

Dr. David L. Hyten Jr.

University of Nebraska-Lincoln
Agronomy & Horticulture
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Education

Ph D, University of Maryland, 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, 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, 1995-1999

- B.A. Microbiology
- Minor Chemistry

Academic, Government, and Professional Positions

Academic

Associate Department Chair, University of Nebraska – Lincoln. (January 1, 2019 – present)

Supports the Department Head by contributing to the annual faculty evaluation, co-develop strategic visioning and priorities, supervise staff members, advise on resource allocations including the development of a graduate student fellowship, lead an ad hoc graduate working group committee to enhance the department's graduate program and served as liaison to the graduate program.

- Drafted and obtained faculty approval of faculty mentoring guidelines for new and not fully promoted faculty.

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

Leads a research lab focused on taking basic genetic and genomic discoveries in soybean and translating those discoveries into applied methods that can be used for the real-world improvement of soybean varieties. This research focuses specifically on improving agronomically important traits such as yield, drought tolerance and response to stress. Translate basic discoveries into applied breeding methods through developing better methods, tools, and genomic breeding strategies for improving soybean breeding programs. Responsible for teaching two graduate level courses focused on molecular plant breeding and crop genomics. Mentors graduate students to help them further develop their professional knowledge, skills, and abilities in crop research.

- Developed improved methods for using next generation sequencing to detect markers in soybean lines

- Developed and teach two graduate courses at UNL

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

Professorship given based upon academic promise in contributing to the teaching and research programs in plant genetics consistent with the strategic plan of the Department of Agronomy and Horticulture.

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

Work collaboratively with interdisciplinary research teams to gain a better understanding of biological plant systems to develop applied technologies for the improvement of crop productivity.

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

Work with a multi-campus, interdisciplinary research team to understand the effects of common bean and soybean genomic variation on the health of the human microbiome.

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

Worked to determine how genetic bottlenecks within the history of soybean domestication and modern improvement has affected genetic diversity, allele frequencies, and linkage disequilibrium in the soybean genome.

- Published data that refuted the widely held assumption that the low sequence diversity in N. Am. soybean cultivars was the result of a narrow genetic base and intensive plant breeding.
- Characterized the structure of linkage disequilibrium (LD) in soybean by sequence analysis of three large genomic regions in multiple soybean populations which gave estimates of how many markers are needed for association analysis and to create a soybean HapMap in cultivated soybean.
- Designed and managed the SNP database at Beltsville, MD using FileMaker Pro.

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

Explored how genetic variation affected key agronomic traits within soybean. Successfully set-up the University of Tennessee soybean breeding program marker assisted selection lab with high-throughput genotyping capabilities for gene mapping and marker assisted selection. This lab gave the breeding program the capability to release a conventional line of soybean followed quickly with a Roundup Ready® backcross version of the same conventional line. Responsible for working in the soybean breeding program performing field work which included planting, plot maintenance, plant pathogen quantification in the field through SDS field scoring, data collection, harvesting, soybean pollination, and single seed descent.

- Co-principal investigator on two research grants for enhanced soybean protein concentration and quality and for rapid molecular marker-assisted development of University of Tennessee Roundup Ready® TN96-58 soybean.

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

Managed the soybean marker-assisted selection lab at Southern Illinois University. Regularly worked in the soybean breeding program performing field work which included planting, plot maintenance, data collection, harvesting, soybean pollination, single seed descent, plant pathogen detection through SDS scoring in the field, SCN screening in greenhouse, and greenhouse management for DNA extraction of samples for marker-assisted selection program. Supervised two research technicians and two to six student workers each semester and trained

undergraduate, graduate, postdoctoral, and visiting scientists in marker-assisted selection protocols.

- Developed protocols for the marker-assisted selection lab including a novel DNA extraction method that produced high quality DNA that could be used in marker-assisted selection.

Government

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

Performed novel research to discover, develop, and to utilize single nucleotide polymorphism markers for the improvement of soybean. Demonstrated how genetic bottlenecks and selection have affected genetic diversity, allele frequencies, and linkage disequilibrium in soybean.

- Led the development of a soybean 50,000 SNP Infinium chip.
- Led the project to genotype the USDA soybean germplasm collection with the soybean 50k SNP Infinium chip.
- Applied high-throughput methods for sequencing and genotyping soybean, wheat, and common bean DNA for the discovery of single nucleotide polymorphisms (SNPs), the creation of high density genetic maps, quantitative trait loci (QTL) discovery, and haplotype map (HapMap) analysis.

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

Performed novel research to discover, develop, and utilize single nucleotide polymorphism markers for the improvement of soybean. Responsible for developing new technologies for high density genotyping and gene discovery within soybean.

- The first researcher in the public sector to develop and implement the high-throughput genotyping technology known as the GoldenGate assay in soybean.
- The first researcher to utilize the GoldenGate assay for bulked segregant analysis (BSA) by using it to map the soybean rust resistant gene known as Rpp3.
- Phenotyped the plant pathogen *Phakopsora pachyrhizi* in the biosafety level-3 plant pathogen containment facility at Ft. Detrick, MD.
- The first researcher to develop high-throughput SNP discovery methods in soybean using next generation sequencing.
- Responsible for developing and maintaining a *G. soja* x *G. max* mapping population consisting of 1,000 recombinant inbred lines. The mapping population has been used to create a high quality, high density genetic map that was utilized to help assemble the soybean draft genome sequence.

Professional

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

Lead the Technology Development and Deployment Unit within the Global Marker Technology Division. The Technology Development and Deployment Unit is a multidisciplinary unit responsible for scouting, discovering, developing, and globally deploying new genotyping technology which significantly reduces genotyping costs, increases data quality, reduces time to obtain genotyping data, and/or provides new capabilities for customers of the Global Marker Technology Division. The unit focused on new and novel technologies within the areas of single nucleotide polymorphism genotyping, real time PCR, digital PCR, next generation resequencing, liquid handling, automation, and DNA extraction.

- Program leader of a multimillion dollar, multidisciplinary scientific research program with the goal of developing the next generation genotyping platform that will be deployed globally for the Global Marker Technology Division.
- Supervised the development of a process improvement that had an estimated net present value in excess of \$1.5 million over five years.
- Supervised a project that created a new lab information management system for production genotyping.
- Successfully negotiated multi-million dollar agreement with external technology provider to jointly develop new genotyping technology.
- Member of the Global Marker Technology Leadership Team
- Member of the Global Marker Technology R&D Steering Team

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

Led the Soybean and Wheat Genomics Development Team which is part of the Marker Development Unit within the Global Marker Technology Development Division. The team provided innovative genomic solutions that enhanced DuPont Pioneer molecular breeding strategies for the production of high-performance cultivars. Genomic solutions developed by this team under my leadership included production marker development for soybean and wheat, gene discovery for agronomic traits, biotic and abiotic stresses through QTL mapping and fine mapping. Team extensively applied next generation resequencing for the discovery and characterization of single nucleotide polymorphisms within soybean and wheat.

- Built and led a multidisciplinary team in a next generation sequencing project to characterize the genetic diversity within DuPont Pioneer soybean germplasm.
- Built and led a multidisciplinary team, which developed and deployed a new production genotyping protocol. The new method reduced breeders' genotyping cost by 72%.
- Nominated into DuPont Pioneer's Advanced Leadership Development Program.
- Actively led or member of nine multidisciplinary teams composed of product development scientists, legal, finance, project management, applied biotechnology scientists, information technology scientists and support staff, and bioinformatics scientists.

Professional Memberships

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

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

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

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

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

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

TEACHING

Teaching Experience

University of Nebraska-Lincoln

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

AGRO919, Advanced Crop Genetics and Genomics, instructor, 2019-present.

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

Chelsie Metzler, Online Masters (committee chair), Agronomy & Horticulture, 2018-present.

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

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

Madison Hale, Online Masters (committee chair), Agronomy & Horticulture, 2017-present.

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

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

Committee member

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

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

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

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

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

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

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

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

RESEARCH

Published Intellectual Contributions

66 peer reviewed publications and 1 book chapter (h-index=42, i10-index=58, total citations 10,359, verified: Google Scholar, March 11, 2020)

Book Chapter

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

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.

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.

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. *Genetics Society of America G3*. Song, Q., Hyten, D.L., Jia, G., Quigley, C.V., Fickus, E.W., Nelson, R.L., and Cregan, P.B. 2015. Fingerprinting soybean germplasm and its utility in genomic research. *G3: Genes|Genomes|Genetics* 8(10), 3367-3375.

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.

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.

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.

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.

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.

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.

Hyten, D.L. and Lee, D. J. (2016). *Plant Genetic Mapping Techniques*. eLS. 1-8.

- 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.
- 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.
- 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.
- 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.
- 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.
- 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.
- 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.
- 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).
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- 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.
- 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.
- 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.
- 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.
- 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.
- 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.
- 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.
- 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).
- 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.
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- McHale, L.K., Haun, W.J., Xu, W.W., Bhaskar, P.B., Anderson, J.E., **Hyten, D.L.**, Gerhardt, D.J., Jeddelloh, 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.
- 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.
- 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.
- 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.
- 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.
- 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.
- 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.

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- 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.
- 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.
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- 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.
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- 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.
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- 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.
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- 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.
- 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.
- 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.
- 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.
- 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.
- 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.
- 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.
- 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.
- 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 (7) and Patent Applications (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.
- Daines B., Hyten D., Schneider N., Woodward J.* (2018). *U.S. Patent No 9,988,693*. Washington, DC: U.S. Patent and Trademark Office.
- Daines B., Hyten D., Schneider N., Woodward J.* (2018). *U.S. Patent No 9,957,577*. Washington, DC: U.S. Patent and Trademark Office.
- Daines B., Hyten D., Schneider N., Woodward J.* (2018). *U.S. Patent No 9,957,578*. Washington, DC: U.S. Patent and Trademark Office.
- Hyten, D.L., Kalvig, A.B., Kuhlman, L.C., Kyle, D., Liu, J., Shendelman, J.M., Thompson, J.A., Woodward, J., Yang, M.* (2018). *U.S. Patent No 9,894,857*. Washington, DC: U.S. Patent and Trademark Office.
- 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.
- Daines B., Hyten D., Schneider N., Woodward J.* (2016). *U.S. Patent No 9,347,105*. Washington, DC: U.S. Patent and Trademark Office.
- Chaky J., Fabrizio M., Hyten D., Krashenninnik N., Spear J., Woodward J., Xiong Y.* (2012). *U.S. Patent Application No CA2834153 A1*, Washington, DC: U.S. Patent and Trademark Office.
- 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.
- 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.

*Author order determined alphabetically of last name

Research Grants and Donations

Grants

- Hyten Jr, D., 2019-2020, "Whole Genome Sequencing of the USDA Soybean Germplasm Collection and Applications for New Gene Discovery." United Soybean Board, \$240,412.
- Hyten Jr, D. and Graef, G. 2019-2020. "Screening for stem borer resistance," Ne Soybean Board, \$55,332.
- Hyten Jr, D. and Graef, G. 2019-2020. "Increasing yield and seed composition stability through diverse germplasm and genomic selection," Ne Soybean Board, \$229,139.
- 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. 2019-2020. "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, \$866,514 (\$121,887 to Hyten lab).
- 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. 2019-2021, "Increasing genetic diversity, yield, and protein of US commercial soybean germplasm." United Soybean Board, \$1,429,751 (\$58,280 to Hyten lab).

- 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 UNL).
- Hyten Jr, D. and Graef, G. 2016-2019. "Genetic Mapping of Yield Stability," Ne Soybean Board, Associations/Foundations, \$229,139.
- 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).
- 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).
- 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).
- Graef, G., Hyten Jr, D., 2016-2017. "Genomic Selection in Soybean," Ne Soybean Board, Associations/Foundations, \$96,339.00.
- 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).
- Hyten Jr, D., 2016-2017. "Development of next generation sequencing applications for improving soybean," Ne Soybean Board, \$200,000.
- 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.
- McClellan, 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).
- Jackson, S., Schmutz, J., Rokhsar, D., McClellan, 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).
- 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).
- 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).
- 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.

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.

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

Donation

Hyten Jr, D., 2019-2020. "Plant Breeding Symposium," Corteva, \$6,000.00.

Hyten Jr, D., 2018-2019. "Plant Breeding Symposium," DuPont Pioneer, \$6,000.00.

Hyten Jr, D., 2017-2018. "Plant Breeding Symposium," DuPont Pioneer, \$6,000.00.

Hyten Jr, D., 2016-2017. "Plant Breeding Symposium," DuPont Pioneer, \$6,000.00.

Invited Oral Presentations

"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.

"Integrating targeted and skim sequencing into the molecular breeding toolbox." University of Hawaii at Manoa Seminar, Honolulu, HI, 2019.

"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.

"Soybean Breeding – New Tools, Challenges and Future." VIII Brazilian Soybean Congress, Goiânia, Goiás State, Brazil, 2018. (Plenary Speaker)

"Development of High-throughput SNP Genotyping Technologies for Soybean." University of Guelph Plant Agriculture Seminar, Guelph, Canada, 2018.

"Development of Sequencing for Genotyping within Soybean Breeding Programs." The Plant & Animal Genome XXVI conference, San Diego, CA, 2018.

"Enhancing Soybean Improvement through genomics." Animal Breeding and Genetics seminar, UNL Dept. of Animal Science, Lincoln, 2017.

"Genomic Sequencing and Accelerated Plant Breeding." Nebraska Independent Crop Consultant Association Spring Meeting, NICCA, Lincoln, NE, 2017.

"Genomics for soybean improvement at UNL." UNL Plant Science Retreat, PSI, Nebraska City, NE, 2016.

"Development of genomic tools for soybean improvement." Oil Crops Research Institute, Chinese Academy of Agricultural Sciences, Wuhan, China, 2016.

"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.

"Improving Nebraska soybean yield." Ag Builders of Nebraska, Lincoln, NE, 2016.

"Future Plans for Genomics/Genetics at the Institute of Agriculture and Natural Resources," Nebraska Soybean Board Quarterly Meeting, Lincoln, NE. 2015.

"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.

“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.

“The soybean HapMap Project.” University of Minnesota seminar series, Minneapolis, MN, 2010.

“The soybean HapMap project.” 57th Brazilian Congress of Genetics. Guarujá, Brazil, 2010.

“SNP marker discovery, development and mapping in Phaseolus vulgaris.” 57th Brazilian Congress of Genetics. Guarujá, Brazil, 2010.

“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.

“SNP marker applications.” Soybean genomics strategic planning workshop, St. Louis, MO, 2010.

“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.

“High-throughput SNP analysis and the creation of a HapMap in soybean.” Seminar at Frostburg State University, Frostburg, MD, 2010.

“High-throughput SNP analysis in soybean.” University of Nebraska, Biotechnology/Life Sciences seminar series, Lincoln, NE, 2010.

“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.

“Genomics for crop improvement.” Beltsville Area’s Research Leaders’ Conference, Shepherdstown, WV, 2009.

“Creation of a 50,000 SNP Infinium assay and two high resolution maps for soybean.” World Soybean Research Conference VIII, Beijing, China, 2009.

“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.

“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.

“NAM Project & Soy HapMap.” Soybean Breeders Workshop. St. Louis, MO, 2009.

“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.

“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.

“Discovering the Power of Soybean Genomics.” USB Production Committee’s workshop entitled, “Probing the Needs of the Global Soybean Industry.” St. Louis, MO, 2008.

“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.

- “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.
- “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.
- “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.
- “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.
- “Defining Linkage Disequilibrium – Is Associated Analysis Possible?” Soybean Breeders/Agronomists/Plant Physiologists Workshop. St. Louis, MO, 2006.
- “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.
- “Genetic Regions Governing Soybean Protein and Oil.” The 93rd AOCs Annual Meeting & Expo. Montreal, Quebec, Canada, 2002.

SERVICE

University Service

- Faculty Advisor, Plant Breeding Symposium. (September 9, 2015 - Present).
- Committee Member/Ad hoc member, Agronomy and Horticulture Graduate Committee. (August 21, 2017 – Present).
- Committee Member, Biotech Faculty Advisory Committee. (May 10, 2016 - Present).
- Committee Member, Coyne Lectureship Committee. (April 26, 2016 – Present).
- Committee Member/Chair elect/Chair, ARD Advisory Council. (August 22, 2016 - 2019).
- Committee Member, Agronomy and Horticulture Safety Committee. (June 28, 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 APR 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

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

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

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

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 – Present).

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).

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.