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A U.S. citizen
I am not a Veteran

Educational and Professional Preparation

Brigham Young University - Botany/Biotechnology - B.S. 1995

Genetics credits: Gen & Cell Biol 1 (4 cr.)

Plant Breeding (3 cr.)

University of Idaho - Plant Science - M.S. 1997

Genetics credits: Plant Mol. Genetics (3 cr.)

Plant Breeding (3 cr.)

University of Wisconsin - Plant Breeding and Genetics - Ph.D. 2003

Genetics credits: Mol. Approaches to Crop Improvement (3 cr.)

Population and Quantitative Genetics (1 cr.)

Advanced Plant Breeding (3 cr.)

Biometric Proc-Plant Breeding (3 cr.)

Plant Genetics (3 cr.)

Selection Theory-Quant. Traits (3 cr.)

Chromosome Manipulation in Plants (2 cr.)

Professional Appointments

2003-2006	Postdoctoral Research Associate, Ecology, Evolution, and Organismal Biology, Iowa State University (100% research)
2006-2012	Assistant Professor, Plant and Wildlife Sciences Dept., BYU (50% teaching, 50% research)
2012-2017	Associate Professor, Plant and Wildlife Sciences Dept., BYU (50% teaching, 50% research)

Advances to field from my research (2016 – present)

My research discoveries of SNP discovery in cotton between the A- and D-genomes within the tetraploid nucleus have advanced our understanding plant genetics to a major extent. For example, not only has my research been highly cited, but cotton was often used an example of polyploid genome evolution to such an extent that I published an article in PLOS Genetics summarizing my findings of interactions between genomes of tetraploid cotton.

Page JT, Liechty ZS, Alexander R, Clemons K, Hulse-Kemp AM, Ashrafi H, Deynze AV, Stelly DM, Udall JA. 2016. DNA sequence evolution and homoeologous conversion in allotetraploid cotton. PLOS Genetics. 12(5):e1006012.
[doi:10.1371/journal.pgen.1006012](https://doi.org/10.1371/journal.pgen.1006012)

A second, more recent example is the publication of a review article in Plant Cell (impact factor 8.5) regarding genome assembly. The impetus of this commentary was to educate my scientific

colleagues of recent advances in genome sequence assembly. Too many poor, fragmented, and 'draft' genome assemblies were being submitted and accepted by good journals. These genome sequences are not what our discipline needs because they often are incomplete and can often cause more work repeating the genome assembly in future papers. The technology has sufficiently advanced that high-quality genomes can be routinely assembled.

Udall JA, Dawe K. 2018. Is it ordered correctly? Validating genome assemblies by optical mapping. *Plant Cell*. 30:7-14.

National and International invitations to present research findings (2012 – present)

This previous work, and my current research efforts, have led to National and International speaking invitations. Below I list only those that occurred since 2012 (while as an Assoc. Prof.)

- International Cotton Genome Initiative, 2018
- Cotton Workshop, International Plant and Animal Genome Conference, San Diego CA, 2018
- Department Seminar, University of North Texas, 2017
- MapNET 2017, Palmerston North, New Zealand
- BGI Workshop International Plant and Animal Genome Conference, San Diego CA, 2017
- University of Georgia, Plant Biology Department Seminar, 2016
- Departmental Seminar Speaker, Texas Tech University, Oct. 2015
- **Organizer**, Utah Plant Genetics Conference 2015, Aspen Grove, UT, USA
- American Society of Plant Biologists (Southern Section), Plenary Speaker, 2015
- International Plant and Animal Genome Conference, Evolution of Genome Size Workshop, CA, 2015
- Plant Genomics Congress 2013, St. Louis, MO
- International Cotton Genome Initiative Workshop, PAG 2013, San Diego, CA
- Genome Evolution, Minisymposium, Conference of ASPB 2012, Austin, TX
- Next Generation Sequencing Workshop, 2012, Temuco, Chile
- ICGI Research Conference 2012, Cary, NC
- 2nd Progress and Applications of Next-Generation Sequencing Workshop 2012, Saskatoon, Canada
- Sequence Capture/454 Sequencing Seminar 2012, University of Utah, SLC, UT, USA
- **Organizer**, Utah Plant Genetics Conference 2012, Aspen Grove, UT, USA

Strategic forward thinking to advance the field of plant genetics (using cotton as a model), and outreach to stakeholders (2008 – present)

My forward thinking is evident in my consistent, year-to-year procurement of major external funding at BYU. Those procurements were awarded to me as federal research grants from the National Science Foundation or private grants from Cotton Incorporated, Inc. (even though research was conducted outside of cotton growing areas). None of these awards would have occurred without conceptualizing and anticipating the direction of plant science and the needs of

cotton researchers for cotton improvement. Each of the projects required detailed planning, execution, and reporting.

- Cotton Inc. (Udall) Sequencing of the *G. longicalyx* genome. 1/1/2017 – 12/31/2017 (\$15,000)
Cotton Inc. (Udall) Sequencing of the *G. herbaceum* genome. 1/1/2016 – 12/31/2016 (\$30,000)
NSF MRI (Bybee, Udall, et al.) Acquisition of a PacBio Sequel Sequencer. 9/1/2016 – 8/31/2019. (\$307,723)
NSF PGRP (Udall (PI), Wendel, Ramaraj) Genomic Sequence Resources of Allotetraploid Cotton 11/15/2015 – 11/14/2018 (\$2,985,081)
NSF PGRP (Udall (PI), Ramaraj, Stark) Structural variation of diploid and polyploid plant genomes 6/1/2014 – 5/30/2018 (\$1,491,000)
USDA Forest Service (Udall). Associating Genomic Properties to Adaptive Traits in Big Sagebrush 6/1/2013 – 5/30/2018 (\$78,000)
Cotton Inc. (Udall) Cotton Inc. Fellowship. 1/1/2014 – 12/31/2016 (\$150,000)
NSF PGRP (Wendel, Paterson, and Udall) GEPR: Comparative Evolutionary Genomics of Cotton 3/1/2009 – 2/28/2014 (\$5,120,000 of which \$700,000 will come to BYU. An additional supplement of \$61,900 was awarded during 2010).
USDA SCRI (Daniels, Moore, Swanson, Ross, Fernandez, Finn Martin, Ming, Udall, Weber, Zasada) Development of a roadmap for U.S. raspberry producers that leads to improved tools for breeding programs (10/1/2011 – 9/30/2012) \$49,506
USDA Specialty Block Grant (Udall and Clement) Sequencing the genome of red raspberry. (10/1/2011 – 9/30/2012) \$51,635
NSF MRI: Acquisition of Genome Sequencer FLX system. (Udall et al.). National Science Foundation 9/1/2008 – 8/31/2011 (\$630,000, NSF; \$270,000 BYU matching)

Outreach to stakeholder groups include 1) hosting regular visits by Cotton Inc. to my lab at BYU. This allowed Cotton Inc. to assess ongoing research as well as provide my employees (students) opportunity to visit with CI representatives. 2) Regular attendance at the Cotton Breeder Tour has allowed me connect with the research needs of cotton breeders as well as receive feedback about the critical areas to address research from grower groups. At the 2017 Breeders tour in Arizona, I present my research as well as provided an overview of CottonGen to cotton breeders. 3) I serve on the ICGI steering committee for CottonGen, the database of cotton genetics. This allows me to directly assess and address the needs of stakeholders through the online material developed in research across the country (and world).

Recognition by scientific community (2012 – present)

I have received several awards and served in various capacities to the scientific community of plant genetic research.

- **2016-present**, I serve as an Associate Editor of two different peer reviewed journals 1) G3: Genes, Genomes, and Genetics and 2) Theoretical and Applied Genetics.
- **2013-2015** I was elected to serve as the Functional Genomics officer for ICGI (International Cotton Genomics Initiative),
- **2016-2018** I was elected to serve as the Bioinformatics and Comparative Genomics officer.

- **2012-present**, I am a **current** member of Genetics Society of America, American Society of Plant Biologists, and Crop Science Society of America.
- The significance of my research is reflected in the high Google Scholar Index (June 2018, see figure below).

Awards

2008 Graduate Mentoring in Research, ORCA, BYU

2013 Outstanding Faculty Researcher, College of Life Science, Brigham Young University

2014 Cotton Biotechnology Award for Outstanding Contribution to Cotton Genomics Research, International Cotton Genomics Initiative

Professional Service (2009 – present)

Advisory Committee (2017), PGRP Grant, Univ. of Texas, Jeff Chen, PI

NSF Plant Genome Panelist (2x), NSF Post-doc Fellowship Panelist (3x, 2016-2018), USDA-ARS Genomics of Feedstocks Panelist

Organizer of the Utah Plant Genetics Conference 2012, 2015

Ad hoc reviewer NSF MRI and PGRP 2009, 2010, 2011, 2015, 2016

International Cotton Genomics Initiative Steering Committee (2012-2015) - Functional Genomics

Numerous invitations to review international proposals and Ph.D. dissertations

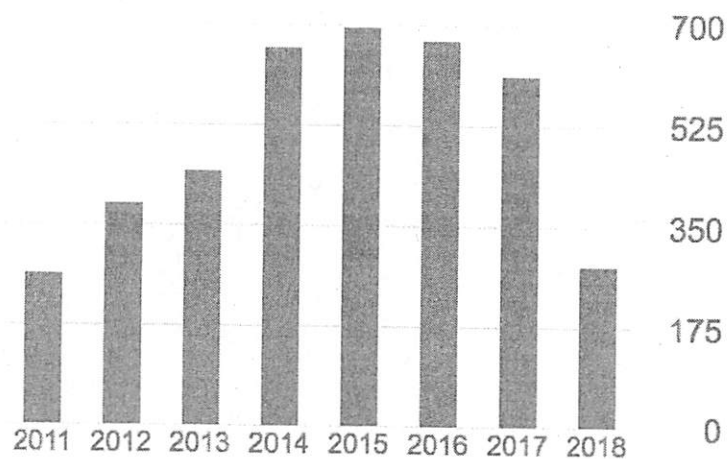
Journal Reviewer (and number of reviewed articles, 2012-present)

(2018) BMC Genetics, Molecular Plant, Theoretical and Applied Genetics

(2017) BMC Genomics, G3, MPE, Nature Genetics, PLOS ONE, Scientific Reports (2), Theoretical and Applied Genetics (2), Plant Cell, The Plant Journal

(2016) G3, Mol. Breeding, Nature Genetics, New Physiologist, Plant Cell, Plant Phys., PLOS One, Scientific Reports, TAG, The Plant Genome, The Plant Journal (2015) DNA Research, G3, Genome Biology, Journal of Heredity, Molecular Biology and Evolution, Molecular Genetics and Genomics, Nature Genetics, Plant Physiology, Planta, PLOS ONE, Theoretical and Applied Genetics, Trends in Plant Science (2014) Nature Genetics, TAG (2013) Nature Genetics, Nature Communications, Plant and Cell Biology, BMC Plant Biology (2 papers), Genome Biology and Evolution, Nucleic Acids Research, PLOS Genetics, PLOS ONE (2), Theoretical and Applied Genetics (2012) Theoretical and Applied Genetics, BMC Genomics (2), Molecular Ecology Resources, Bioinformatics, The Plant Journal, Crop Science, G3:Gene|Genetics|Genomes (3), PLoS ONE, Functional and Integrative Genomics

	All	Since 2013
Citations	4858	3362
h-index	38	33
i10-index	62	56



Complete list of publications

(authors in *italics* under my membership and direction)
(my name is in bold)

- Wang M, Tu L, *Yuan D*, Zhu D, Shen C, Li J, Liu F, Pei L, Wang P, Zhao G, Ye Z, Huang H, Yan F, Zhang L, Zhu L, Jin Z, Yang X, Min L, Li G, Chen L, Zheng H, *Lindsey K*, Lin Z, **Udall JA**, Zhang X. (In Review). Reference genome sequences of two cultivated cotton species provide a rational approach to genomics-based fiber improvement. Submitted. *Nature Genetics*.
- Udall JA**, Dawe K. 2018. Is it ordered correctly? Validating genome assemblies by optical mapping. *Plant Cell*. 30:7-14.
- Osorio CE, del Canto GA, Lichtin NV, Rupayán AN, **Udall JA**, Salvo-Garrido H, Maureira-Butler IJ. 2018. Development and characterization of InDel markers for *Lupinus luteus* L. (Fabaceae) and cross-species amplification in other Lupin species *Electronic Journal of Biotechnology* 31:44-47.
- C.E. Grover, M.A. Arick, J.L. Conover, A. Thrash, G. Hu, W.S. Sanders, C.-Y. Hsu, R.Z. Naqvi, M. Farooq, X. Li, L. Gong, J. Mudge, *T. Ramaraj*, **J.A. Udall**, D.G. Peterson, J.F. Wendel. 2017. Comparative Genomics of an Unusual Biogeographic Disjunction in the Cotton Tribe (Gossypieae) Yields Insights into Genome Downsizing. *Genome Biology and Evolution* 9:3328-3344

- Hinze L, Hulse-Kemp AM, Wilson LW, Zhu Q, Llewellyn DJ, Taylor JM, Spriggs A, Fang DD, Ulloa M, Burke J, Gilband M, Lacape J, Van Deynze A, Udall JA, Scheffler JA. 2017. Diversity analysis of cotton (*Gossypium hirsutum* L.) germplasm using the CottonSNP63K Array. *BMC Plant Biology* 17:37
- Reddy U, Kimmakayala P, Abburi VL, Reddy CM, Saminathan T, Percy RG, Yu JZ, Frelichowski J, Udall JA, Page JT, et al. 2017. Genome-wide divergence, haplotype distribution and population demographic histories for *Gossypium hirsutum* and *Gossypium barbadense* as revealed by genome-anchored SNPs. *Scientific Reports*. 7:41285. <website>
- Niederhuth CE, Bewick AJ, Lexiang Ji MA, Kim KD, Qing Li NR, Rambani A, Burke JM, Udall JA, Chiedozi Egesi JS, Grimwood J, et al. 2016. Widespread natural variation of DNA methylation within angiosperms. *Genome Biology* 17:194. <website> doi:10.1186/s13059-016-1059-0
- Renny-Byfield S, Page JT, Udall JA, Sanders WS, Peterson DG, Arick MA, Grover CE, Wendel JF. 2016. Independent domestication of two Old World cotton species. *Genome Biol. Evol.* 8(7):1940-1947. <website> doi:10.1093/gbe/evw129
- Chaney L, Sharp AR, Evans CR, Udall JA. 2016. Genome Mapping in Plant Comparative Genomics. *Trends in Plant Science*. 9:770-780. <website> doi:10.1016/j.tplants.2016.05.004
- Page JT, Liechty ZS, Alexander R, Clemons K, Hulse-Kemp AM, Ashrafi H, Deynze AV, Stelly DM, Udall JA. 2016. DNA sequence evolution and homoeologous conversion in allotetraploid cotton. *PLOS Genetics*. 12(5):e1006012. doi:10.1371/journal.pgen.1006012
- Clouse JW, Adhikary D, Page JT, Ramaraj T, Deyholos MK, Udall JA, Fairbanks D, Jellen EN, Maughan PJ. 2016. The Amaranth (*Amaranthus hypochondriacus*) Genome: Genome, Transcriptome and Physical Map Assembly. *The Plant Genome*. 8(2). <website> doi:10.3835/plantgenome2014.08.0040
- Huynh MD, Page JT, Richardson BA, Udall JA. 2015. Insights into Transcriptomes of Big and Low Sagebrush. *PLOS One*. doi.org/10.1371/journal.pone.0127593
- Hulse-Kemp AM, Lemm J, Joerg Plieske HA, Ramesh Buyyarapu DF, Frelichowski J, Giband M, Hague S, Hinze LL, Kochan KJ, Riggs PK, Scheffler J, Udall JA, ... Byers R, ... Harker DB, ... Yourstone SM et al. 2015. Development of a 63K SNP Array for Cotton and High-density Mapping of Intra- and Inter-specific Populations of *Gossypium* spp. *G3: Genes|Genetics|Genomes*. 5:1187-1209. <website>
- Gallagher JP, Jareczek JJ, Page JT, Udall JA, Gore M, Wendel JF, Grover C. 2015. Re-evaluating the phylogeny of allopolyploid *Gossypium* L. *Molecular Phylogenetics and Evolution*. 92:45-52. <website> doi:http://dx.doi.org/10.1016/j.ympev.2015.05.023
- Page JT, Udall JA. 2015. Methods for mapping and categorization of DNA sequence reads from allopolyploid organisms. *BMC Genetics*. 16(Suppl 2):S4. <website> doi:10.1186/1471-2156-16-S2-S4
- Page JT, Clement MJ, Udall JA. 2014. Genome Sequence Assembly by Suffix Tree Branch Extension. *Journal of Bioinformatic Research Studies*. 1(2). <website>
- Yurchenko OP, Park S, Ilut DC, Millhollon JC, Inmon JJ, Liechty Z, Page JT, Jenks MA, Chapman KD, Udall JA, et al. 2014. Genome-wide analysis of the omega-3 fatty acid desaturase gene family in *Gossypium*. *BMC Plant Biology*. 14(312). <website> doi:10.1186/s12870-014-0312-5

- Page JT, Liechty ZS, Huynh MD, Udall JA.* 2014. BamBam: genome sequence analysis tools for biologists. *BMC Research Notes.* 7:829. <website> doi:10.1186/1756-0500-7-829
- Hulse-Kemp AM, Ashrafi H, Zheng X, Wang F, Hoegenauer KA, Maeda AB, Yang SS, Stoffel K, Matvienko M, *Clemons K, Udall JA,* et al. 2014. Development and bin mapping of gene-associated interspecific SNPs for cotton (*Gossypium hirsutum* L.) introgression breeding efforts. *BMC Genomics.* 15:945. <website>
- Guan X, Nah G, Song Q, *Udall JA,* Stelly DM, Chen ZJ. 2014. Transcriptome analysis of extant cotton progenitors revealed tetraploidization and identified genomespecific single nucleotide polymorphism in diploid and allotetraploid cotton. *BMC Research Notes.* 7:493. <website> doi:10.1186/1756-0500-7-493
- Naumkina M, Thyssen G, Fang DD, Hinchliffe DJ, Florane C, Yeater KM, *Page JT, Udall JA.* 2014. The Li2 mutation results in reduced subgenome expression bias in elongating fibers of allotetraploid cotton (*Gossypium hirsutum* L.). *PLOS One.* 9(3):e90830. <website> doi:10.1371/journal.pone.0090830
- Renny-Byfield S, Gallagher JP, Grover CE, Szadkowski E, *Page JT, Udall JA,* Wang X, Paterson AH, Wendel JF. 2014. Ancient gene duplicates in *Gossypium* (cotton) exhibit near-complete expression divergence. *Genome Biology and Evolution.* 6(3):559-571. <website> doi:10.1093/gbe/evu037
- Tyagi P, Gore MA, Bowman DT, Campbell BT, *Udall JA,* Kuraparthi V. 2014. Genetic diversity and population structure in the U.S. Upland cotton (*Gossypium hirsutum* L.). *Theoretical and Applied Genetics.* 127(2):283-295. <website> doi:10.1007/s00122-013-2217-3
- Raney JA, Reynolds DJ, Elzinga DB, *Page JT, Udall JA,* Jellen EN, Bonfacio A, Fairbanks D, Maughan PJ. 2014. Transcriptome Analysis of Drought Induced Stress in *Chenopodium quinoa*. *Am. J. Plant Sci.* 5(3):338-357. <website>
- Rambani A, Page JT, Udall JA.* 2014. Polyploidy and the petal transcriptome of *Gossypium*. *BMC Plant Biology.* 14:3. <website> doi:10.1186/1471-2229-14-324393201
- Bowman MJ, Park W, Bauer PJ, *Udall JA, Page JT, Raney J,* Scheffler BE, Campbell BT. 2013. RNA-seq transcriptome profiling of upland cotton (*Gossypium hirsutum* L.) root tissue under water deficit stress. *PLOS One.* 8(12):e82634. <website> doi:10.1371/journal.pone.0082634
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- Page JT, Huynh MD, Liechty ZS,* Grupp K, Stelly D, Hulse AM, Ashrafi H, Van Deynze A, Wendel JF, *Udall JA.* 2013. Insights into the Evolution of Cotton Diploids and Polyploids from Whole-Genome Re-sequencing. 3(10):1809-1818. <website> doi:10.1534/g3.113.007229
- Page JT, Gingle AR, Udall JA.* 2013. PolyCat: A Resource for Genome Categorization of Sequencing Reads from Allopolyploid Organisms. *G3: Genes, Genomes, and Genomics.* 3(3):517-525. <website> doi:10.1534/g3.112.005298
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- Maughan PJ, Smith SM, Rojas-Beltrán JA, Elzinga D, Raney JA, Jellen EN, Bonifacio A, Udall JA, Fairbanks D. 2012. Single nucleotide polymorphisms identification, characterization and linkage mapping in *Chenopodium quinoa*. *The Plant Genome*. 5(3):1-7. <website>
- Salmon A, Udall JA, Jeddloh J, Wendel JF. 2012. Targeted capture of homoeologous coding and non-coding sequence in polyploid cotton. *G3: Genes, Genomes, and Genetics*. 2:921-930. <website>
- Parra-Gonzalez LB, Aravena-Abarzúa GA, Navarro-Navarro CS, Udall JA, Maughan PJ, Peterson LM, Salvo-Garrido HE, Maureira-Butler IJ. 2012. Yellow lupin (*Lupinus luteus* L.) transcriptome sequencing: molecular marker development and comparative studies. *BMC Genomics*. 13:425-440. <website>
- Flagel LE, Wendel JF, Udall JA. 2012. Duplicate gene evolution, homoeologous recombination, and transcriptome characterization in allopolyploid cotton. *BMC Genomics*. 13:302. <website>
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- Cronn R, Knaus B, Liston A, Maughan PJ, Parks M, Syring J, Udall JA. 2012. Targeted enrichment strategies for Next-Generation plant biology. *American Journal of Botany*. 99:1-22. <website>
- Byers RL, Harker DB, Yourstone SM, Maughan PJ, Udall JA. 2012. Development and Mapping of SNP Assays in Allotetraploid Cotton. *Theoretical and Applied Genetics*. 124:1201-1214. <website>
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- Morales, A.J., P. Bajgain, Z. Garver, P.J. Maughan, J.A. Udall. 2011. Physiological responses of *Chenopodium quinoa* to salt stress. (In Press)
- Bajgain, P., R.A. Richardson, J.C. Price, R.C. Cronn, and J.A. Udall. 2011. Transcriptome characterization and polymorphism detection between subspecies of big sagebrush (*Artemisia tridentata*). *BMC Genomics* 12:370.
- Rapp R.A, C.H. Haigler, L.E. Flagel, R.H. Hovav, J.A. Udall, J.F. Wendel. 2010. Gene expression in developing fibers of upland cotton (*Gossypium hirsutum* L.) was massively altered by domestication *BMC Biology* 8:139

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- Paterson, A.H., J. Rong, A.R. Gingle, P.W. Chee, E.S. Dennis, D. Llewellyn, L.S. Dure III, C. Haigler, G.O. Myers, D.G. Peterson, M. Rahman, Y. Zafar, U. Reddy, Y. Saranga, J.M. Stewart, J.A. Udall, V.N. Waghmare, J.F. Wendel, T.A. Wilkins, R.J. Wright, E. Zaki, E. Hafez, J. Zhu. 2010. Sequencing and utilization of the *Gossypium* genomes. *Tropical Plant Biology* 3:71-74.
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- Maughan, P.J., T. Turner, C.E. Coleman, D. Elzinga, E.N. Jellen, A.J. Morales, J.A. Udall, D. Fairbanks, and A. Bonifacio 2009. Characterization of salt overly sensitive (SOS1) gene homoeologs in quinoa (*Chenopodium quinoa* Willd). *Genome* 52:647-657
- Chaudhary, B., L.E. Flagel, R. Stupar, J.A. Udall, N. Verma, N. Springer, and J.F. Wendel 2009. Reciprocal silencing, transcriptional bias and functional divergence of homoeologs in polyploid cotton *Genetics* 182:503-517.
- Rapp, R.A., J.A. Udall, and J.F. Wendel. 2009. Genomic expression dominance in allopolyploids *BMC Biology* 7:18.
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- Chaudhary, B., R.H. Hovav, R.A. Rapp, N. Verma, J.A. Udall, and J.F. Wendel. 2008. Global analysis of gene expression in cotton fibers from wild and domesticated *Gossypium barbadense*. *Evolution and Development* 10:567-582.
- Hovav R.H., B. Chaudhary, J.A. Udall, L.E. Flagel, J.F. Wendel 2008. Parallel domestication, convergent evolution and duplicated gene recruitment in allopolyploid Cotton. *Genetics* 179:1725-1733
- Hovav, R.H., J.A. Udall, B. Chaudhary, L. Flagel, E. Hovav, R.A. Rapp, and J.F. Wendel. 2008. Partitioned expression of duplicated genes during development of a single cell in a polyploid plant. *Proceedings of the National Academy of Sciences* 105:6191-6195
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Turley, H. McFadden, P. Payton, N. Klueva, R. Allen, D. Zhang, C. Haigler, C. Wilderson, J. Suo, S.T. Schulze, M.L. Pierce, M. Essenberg, H. Kim, D.J. Llewellyn, E.S. Dennis, D. Kudrna, R. Wing, A.H. Paterson, C. Soderlund, and J.F. Wendel. 2006. A large global assembly of cotton ESTs. *Genome Research* 16: 441 - 450.

Amarasinghe, B.R., E.F. Nitschke, Y. Wu, J.A. Udall, E.S. Dennis, G. Constable, and D.J. Llewellyn. 2006. Genomic approaches to the discovery of promoters for sustained expression in cotton (*Gossypium hirsutum* L.) under field conditions: expression analysis in transgenic cotton and Arabidopsis of a Rubisco small subunit promoter identified using EST sequence analysis and cDNA microarrays. *Plant Biotechnology* 5: 437 - 450.

Ph.D. Thesis Abstract

A genetic study of oilseed *Brassica napus* L. : mapping chromosome rearrangements and quantitative trait loci

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Chromosome rearrangements were detected in four DH populations of *Brassica napus* L. Four sources of unadapted germplasm, a Chinese winter cultivar, 'Hua-db12', a resynthesized *B. napus*, and two French winter germplasm sources were each crossed to a common male parent to create four DH populations (HUA, SYN, MS, and SW, respectively). A genetic map for each population and a consensus map were constructed with RFLP markers. Within each DH population, chromosome rearrangements were identified and classified as either de novo non-reciprocal translocations (NRTs), segregating NRTs, or segregating reciprocal translocations (RT). These likely resulted from recombination between homoeologous chromosomes, and were most prevalent in the SYN population. We found that chromosome rearrangements may occur frequently in *B. napus*, and may impact recombination, and allelic and phenotypic diversity. The seed yields of hybrid spring canola could be improved by introducing alleles from these unadapted germplasm sources. The common male parent used in the mapping populations was part of a *B. napus* hybrid combination and contained a genetically engineered male-fertility restorer gene. F1 hybrid seed was created for the HUA and SYN DH populations by crossing each DH line to a single tester of a heterotic group which complements the male-fertility restorer line. The HUA and SYN DH lines were evaluated in two environments (Wisconsin) and testcrosses (TxHUA and TxSYN hybrid populations) were evaluated in three or four environments (Wisconsin and Canada). Many of the hybrids had significantly higher seed yields than the starting hybrid combination. QTL mapping was used to identify favorable alleles from these two unadapted germplasm sources. The map position of QTL for days to flower and resistance to a bacterial disease coincided with QTL for other agronomic traits suggesting the occurrence of pleiotropic or linked effects. Four quantitative trait loci (QTL) for seed yield were found in the hybrid populations which contained favorable alleles increasing seed yield from the unadapted parent. One of these regions was detected in multiple environments and in both populations. Lines containing favorable QTL alleles from the unadapted parents of some seed yield QTL have been selected for transfer and testing in different genetic backgrounds.

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