 11(12), e0164493.
20. Phansak, P., Soonsuwon, W., **Hyten, D.L.**, Song, Q., Cregan, P., Graef, G., Specht, J. (2016). Multi-Population Selective Genotyping to Identify Soybean (*Glycine max* (L.) Merr.) Seed Protein and Oil QTLs. *G3: Genes*|*Genomes*|*Genetics,* 6(6), 1635-1648.
21. Song, Q., Jenkins, J., Jia, G., **Hyten, D.L.**, Pantalone, V., Jackson, S., Schmutz, J., Cregan, P. (2016). Construction of high resolution genetic linkage maps to improve the soybean genome sequence assembly Glyma1.01. *BMC Genomics*, 17:33.
22. **Hyten, D.L.** and Lee, D. J. (2016). *Plant Genetic Mapping Techniques*. eLS. 1-8.
23. Song, Q., Jia, G., **Hyten, D.L.**, Jenkins, J., Hwang, E. Y., Schroeder, S. G., Osorno, J. M., Schmutz, J., Jackson, S. A., McClean, P. E., Cregan, P. B. (2015). SNP Assay Development for Linkage Map Construction, Anchoring Whole Genome Sequence and Other Genetic and Genomic Applications in Common Bean. *G3: Genes*|*Genomes*|*Genetics*, 5(11), 2285-2290.
24. Song, Q., **Hyten, D.L.**, Jia, G., Quigley, C. V., Fickus, E. W., Nelson, R. L., Cregan, P. B. (2015). Fingerprinting Soybean Germplasm and Its Utility in Genomic Research. *G3: Genes*|*Genomes*|*Genetics,* 5(10), 1999-2006.
25. Warrington, C. V., Abdel-Haleem, H., **Hyten, D.L.**, Cregan, P. B., Orf, J. H., Killam, A. S., Bajjalieh, N., Li, Z., Boerma, H. R. (2015). QTL for seed protein and amino acids in the Benning x Danbaekkong soybean population. *Theoretical and Applied Genetics,* 128(5), 839-850.
26. Fallen, B., Allen, F., Kopsell, D., Saxton, A., McHale, L., Shannon, G., Kantartzi, S., Cardinal, A., Cregan, P., **Hyten, D.L.**, Pantalone, V. (2015). Selective Genotyping for Marker Assisted Selection Strategies for Soybean Yield Improvement. *Plant Genetics, Genomics, and Biotechnology*, 2(1): 95-119.
27. Wang, X. Z., Jiang, G. L., Green, M., Scott, R. A., Song, Q. J., **Hyten, D.L.**, Cregan, P. B. (2014). Identification and validation of quantitative trait loci for seed yield, oil and protein contents in two recombinant inbred line populations of soybean. *Molecular Genetics and Genomics, 289*(5), 935-949.
28. Schmutz, J., McClean, P. E., Mamidi, S., Wu, G. A., Cannon, S. B., Grimwood, J., Jenkins, J., Shu, S. Q., Song, Q. J., Chavarro, C., Torres-Torres, M., Geffroy, V., Moghaddam, S. M., Gao, D. Y., Abernathy, B., Barry, K., Blair, M., Brick, M. A., Chovatia, M., Gepts, P., Goodstein, D. M., Gonzales, M., Hellsten, U., **Hyten, D.L.**, Jia, G. F., Kelly, J. D., Kudrna, D., Lee, R., Richard, M. M. S., Miklas, P. N., Osorno, J. M., Rodrigues, J., Thareau, V., Urrea, C.

A., Wang, M., Yu, Y., Zhang, M., Wing, R. A., Cregan, P. B., Rokhsar, D. S., Jackson, S. A. (2014). A reference genome for common bean and genome-wide analysis of dual domestications. *Nature Genetics,* 46(7), 707-713.

29. Abdelmajid, K., Ramos, L., **Hyten, D.L.**, Bond, J., Bendahmane, A., Arelli, P., Njiti, V., Cianzio, S., Kantartzi, S., Meksem, K. (2014). Quantitative Trait Loci (QTL) that Underlie SCN Resistance in Soybean [Glycine max (L.) Merr.] PI438489B by 'Hamilton' Recombinant Inbred Line (RIL) Population. *Atlas Journal of Plant Biology* 1(3), 29-38.

30. Bolon, Y. T., **Hyten, D.L.**, Orf, J. H., Vance, C. P., Muehlbauer, G. J. (2014). eQTL Networks Reveal Complex Genetic Architecture in the Immature Soybean Seed. *Plant Genome, 7*(1).

31. Zhang, Z. N., Hao, J. J., Yuan, J. Z., Song, Q. J., **Hyten, D.L.**, Cregan, P. B., Zhang, G. R., Gu, C. H., Li, M., Wang, D. C. (2014). Phytophthora Root Rot Resistance in Soybean E00003. *Crop Science,* 54(2), 492-499.

32. Wang, X. Z., Jiang, G. L., Green, M., Scott, R. A., **Hyten, D.L.**, Cregan, P. B. (2014). Quantitative trait locus analysis of unsaturated fatty acids in a recombinant inbred population of soybean. *Molecular Breeding,* 33(2), 281-296.

33. Smallwood, C. J., Nyinyi, C. N., Kopsell, D. A., Sams, C. E., West, D. R., Chen, P. Y., Kantartzi, S. K., Cregan, P. B., **Hyten, D.L.**, Pantalone, V. R. (2014). Detection and Confirmation of Quantitative Trait Loci for Soybean Seed Isoflavones. *Crop Science,* 54(2), 595-606.

34. Hwang, E. Y., Song, Q. J., Jia, G. F., Specht, J., **Hyten, D.L.**, Costa, J., Cregan, P. B. (2014). A genome-wide association study of seed protein and oil content in soybean. *BMC Genomics,* 15:1.

35. Cardinal, A. J., Whetten, R., Wang, S. B., Auclair, J., **Hyten, D.L.**, Cregan, P., Bachlava, E., Gillman, J., Ramirez, M., Dewey, R., Upchurch, G., Miranda, L., Burton, J. W. (2014). Mapping the low palmitate fap1 mutation and validation of its effects in soybean oil and agronomic traits in three soybean populations. *Theoretical and Applied Genetics, 127*(1), 97-111.

36. Fallen, B., Hatcher, C., Allen, F., Kopsell, D., Saxton, A., Chen, P., Kantartzi, S., Cregan, P., **Hyten, D.L.**, Pantalone, V. (2013). Soybean Seed Amino Acid Content QTL Detected Using the Universal Soy Linkage Panel 1.0 with 1,536 SNPs. *Journal of Plant Genome Sciences,* 1(3), 68-79.

37. Bales, C., Zhang, G. R., Liu, M. H., Mensah, C., Gu, C. H., Song, Q. J., **Hyten, D.L.**, Cregan, P., Wang, D. C. (2013). Mapping soybean aphid resistance genes in PI 567598B. *Theoretical and Applied Genetics, 126*(8), 2081-2091.

38. Pathan, S. M., Vuong, T., Clark, K., Lee, J. D., Shannon, J. G., Roberts, C. A., Ellersieck, M. R., Burton, J. W., Cregan, P. B., **Hyten, D.L.**, Nguyen, H. T., Sleper, D. A. (2013). Genetic Mapping and Confirmation of Quantitative Trait Loci for Seed Protein and Oil Contents and Seed Weight in Soybean. *Crop Science, 53*(3), 765-774.

39. Song, Q. J., **Hyten, D.L.**, Jia, G. F., Quigley, C. V., Fickus, E. W., Nelson, R. L., Cregan, P. B. (2013). Development and Evaluation of SoySNP50K, a High-Density Genotyping Array for Soybean. *Plos One, 8*(1).

40. Kim, K.-S., Diers, B.W., **Hyten, D.L.**, Rouf Mian, M.A., Shannon, J.G., Nelson, R.L. 2012. Identification of positive yield QTL alleles from exotic soybean germplasm in two backcross populations. *Theor. Appl. Genet.* 125:1353-1369.

41. Abdelmajid, K.M., Ramos, L., Leandro, L., Mbofung, G., **Hyten, D.L.**, Kantartzi, S.K., Grier, R.L., Njiti, V.N., Cianzio, S., and Meksem, K. 2012. The 'PI 438489B' by 'Hamilton' SNP-based genetic linkage map of soybean [Glycine max (L.) Merr.] identified quantitative trait loci that underlie seedling SDS resistance. *J. of Plant Gen. Sci.* 1:18-30.

42. McHale, L.K., Haun, W.J., Xu, W.W., Bhaskar, P.B., Anderson, J.E., **Hyten, D.L.**, Gerhardt, D.J., Jeddeloh, J.A., Stupar, R.M. 2012. Structural variants in the soybean genome localize to clusters of biotic stress-response genes. *Plant Physiol.* 159:1295-1308.

43. Wang, X., Jiang, G.-L., Green, M., Scott, R.A., **Hyten, D.L.**, Cregan, P.B. 2012. Quantitative trait locus analysis of saturated fatty acids in a population of recombinant inbred lines of soybean. *Molecular Breeding* 30:1163-1179.

44. Kim, K.-S., Unfried, J.R., **Hyten, D.L.**, Frederick, R.D., Hartman, G.L., Nelson, R.L., Song, Q., Diers, B.W. 2012. Molecular mapping of soybean rust resistance in soybean accession PI 561356 and SNP haplotype analysis of the Rpp1 region in diverse germplasm. *Theor. Appl. Genet.* 125:1339-1352.

45. Mamidi, S., Chikara, S., Goos, R.J., **Hyten, D.L.**, Annam, D., Moghaddam, S.M., Lee, R.K., Cregan, P.B., and McClean, P.E. 2011. Genome-wide association analysis identifies candidate genes associated with iron deficiency chlorosis in soybean. *The Plant Genome* 4:154-164.

46. Polacco, J.C., **Hyten, D.L.**, Medeiros-Silva, M., Sleper, D.A., Bilyeu, K.D. 2011. Mutational analysis of the major soybean UreF paralogue involved in urease activation. *J. of Experimental Botany* 62:3599-3608.

47. Kendrick, M.D., Harris, D.K., Ha, B.-K., **Hyten, D.L.**, Cregan, P.B., Frederick, R.D., Boerma, H.R., Pedley, K.F. 2011. Identification of a second Asian soybean rust resistance gene in Hyuuga soybean. *Phytopathology* 101:535-543.

48. Kim, M., **Hyten, D.L.**, Niblack, T.L., Diers, B.W. 2011. Stacking resistance alleles from wild and domestic soybean sources improves soybean cyst nematode resistance. *Crop Sci.* 51:934-943.

49. Haun, W.J., **Hyten, D.L.**, Xu, W.W., Gerhardt, D.J., Albert, T.J., Richmond, T., Jeddeloh, J.A., Jia, G., Springer, N.M., Vance, C.P., Stupar, R.M. 2011. The composition and origins of genomic variation among individuals of the soybean reference cultivar Williams 82. *Plant Physiol.* 155:645-655.

50. **Hyten, D.L.**, Q. Song, E.W. Fickus, C.V. Quigley, J-S. Lim, I-Y. Choi, E-Y Hwang, M. Pastor-Corrales, and P.B. Cregan. 2010. High-throughput SNP discovery and assay development in common bean. *BMC Genomics* 11:475.

51. Lin, Y-Y., Stupar, R.M., Hans, C., **Hyten, D.L.**, and Jackson, S. 2010. Structural and functional divergence of a 1-Mb duplicated region in the soybean (Glycine max) genome and comparison to Phaseolus vulgaris. *Plant Cell* 22:2545-2561.

52. Severin, A.J., Peiffer, G., Xu, W.W., **Hyten, D.L.**, Bucciarelli, B., O'Rourke, J.A., Bolon, Y-T., Grant, D., Farmer, A.D., May, G.D., Vance, C.P., Shoemaker, R.C., and Stupar, R.M. 2010. An integrative approach to genomic introgression mapping. *Plant Physiol.* 154:3-12.

53. Song, Q., Jia, G., Zhu, Y., Hwang, E-Y., **Hyten, D.L.**, and Cregan P.B. 2010. Abundance of SSR motifs and development of candidate polymorphic SSR markers (BARCSOYSSR_1.0) in soybean. *Crop Sci.* 50:1950-1960.

54. Kim, K. S., Hill, C. B., Hartman, G. L., **Hyten, D. L.**, Hudson, M. E., Diers, B. W. 2010. Fine mapping of the soybean aphid-resistance gene Rag2 in soybean PI 200538. *Theor. Appl. Genet.*121:599-610.

55. **Hyten, D.L.**, I.-Y. Choi, Q. Song, J.E. Specht, T.E. Carter, R.C. Shoemaker, E.-Y. Hwang, L.K. Matukumalli, and P.B. Cregan. 2010. A high density integrated genetic linkage map of soybean and the development of a 1,536 Universal Soy Linkage Panel for QTL mapping. *Crop Sci.* 50:960-968.

56. **Hyten, D.L.**, S.B. Cannon, Q. Song, N. Weeks, E.W. Fickus, R.C. Shoemaker, J.E. Specht, A.D. Farmer, G.D. May, and P.B. Cregan. 2010. High-throughput SNP discovery through deep resequencing of a reduced representation library to anchor and orient scaffolds in the soybean whole genome sequence. *BMC Genomics* 11:38.

57. Schmutz, J., S. Cannon, J. Schlueter, J. Ma, T. Mitros, W. Nelson, **D.L. Hyten**, Q. Song, J. Thelen, J. Cheng, D. Xu, U. Hellsten, G. May, Y. Yu, T. Sakurai, T. Umezawa, M. Bhattacharyya, D. Sandhu, B. Valliyodan, E. Lindquist, M. Peto, D. Grant, S. Shu, D. Goodstein, K. Barry, M. Futrell-Griggs, J. Du, Z. Tian, L. Zhu, N. Gill, T. Joshi, M. Libault, A. Sethuraman, X.-C. Zhang, K. Shinozaki, H. Nguyen, R. Wing, P. Cregan, J. Specht, J. Grimwood, D. Rokhsar, G. Stacey, R. Shoemaker, and S. Jackson. 2010. Genome seqeunce of the paleopolyploid soybean. *Nature* 463:178-183.

58. Kim, K-S., Bellendir, S., Hudson, K., Hill, C., Hartman, G., **Hyten, D.L.**, Hudson, M., and Diers, B. 2010. Fine mapping the soybean aphid resistance gene Rag1 in soybean. *Theor. Appl. Genet.* 120:1063-1071.

59. Chakraborty, N., Curley, J., Frederick, R.D., **Hyten, D.L.**, Nelson, R.L., Hartman, G.L., and Diers, B.W. 2009. Mapping and confirmation of a new allele at Rpp1 from soybean PI 594538A conferring RB lesion type resistance to soybean rust. *Crop Sci.* 49: 783-790.

60. **Hyten, D.L.**, J.R. Smith, R.D. Frederick, M.L. Tucker, Q. Song, and P.B. Cregan. 2009. Bulked segregant analysis using the GoldenGate assay to locate the Rpp3 locus that confers resistance to Phakopsora pachyrhizi (soybean rust) in soybean. *Crop Sci.* 49: 265-271.

61. **Hyten, D.L.**, Song, Q., Choi, I-Y., Yoon, M-S., Specht, J.E., Matukumalli, L.K., Nelson, R.L., Shoemaker, R.C., Young, N.D., and Cregan, P.B. 2008. High-throughput genotyping with the GoldenGate assay in the complex genome of soybean. *Theor. Appl. Genet.* 116:945-952.

62. Choi, I.-Y., **Hyten, D.L.**, Matukumalli, L.K., Song, Q., Chaky, J.M., Quigley, C.V., Chase, K., Lark, K.G., Reiter, R.S., Yoon, M-S., Hwang, E-Y., Yi, S-In., Young, N.D., Shoemaker, R.C., Van Tassell, C.P., Specht, J.E., and Cregan, P.B. 2007. A soybean transcript map: gene distribution, haplotype and SNP analysis. *Genetics* 176:685-696.

63. **Hyten, D.L.**, Choi, I-Y., Song, Q., Shoemaker, R.C., Nelson, R.L., Costa, J.M., Specht, J.E., and Cregan, P.B. 2007. Highly variable patterns of linkage disequilibrium in multiple soybean populations. *Genetics* 175:1937-1944.

64. **Hyten D.**, Hartman G., Nelson R., Frederick R., Concibido V., and Cregan P. 2007. Map Location of the Rpp1 locus that confers resistance to Phakopsora pachyrhizi (Soybean Rust) in soybean. *Crop Sci.* 47:835-838.

65. Yoon M-S., Song Q., Choi I-Y., Specht J., **Hyten D.**, and Cregan P. 2007. BARCSoySNP23: A panel of 23 selected SNPs for soybean cultivar identification. *Theor. Appl. Genet.* 114:885-899.

66. **Hyten D.**, Song Q., Zhu Y., Choi I-Y., Nelson R., Costa J., Specht J., Shoemaker R., and Cregan P. 2006. Impacts of genetic bottlenecks on soybean genome diversity. *Proc. Natl. Acad. Sci. U.S.A.* 103:16666-16671.

67. Matukumalli, L., Grefenstette J., **Hyten D.**, Choi, I-Y., Cregan P., and Van Tassell C. 2006. SNP-PHAGE – High throughput SNP discovery pipeline. *BMC Bioinformatics* 7:468.

68. Matukumalli, L., Grefenstette J., **Hyten D.**, Choi, I-Y., Cregan P., and Van Tassell C. 2006. SNP-PHAGE-ML: Application of machine learning in SNP discovery. *BMC Bioinformatics* 7:4.

69. Stefaniak T., **Hyten D.**, Pantalone V., Klarer A., and Pfeiffer T. 2006. Soybean cultivars resulted from more recombination events than unselected lines in the same population. *Crop Sci.* 46:43-51.

70. **Hyten D.**, Pantalone V., Saxton A., Schmidt M., and Sams C. 2004. Molecular mapping and identification of soybean fatty acid modifier quantitative trait loci. *J. Am. Oil Chem. Soc.* 81:1115-1118.

71. **Hyten D.**, Pantalone V., Sams C., Saxton A., Landau-Ellis D., Stefaniak T., Schmidt M. 2004. Seed quality QTL in a prominent soybean population. *Theor. Appl. Genet.* 109: 552-561.

72. Zhu Y., Song Q., **Hyten D.**, Van Tassell C., Matukumalli L., Grimm D., Hyatt S., Fickus E., Young N., and Cregan P. 2003. Single-nucleotide polymorphisms in soybean. *Genetics* 163:1123-1134.

73. Spencer M., Pantalone V., Meyer E., Landau-Ellis D., **Hyten D.** 2003. Mapping the Fas locus controlling stearic acid content in soybean. *Theor. Appl. Genet.* 106:615-619.

74. Meksem K., Ruben E., **Hyten D.**, Triwitayakorn K., Lightfoot D. A. 2001. Conversion of AFLP bands to high-throughput DNA markers. *Mol. Genet. Genomics* 265:207-214.

75. Meksem K., Ruben E., **Hyten D.**, Lightfoot D. 2001. Highthroughput genotyping for the detection of polymorphism physically linked soybean cyst nematode resistance gene Rhg4 using Taqman Probes. *Mol. Breeding* 77:63-71.

76. Meksem K., Pantazopoulos P., Njiti V., **Hyten D.**, Arelli P., Lightfoot D. 2001. “Forrest” resistance to the soybean cyst nematode is bigenic: saturation mapping of the Rhg1 and Rhg4 loci. *Theor. Appl. Genet.* 103:710-717.

77. Meksem K., Njiti V., Banz W., Iqbal M., Kassem M., **Hyten D.**, Yuang J., Winters T., and Lightfoot D. 2001. Genomic regions that underlie soybean seed isoflavone content. *J. Biomed. Biotechnol.* 1:35-42.

78. Meksem K., Zobrist K., Ruben E., **Hyten D.**, Quanzhou T., Zhang H-B., Lightfoot D. 2000. Two large-insert soybean genomic libraries constructed in a binary vector: applications in chromosome walking and genome wide physical mapping. *Theor. Appl. Genet.* 101:747-755.

Patents (9) and Patent Applications (3) *Author order determined alphabetically of last name

1. *Forth, K.A., Hyten, D.L., Kalvig, A.B., King, K.E., Kuhlman, L.C., Kyle, D., Lee, T., Massman, J.M., Mendez, E.J., Santiago-Parton, S.A., Shendelman, J.M., Spear, J.D., Woodward, J.B., Xiong, Y. (2020). *U.S. Patent No 10,577,666* Washington, DC: U.S. Patent and Trademark Office.

2. *Hyten, D.L., Kalvig, A.B., Kuhlman, L.C., Kyle, D., Liu, J., Shendelman, J.M., Thompson, J.A., Woodward, J.B., Yang, M. (2020) *U.S. Patent No 10,568,280* Washington, DC: U.S. Patent and Trademark Office.

3. *Forth, K.A., Hyten, D.L., Kalvig, A.B., King, K.E., Kuhlman, L.C., Kyle, D., Lee, T., Massman, J.M., Mendez, E.J., Santiago-Parton, S.A., Shendelman, J.M., Spear, J.D., Woodward, J.B., Xiong, Y. (2018). *U.S. Patent No 9,951,391* Washington, DC: U.S. Patent and Trademark Office.

4. *Daines B., Hyten D., Schneider N., Woodward J. (2018). *U.S. Patent No 9,988,693*. Washington, DC: U.S. Patent and Trademark Office.

5. *Daines B., Hyten D., Schneider N., Woodward J. (2018). *U.S. Patent No 9,957,577*. Washington, DC: U.S. Patent and Trademark Office.

6. *Daines B., Hyten D., Schneider N., Woodward J. (2018). *U.S. Patent No 9,957,578*. Washington, DC: U.S. Patent and Trademark Office.

7. *Hyten, D.L., Kalvig, A.B., Kuhlman, L.C., Kyle, D., Liu, J., Shendelman, JM., Thompson, J.A., Woodward, J., Yang, M. (2018). *U.S. Patent No* 9*,894,857*. Washington, DC: U.S. Patent and Trademark Office.

8. *Allen J., Daines B., Hyten D., Kyle D., Mapel C., Shendelman, J. Thompson J., Woodward J., Xiong Y., Yang M. (2016) *U.S. Patent No* 9*,464,330*. Washington, DC: U.S. Patent and Trademark Office.
9. *Daines B., Hyten D., Schneider N., Woodward J. (2016). *U.S. Patent No 9,347,105*. Washington, DC: U.S. Patent and Trademark Office.
10. *Chaky J., Fabrizius M., Hyten D., Krasheninnik N., Spear J., Woodward J., Xiong Y. (2012). *U.S. Patent Application No CA2834153 A1*, Washington, DC: U.S. Patent and Trademark Office.
11. *Hood M., Hyten D., Kalvig A., Raines J., Shendelman J., Woodward J., Xiong Y. (2012). U.S. *Patent Application No US 20140162250 A1*, Washington, DC: U.S. Patent and Trademark Office.
12. Kim K-S., Hill C. Hartman G., Hyten D., Hudson M., Diers B. (2010). *U.S. Patent Application No WO2011116131 A3*, Washington, DC: U.S. Patent and Trademark Office.

Research Grants and Donations

Grants

1. Hyten, D., Graef, G. 2023-2025. “Genetic control of Soybean Nodulation Bradyrhizobium Strains in Nebraska Soils” NE Soybean Board, Awarded. $210,973.
2. Hudson, M., Bernard, G., Bilyeu, K., Cannon, S., Hyten, D., Hudson, K., Lorenz, A., Ma, J., and Stupar, B. 2023-2025. “A Reference Level Pangenome of Soybean Founder Lines.” Department of Defense, Joint Genome Institute, Community Science Program. Awarded. $0 to PIs: DoE sequencing budget TBD.
3. Lorenz, A., Chen, P., Diers, B., Graef, G., Hudson, M., Hyten, D., Miranda, C., Rainey, K., Martin, N., McHale, L., Scaboo, A., Schapaugh, W., Singh, W., Singh, A., Wang, D., and Nelson, R. 2022-2025. “SOYGEN3: Building capacity to increase soybean genetic gain in future environments for seed yield and composition through combining genomics-assisted breeding with environmental characterization” North Central Soybean Research Program, Awarded. $2,605,238 ($132,933 to Hyten lab).
4. Hyten Jr, D., Graef, G. 2021-2024, “Assessing the Genetic Diversity and Vulnerability of Nebraskan Soybean.” NE Soybean Board, Awarded. $172,325.
5. Hyten Jr, D., 2019-2022, "Whole Genome Sequencing of the USDA Soybean Germplasm Collection and Applications for New Gene Discovery." United Soybean Board, $733,148.
6. Hyten Jr, D. and Graef, G. 2019-2022. "Increasing yield and seed composition stability through diverse germplasm and genomic selection," Ne Soybean Board, $306,990.
7. McHale, L., Chen, P., Diers, B., Graef, G., Hudson, M., Hyten, D., Lorenz, A., Rainey, K., Martin, N., Nelson, R., Scaboo, A., Schapaugh, B., Singh, A., and Wang. D. 2019-2022. “SOYGEN 2: Increasing soybean genetic gain for yield and seed composition by developing tools, know-how and community among public breeders in the north central US” North Central Soybean Research Program, $2,466,237 ($358,126 to Hyten lab).
8. Graef, G., and Hyten, D., 2019-2022. “Creating Five High-Yield Soybean Variety Pairs with Contrasting Biological Nitrogen Fixation Capabilities,” Ne Soybean Board, $134,565.
9. Graef, G., Schapaugh, W., Singh, D., Walker, D., Smith, J., Lorenz, A., Diers, B., Scaboo, A., Krishnan, H., Hyten, D., Clemente, T., and Hudson, M. 2019-2022, " Increasing genetic diversity, yield, and protein of US commercial soybean germplasm." United Soybean Board, $2,692,740 ($79,347 to Hyten lab).
10. Hyten Jr, D. and Graef, G. 2019-2021. "Screening for stem borer resistance," Ne Soybean Board, $112,904.

11. Stupar, R., Muehlbauer, G., Hyten, D. 2018-2020. “Discovering and (finally) understanding the functions of genes that underlie major agricultural traits in soybean.” North Central Soybean Research Program, $200,000 ($60,000 to Hyten lab).
12. Hyten Jr, D. and Graef, G. 2016-2019. "Genetic Mapping of Yield Stability," Ne Soybean Board, Associations/Foundations, $229,139.
13. Graef, G., Schapaugh, W., Hyten Jr, D., Lorenz, Aaron, Diers, B., Krishnan, H., Smith, J., Singh, A., Walker, D. 2018-2019. "Utilizing unique genetic diversity to combine elevated protein concentration with high yield in new varieties and experimental lines," United Soybean Board, $524,867 ($141,555 to UNL).
14. McHale, L., Beavis, B., Chen, P., Diers, B., Graef, G., Hudson, M., Hyten, D., Lorenz, A., Ma, J., Rainey, K., Clough, S., Scaboo, A., Schapaugh, B., Singh, A., and Wang. D. 2016-2019. “Increasing the Rate of Genetic Gain for Yield in Soybean Breeding Programs.” North Central Soybean Research Program, $2,989,646 ($703,129 to UNL).
15. Graef, G., Schapaugh, W., Hyten Jr, D., Lorenz, Aaron, Diers, B., Krishnan, H., Smith, J., Singh, A., Walker, D. 2017-2018. "Utilizing unique genetic diversity to combine elevated protein concentration with high yield in new varieties and experimental lines," United Soybean Board, $515,426 ($150,396 to UNL).
16. Graef, G., Hyten Jr, D., 2016-2017. "Genomic Selection in Soybean," Ne Soybean Board, Associations/Foundations, $96,339.00.
17. Nelson, R., Diers, B., Smith, J., Singh, A., Lorenz, A., Graef, G., Hyten, D., Schapaugh, W., Krishnan, H. 2016-2017 “Utilizing unique genetic diversity to combine elevated protein concentration with high yield in new varieties and experimental lines.” United Soybean Board, $456,772 ($79,970 to UNL).
18. Hyten Jr, D., 2016-2017. "Development of next generation sequencing applications for improving soybean," Ne Soybean Board, $200,000.
19. Hyten, D., Cregan, P., and Nelson, R. 2008-2011. “Whole Genome Analysis of the USDA Soybean Germplasm Collection and Applications for New Gene Discovery (50,000 SNPs).” United Soybean Board, $2,913,480.
20. McClean, P., Garden-Robinson, J., Johnson, C., Osorno, J., Slator, B., Kelly, J., Brick, M., Ryan, E., Thompson, H., Meyers, J., Gepts, P., Urrea, C., Grusak, M., Cregan, P., Hyten, D., Cichy, K., Porch, T., and Miklas, P. 2009-2013. “Common Bean Coordinated Agricultural Project.” USDA, AFRI. $4,000,000 ($727,356 to Beltsville).
21. Jackson, S., Schmutz, J., Rokhsar, D., McClean, P., Cregan, P., Hyten, D. 2009-2011. “A sequence map of the common bean genome for bean improvement.” USDA, AFRI. $996,554. ($60,000 to Beltsville).
22. Diers, B., Boerma, R., Hyten, D., Cregan, P., Hartman, G., Nelson, R., and Cianzio, S. 2009-2010. “Identification and Utilization of Resistance to Soybean Rust.” United Soybean Board. $572,143 ($75,000 to Beltsville).
23. Cregan, P., Hyten, D., Specht, J., and Diers, B. 2008-2011. “Nested Association Mapping to Identify Yield QTL in Diverse High Yielding Elite Soybean Lines.” United Soybean Board. $280,000 ($160,000 to Beltsville).
24. Burton, J., Boerma, R., Pantalone, V., Kenworthy, B., Shannon, G., Sleper, D., Scott, R., Cardinal, A., Cregan, P., Hyten, D., Dewey, R., Chen, P., and Orf, J. 2009-2012. “Development of Mid-Oleic, Low-Linolenic, Low-Saturated Substitutes for Partially Hydrogenated Soybean Oil.” United Soybean Board. ($180,000 to Beltsville).

25. Pantalone, V.R., Spencer, M., Landau-Ellis, D., and Hyten, D. 2001-2002. “Rapid Molecular Marker Assisted Development of University of Tennessee Roundup Ready TN96-58 Soybean.” Tennessee Soybean Promotion Board. $31,000.

26. Pantalone, V., and Hyten, D. 2001-2005. “Enhanced Soybean Protein Concentration and Quality: QTL Discovery and Marker Assisted Selection.” United Soybean Board. $147,394.

Donations

Hyten Jr, D., 2024. "Plant Science Symposium," Corteva, $6,000.00.

Hyten Jr, D., 2023. "Plant Science Symposium," Corteva, $6,000.00.

Hyten Jr, D., 2022. "Plant Science Symposium," Corteva, $6,000.00.

Hyten Jr, D., 2019. "Plant Breeding Symposium," Corteva, $6,000.00.

Hyten Jr, D., 2018. "Plant Breeding Symposium," DuPont Pioneer, $6,000.00.

Hyten Jr, D., 2017. "Plant Breeding Symposium," DuPont Pioneer, $6,000.00.

Hyten Jr, D., 2016. "Plant Breeding Symposium," DuPont Pioneer, $6,000.00.

Invited Oral Presentations

1. “Signatures of Selection Associated with GxE Loci in Soybean Breeding,” American Society of Plant Biologists Plant Biology Conference, Milwaukee, WI. 2025.

2. “Signatures of Selection Associated with GxE Loci in Soybean Breeding,” UNL Animal Breeding and Genetics Seminar, Lincoln, NE, 2025.

3. “Signatures of Selection Associated with GxE Loci in Soybean Breeding,” The Plant and Animal Genome 32 Conference San Diego, CA. 2025.

4. “Variable Selection Patterns Associated with Constitutive and GxE Effects for Soybean Grain Yield,” Spring 2024 Department of Horticulture and Department of Plant, Soil, and Microbial Sciences joint seminar series, Michigan State University, East Lansing, MI 2024.

5. “Variable Selection Patterns Associated with Constitutive and GxE Effects for Soybean Grain Yield,” The International Conference of the Genetic Society of Thailand 2024, Phitsanulok, Thailand 2024.

6. “The Genetics of Yield Stability in a Local Breeding Program,” Department of Agronomy Seminar, Kasetsart University, Kamphaeng Saen, Thailand 2024.

7. “Developing and Applying Genomic Tools for Soybean Improvement,” Faculty of Science Seminar, Nakhon Phanom University, Muang, Thailand 2024.

8. “Mapping and Selection for Yield Stability in Soybean,” World Soybean Research Conference, Vienna, Austria, 2023.

9. “Mapping and Selection for Yield Stability in Soybean,” Elmer G. Heyne Distinguished Crop Science Lecturer, Kansas State University, Manhattan, KS 2023.

10. “Mapping and Selection for Yield Stability in Soybean,” Iowa State University’s Plant Breeding Seminar Series, Ames, IA 2023.

11. “How Low Can You Go? Reduce Breeding Costs with an Optimized Genotyping and Analysis Strategy,” Genomeweb webinar series Online Webinar, 2020

12. "Developing and Applying Genomic Tools for Soybean Improvement," UNL Agronomy & Horticulture seminar series, Lincoln, NE, 2020.

13. “Generating High Density, Low-Cost Genotype Data in Soybean with Next Generation Genotyping (NGG),” The Plant and Animal Genome XXVIII Conference San Diego, CA. 2020.
14. "Exploring Yield Stability in Soybean." 6th International Symposium on Genomics and Crop Genetic Improvement – Molecular Breeding, Huazhong Agricultural University and Molecular Breeding a Springer journal, Wuhan, China, 2019.
15. "Integrating targeted and skim sequencing into the molecular breeding toolbox." University of Hawaii at Manoa Seminar, Honolulu, HI, 2019.
16. "The mysteries of bean diversity and how we can unlock this diversity to improve human health." Weekly NFHC sponsored meetings, Nebraska Food for Health Center, Lincoln, NE, 2019.
17. “Soybean Breeding – New Tools, Challenges and Future.” VIII Brazilian Soybean Congress, Goiânia, Goiás State, Brazil, 2018. (Plenary Speaker)
18. “Development of High-throughput SNP Genotyping Technologies for Soybean.” University of Guelph Plant Agriculture Seminar, Guelph, Canada, 2018.
19. "Development of Sequencing for Genotyping within Soybean Breeding Programs." The Plant & Animal Genome XXVI conference, San Diego, CA, 2018.
20. "Enhancing Soybean Improvement through genomics." Animal Breeding and Genetics seminar, UNL Dept. of Animal Science, Lincoln, 2017.
21. "Genomic Sequencing and Accelerated Plant Breeding." Nebraska Independent Crop Consultant Association Spring Meeting, NICCA, Lincoln, NE, 2017.
22. "Genomics for soybean improvement at UNL." UNL Plant Science Retreat, PSI, Nebraska City, NE, 2016.
23. "Development of genomic tools for soybean improvement." Oil Crops Research Institute, Chinese Academy of Agricultural Sciences, Wuhan, China, 2016.
24. "Development of genomic tools for soybean improvement." Innovations in Crop Improvement to Meet the Global Grand Challenges of the 21st Century Workshop, Huazhong Agricultural University, Wuhan, China, 2016.
25. "Improving Nebraska soybean yield." Ag Builders of Nebraska, Lincoln, NE, 2016.
26. "Future Plans for Genomics/Genetics at the Institute of Agriculture and Natural Resources," Nebraska Soybean Board Quarterly Meeting, Lincoln, NE. 2015.
27. "Future Plans for Genomics/Genetics at the Institute of Agriculture and Natural Resources," Soybean Researcher Symposium: Linking Together Soybean Researchers, Nebraska Soybean Board, Lincoln, NE. 2015.
28. “The next generation of breeder’s tools available within DuPont Pioneer’s Accelerated Yield Technology (AYTTM) system” National Association of Plant Breeders/Plant Breeding Coordination Committee conference. Indianapolis, IN, 2012.
29. “The soybean HapMap Project.” University of Minnesota seminar series, Minneapolis, MN, 2010.
30. “The soybean HapMap project.” 57th Brazilian Congress of Genetics. Guarujá, Brazil, 2010.
31. “SNP marker discovery, development and mapping in Phaseolus vulgaris.” 57th Brazilian Congress of Genetics. Guarujá, Brazil, 2010.

32. “The soybean HapMap phase I.” Biennial Conference on Molecular and Cellular Biology of the Soybean session entitled “Whole Genome Analysis: Focus on Technology” Durham, NC, 2010.
33. “SNP marker applications.” Soybean genomics strategic planning workshop, St. Louis, MO, 2010.
34. “A whole genome SNP panel resource for soybeans.” AEIC 2010 spring meeting session entitled “The development of biotech products in the genomics era”, Gastonia, NC, 2010.
35. “High-throughput SNP analysis and the creation of a HapMap in soybean.” Seminar at Frostburg State University, Frostburg, MD, 2010.
36. “High-throughput SNP analysis in soybean.” University of Nebraska, Biotechnology/Life Sciences seminar series, Lincoln, NE, 2010.
37. “High-throughput SNP analysis in soybean.” Annual Meeting of the American Society of Agronomy in the Symposium session entitled “Footprints of Genetic Progress: Looking Forward Using Genomics, Biotechnology, and Bioinformatics to Enhance Gains” Pittsburgh, PA, 2009.
38. “Genomics for crop improvement.” Beltsville Area’s Research Leaders’ Conference, Shepherdstown, WV, 2009.
39. “Creation of a 50,000 SNP Infinium assay and two high resolution maps for soybean.” World Soybean Research Conference VIII, Beijing, China, 2009.
40. “Discovering the power of soybean genomics.” 100th AOCS Annual Meeting & Expo hot topic session entitled “How Genomics & Biotechnology will Revolutionize Soybean Productivity & Quality.” Orlando, FL, 2009.
41. “The accelerating pace of soybean genomics for marker development, quantitative trait loci discovery, and germplasm characterization.” Syngenta Seeds, Inc. in Research Triangle Park, NC, 2009.
42. “NAM Project & Soy HapMap.” Soybean Breeders Workshop. St. Louis, MO, 2009.
43. “The Accelerating Pace of Soybean Genomics for Marker Development, Quantitative Trait Loci Discovery, and Germplasm Characterization.” The Plant and Animal Genome Conference XVII in the workshop entitled “Soybean Genomics”. San Diego, CA, 2009.
44. “Development of Genomic Tools for High-throughput QTL Discovery and Germplasm Characterization for Soybean Improvement.” Iowa State University Workshop on Translational Biology, Ames, IA, 2008.
45. “Discovering the Power of Soybean Genomics.” USB Production Committee’s workshop entitled, “Probing the Needs of the Global Soybean Industry.” St. Louis, MO, 2008.
46. “Defining the Signatures of Positive Selection in the Soybean Genome as Targets for Mining the USDA Germplasm Collection for Crop Improvement.” Biennial Conference on Molecular and Cellular Biology of the Soybean, Indianapolis, IN, 2008.
47. “An Assessment of Genome-wide Linkage Disequilibrium in Soybean.” The Plant and Animal Genome Conference XV in the workshop entitled “Legumes”. San Diego, CA, 2007.
48. “Progress Toward Creation a Universal 1,536 SNP Array for Soybean QTL Discovery.” The Plant and Animal Genome XV in the Illumina sponsored workshop entitled “Microarray Approaches to Analysis of Plant and Animal Genomes”. San Diego, CA, 2007.
49. “An Initial Assessment of Genome-wide Linkage Disequilibrium in Soybean.” The Annual Meeting of the American Society of Agronomy in the Symposium session entitled “Closing the Circle on Plant Genetic Resources Conservation and Utilization: II” Indianapolis, IN, 2006.

50. “The Structure of Soybean Genetic Diversity.” Molecular & Cellular Biology of the Soybean Conference in the plenary session entitled “Molecular Breeding” held in Lincoln, NE, 2006.
51. “Defining Linkage Disequilibrium – Is Associated Analysis Possible?” Soybean Breeders/Agronomists/Plant Physiologists Workshop. St. Louis, MO, 2006.
52. “Highly Variable Patterns of Linkage Disequilibrium in Multiple Soybean Populations.” The Annual Meeting of the American Society of Agronomy in the Symposium session entitled “SNP Marker Symposium-Discovery, Development, Mapping, Utilization” Salt Lake City, UT, 2005.
53. “Genetic Regions Governing Soybean Protein and Oil.” The 93rd AOCS Annual Meeting & Expo. Montreal, Quebec, Canada, 2002.

SERVICE

University Service

Chair, Agronomy and Horticulture Graduate Committee. (January 2023 – Present).

Faculty Advisor, Plant Breeding Symposium. (September 9, 2015 - Present).

Committee Member, PSI Graduate committee. (2024 – Present)

Committee Member, Coyne Lectureship Committee. (April 26, 2016 – Present).

Committee Member, Promotion and Tenure Committee. (July 6, 2022 – 2025).

Committee Member, Agronomy and Horticulture Safety Committee. (June 28, 2016 - 2024).

Organizing Committee Member and session chair, Agriculture & Health Summit. (March 25, 2020-October 13, 2021).

Committee Member, Biotech Faculty Advisory Committee. (May 10, 2016 - 2020).

Committee Member/Ad hoc member, Agronomy and Horticulture Graduate Committee. (August 21, 2017 – December 31, 2020).

Committee Member, Department Peer Evaluation Team. (2019 and 2020).

Committee Member/Chair elect/Chair, Institute of Agriculture and Natural Resources - Agricultural Research Division Advisory Council. (August 22, 2016 - 2019).

Grant Proposal Reviewer, ARD Hatch Multistate funding. (April 5, 2018 – May 17, 2018)

Committee Member, IANR Committee on Teams. (February 2, 2017 - May 31, 2017).

Workshop Co-organizer, UNL Soft Skills Workshop for PSI Postdocs. (January 26, 2017 – May 25, 2017).

Organization Committee Member, 2017 Nebraska EPSCoR Plant Science Conference. (February 22, 2017 – April 7, 2017).

Research Teamwork writing team facilitator, Agronomy and Horticulture academic program review writing team. (January 20, 2017 – October 6, 2017).

Committee Member, Search Committee for Plant Metabolic Biochemist, Plant Quantitative Statistical Genomicist, and Agronomy and Horticulture Department Chair. (2016 and 2018).

Committee Member, Agronomy and Horticulture Faculty Advisory Committee. (June 27, 2016 - 2018).

Committee Member, Faculty Senate Ad Hoc Committee on Academic Honesty. (June 16, 2016 - 2017).

Committee Member, Ad hoc committee to review promotion and tenure committee structure. (April 15, 2016 - June 1, 2016).

Grant Proposal Reviewer, Internal, ARD. (February 19, 2016 - March 31, 2016).

Guest Speaker, Academic Planning Committee. (December 9, 2015).

Professional Service and Synergistic Activities

Co-program chair, “Soybean Genomics” session at the Plant and Animal Genome Conference (2022-present).

Associate Editor, Molecular Breeding. Springer Netherlands. (2018 – Present).

Reviewer for USDA-ARS peer review 301C panel. (2023)

Reviewer, Ad Hoc Reviewer, NSF, Washington, DC. (2022).

Associate Editor, The Plant Genome. Crop Science Society of America, Madison, WI. (2016 - 2021).

Associate Editor, International Journal of Molecular Sciences. MDPI, Basel, Switzerland. (2019-2021)

Guest Presenter, Soybean Science Institute which educates middle school science teachers from Nebraska on soybean science to help them develop curriculums for their classes. (2016 – 2019).

Session Chair, “Abiotic Stress Session” at the 17th Biennial Conference on the Molecular and Cellular Biology of the Soybean. (2018).

Grant Panel Manager, Grant Proposal Panel, NIFA, Washington, DC. (2017).

Reviewer, Grant Proposal Panel, NIFA, Washington, DC. (2016).

Reviewer, Ad Hoc Reviewer, NIFA, Washington, DC. (2015).

Reviewer, Grant Proposal Panel, NIFA, Washington, DC. (2015).

Associate Editor, Crop Science. Crop Science Society of America, Madison, WI. (2008 - 2011).

Chair, 2010, Soybean Genetics Committee. (February 28, 2008 - February 28, 2010).

Co-program chair, “Legumes” session at the Plant and Animal Genome Conference (2009-2010).

Co-chair, “Whole Genome Analysis: Focus on Technology” session at the 13th Biennial Molecular & Cellular Biology of the Soybean Conference (2010).

Co-chair, A symposium at the 2009 World Soybean Research Conference VIII, Beijing, China (2009).

Invited to be a guest speaker and to discuss thoughts on mining native traits to the Pioneer Soybean Breeding Group after the conclusion of the 13th Biennial Molecular & Cellular Biology of the Soybean Conference, (2010).

Consultant to Syngenta Seeds, Inc. during two workshops focused on advancing plant breeding and crop genetic improvement within Syngenta Seeds, (2007 and 2009).

Invited to Dow AgroScience, to consult on what soybean genomic resources are available, gave a presentation on current genomic resources available, and if any private/public collaborations are possible in the future, (2008).

Consulted with BASF Plant Science, L.L.C., to discuss what soybean genomic resources are available and if any collaborations are possible in the future (2009).

Participated at the Soybean Genomics Research Strategic Planning Meeting to strategically plan for the attainment of measurable goals for the next half-decade for soybean genomics. In addition, I chaired a session at the meeting entitled “Genome Resequencing” (2007).

Consulted with the United Soybean Board Production Committee during their “Probing the Needs of the Global Soybean Industry” workshop on what research should be performed in the future for soybean (2008).

Participated in the iPlant Grand Challenge workshop entitled “Plant adaptation”. (2008).

Manuscript reviewer for Crop Science, Genetics, Theoretical and Applied Genetics, BMC Genomics, Journal of Heredity, Canadian Journal of Plant Science, Plant Genome, Plant Science, and Molecular Breeding.