

DAVID M. STELLY, PROFESSOR

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For Additional Information:

See hyperlinks and URLs listed on the last page (5)

EDUCATION

Ph. D.	Plant Breeding & Plant Genetics	University of Wisconsin - Madison	1983
M. Sc.	Plant Breeding & Cytogenetics	Iowa State University	1979
B. Sc.	Genetics	University of Wisconsin - Madison	1975

RESEARCH & PROFESSIONAL EXPERIENCE

Positions

2020 ---:	Director	AgriGenomics Laboratory (AGL) (small core lab.)
2008 -20:	Co-Director	AgriGenomics Laboratory (AGL) (small core lab.)
2003 ---:	Member	Faculty of Biotechnology, TAMU
1993 ---:	<u>Professor</u>	<u>Plant Genetics, Cytogenetics and Breeding, TAMU</u>
1989-93:	<u>Associate Professor</u>	<u>Plant Genetics, Cytogenetics and Breeding, TAMU</u>
1989 ---:	Member	Faculty of Mol. Environmental Plant Sci., TAMU
1984 ---:	Member	Faculty of Genetics, TAMU
1984 ---:	Member	Graduate Faculty, TAMU
1983 ---:	<u>Asst. Professor</u>	<u>Plant Genetics, Cytogenetics and Breeding, TAMU</u>

PROFESSIONAL ACTIVITIES

- 2022 Member, Search Committee, Vice-President for Research (TAMU)
- 2022 Member, TAMU Working Group (#17) on University Studies and Interdepartmental Programs
- 2022 Member, TAMU Working Group (#30) on Vet Med Research Grants and Facilities
- 2021- Chair (elected), Molecular & Environmental Plant Sciences (Graduate Program)
- 2021-2022 Chair (elected), Council of Principle Investigators (TAMU System)
- 2021-2022 Associate Editor (selected), Theoretical and Applied Genetics (retired)
- 2020 -2021 Vice-Chair (elected), Council of Principle Investigators (TAMU System)
- 2019-21: Joint Chair, Awards Committee, College of Agric. & Life Sciences, TAMU
- 2019 ---: Executive Committee (selected), Genetics & Genomics (Graduate Program)
- 2017-18: Executive Committee (selected), Council of Principle Investigators (CPI)
- 2016 ---: College Representative (elected), Council of Principle Investigators
- 2017 ---: Executive Committee, Interdisciplinary Graduate Program in Genetics
- 2016: USDA Program 301 Review Panel, Member

- 2015-7: Chair (elected), International Cotton Genome Initiative (ICGI).
- 2014 ---: Nat'l Academy of Sci. Committee on GE Crops: Past, Present ... Future
- 2014-6: Chair, Calvin Sperling Biodiversity Lectureship, Crop Sci. Soc. Amer.
- 2014-6: Int'l Organizing Committee, World Cotton Research Conference-6
- 2013 ---: Organizer/Co-organizer, "Analysis of Complex Genomes" workshops at PAG
- 2013-5: Co-Chair/Chair, International Cotton Genome Initiative (ICGI)
- 2013: Calvin Sperling Biodiversity Lectureship, Crop Science Soc. of America
- 2009-14: Chair, P&T Committee, Dept. Soil & Crop Sciences, TAMU
- 2009-12: Sec. / VP, President / Past-P., National Association of Plant Breeders
- 2007-9: Chair, Science & Technology group, Plant Breeding Coord. Comm.
- 2002-4: Chair, International Cotton Genome Initiative (ICGI)
- **Association memberships:** American Association for the Advancement of Science (**AAAS**), Crop Science Society of America (**CSSA**), National Association of Plant Breeders (**NAPB**), Int'l Cotton Genome Initiative (**ICGI**), Sigma Xi, Society for Science & the Public

HONORS & AWARDS

- 2018: Fellow, AAAS
- 2018: Cotton Biotechnology Award, Cotton Incorporated
- 2017: Cotton Researcher of the Year, The Int'l Cotton Advisory Comm.
- 2016: Fellow, Crop Science Society of America
- 2016: Lifetime Achievement Award, U. Agricultural Sciences, Dharwad, India
- 2016: B.B. Singh Award for Outstanding Research in Crop Science, TAMU
- 2015: Margaret Annette Peters Advising Award (student nominated)
- 2013: Research Award for 2012 (faculty), Dept. Soil & Crop Sciences, TAMU
- 2008: Cotton Genetics Award, Cotton Incorporated
- 2002: First elected Chair by the International Cotton Genome Initiative (ICGI) -
- 1995: Cotton Genetics Award, Cotton Incorporated

RECENT SIGNIFICANT GRANTS RECEIVED

1. Cotton Inc. 20-724. CIF - *Overcoming Haplotypic Blocks as Barriers to Genetic Progress*. PI. 2020, 2021, 2022 with annual potential for renewal.
2. NSF. 1739092. Co-PI (UT-Austin led). *Genomic and epigenomic analyses of fiber development in allotetraploid cottons*. 01-Aug-2018 to 31-Jul-2022.
3. Cotton Inc. 18-201. *Introgression of Gossypium Germplasm to Increase Genetic Diversity for Cotton Improvement*. PI. 2018-2022, with annual competition for renewal.
4. Texas State Support Committee, via Cotton Inc. 13-466TX. *Improving East Texas Cotton*. Co-PI. 2013-2022, with annual competition for renewal.

PUBLICATIONS (last 5 years)

ORCID: [0000-0002-3468-4119](https://orcid.org/0000-0002-3468-4119), <https://orcid.org>

1. Hinze, LL, AM Hulse-Kemp, IW Wilson, Q-H Zhu, DJ. Llewellyn, JM Taylor, A Spriggs, DD Fang, M Ulloa, JJ Burke, M Giband, J-M Lacape, A Van Deynze, JA Udall, JA Scheffler, S Hague, JF Wendel, AE Pepper, J Frelichowski, CT Lawley, DC Jones, RG Percy, and DM Stelly. 2017. Diversity analysis of cotton (*Gossypium hirsutum* L.) germplasm using the CottonSNP63K Array. *BMC Plant Biology* 17: 37. (20 pg) <https://doi.org/10.1186/s12870-017-0981-y>
2. Saha, S., JN Jenkins, JC McCarty, RW Hayes, DM Stelly and BT Campbell. 2017. Four chromosome-specific (*Gossypium barbadense* chromosome 5sh) Upland cotton RILs with improved elongation. *J. Plant Registrations* 11:165-167. <https://doi.org/10.3198/jpr2015.09.0060crg>
3. Jenkins, JN, JC McCarty, BT Campbell, RW Hayes, J Wu, S Saha, DM Stelly. 2017. "Effects of chromosomes 01, 04, 18 from three tetraploid species of *Gossypium* in topcrosses with five elite cultivars: I. Genetic effects. *Crop Science* 57:1338-1346. <https://doi:10.2135/cropsc:2016.06.0528>
4. Jenkins, JN, JC McCarty, BT Campbell, RW Hayes, J Wu, S Saha and DM Stelly. 2017. Genotypic comparisons of chromosomes 01, 04, and 18 from three tetraploid species of *Gossypium* in topcrosses with five elite cultivars of *G. hirsutum* L." *Euphytica* 213, no. 5 (2017): 107 (16pp). <https://doi:10.1007/s10681-017-1895-3>
5. Saha, S., J. Wu, J.N. Jenkins, J.C. McCarty, R.W. Hayes, D.M. Stelly, D.A. Raska and B.T. Campbell. 2017. Tri-species shuffling of chromosomes to study the effects on fiber traits using chromosome substitution lines. *Crop Science* 57:1211-1226. <https://doi:10.2135/cropsci2016.09.0729>
6. Song, Q, T Zhang, DM Stelly and ZJ Chen. 2017. Epigenomic and functional analyses reveal roles of epialleles in the loss of photoperiod sensitivity during domestication of allotetraploid cottons. *Genome Biology* 18:99 (14pp). <https://doi.org/10.1186/s13059-017-1229-8>
7. Ulloa, M, AM Hulse-Kemp, L De Santiago, DM Stelly and JJ Burke. 2017. Insights into Upland cotton (*Gossypium hirsutum* L.) genetic recombination based on three high-density SNP and a consensus map developed independently with common parents. *Genomics Insights* 10 (2017): 1178631017735104. <https://doi.org/10.1177/1178631017735104>
8. Saski, CA, BE Scheffler, AM Hulse-Kemp, B Liu, Q Song, A Ando, DM Stelly, JA Scheffler, J Grimwood, DC Jones, DG Peterson, J Schmutz, T Zhang and ZJ Chen. 2017. Subgenome-anchored physical frameworks of the allotetraploid Upland cotton (*Gossypium hirsutum* L.) genome, and an approach toward reference-grade assemblies of polyploids. *Scientific Reports* 7:15274. <https://doi.org/10.1038/s41598-017-14885-w>
9. Awasthi, A., Reddy, K.R., Saha, S., Jenkins, J.N. and Stelly, D.M., 2018. Morph-physiological responses of cotton interspecific chromosome substitution lines to low temperature and drought stresses. *Euphytica* 214:218 (19 p). <https://doi.org/10.1007/s10681-018-2300-6>
10. Sripathi, V.R., Choi, Y., Gossett, Z.B., Stelly, D.M., Moss, E.M., Town, C.D., Walker, L.T., Sharma, G.C. and Chan, A.P., 2018. Identification of microRNAs and their targets in four *Gossypium* species

- using RNA sequencing. *Current Plant Biology*. 14:30-40.
<https://doi.org/10.1016/j.cpb.2018.09.008>
11. Saha, S., J. N. Jenkins, J. C. McCarty, R. W. Hayes, D. M. Stelly, and B. T. Campbell. 2018. Registration of two CS-B17-derived Upland cotton recombinant inbred lines with improved fiber micronaire. *J. Plant. Reg.* 12:97-100. doi:10.3198/jpr2015.09.0061crg, doi:10.3198/jpr2019.05.0024crg
 12. Pixley, K.V., Falck-Zepeda, J.B., Giller, K.E., Glenna, L.L., Gould, F., Mallory-Smith, C.A., Stelly, D.M. and Stewart, C.N., 2019. Genome editing, gene drives, and synthetic biology: will they contribute to disease-resistant crops, and who will benefit?. *Annual Review of Phytopathology*, 57:165-88. <https://www.annualreviews.org/doi/abs/10.1146/annurev-phyto-080417-045954>
 13. Jenkins, J. N., J. C. McCarty, R. W. Hayes, D. M. Stelly, and S. Saha. 2019. Registration of RMBHMTUP-C4, a random-mated cotton population containing alleles from four *Gossypium* species. *J. Plant. Reg.* 13:411-415. doi:10.3198/jpr2019.05.0024crg
 14. Alabi, O.J., Isakeit, T., Vaughn, R., Stelly, D., Conner, K., Gaytan, B., Villegas, C., Hitzelberger, C., De Santiago, L., Monclova-Santana, C. and Brown, J.K. 2020. First report of cotton leafroll dwarf virus infecting upland cotton (*Gossypium hirsutum* L.) in Texas. *Plant Disease*. online: <https://apsjournals.apsnet.org/doi/10.1094/PDIS-09-19-2008-PDN>
 15. Ulloa, M., L. M. De Santiago, A. M. Hulse-Kemp, D. M. Stelly. 2020. Enhancing Upland cotton for drought resilience, productivity, and fiber quality: comparative evaluation and genetic dissection. *Molecular Genetics and Genomics* 295:155-176. <https://doi.org/10.1007/s00438-019-01611-6>
 16. Abdelraheem, A., H. Ellassbli, Y. Zhu, V. Kuraparthy, L. Hinze, D. Stelly, T. Wedegaertner and J. Zhang. 2020. A genome-wide association study uncovers consistent quantitative trait loci for resistance to *Verticillium* wilt and *Fusarium* wilt in the U.S. Upland cotton. *Theor. Appl. Genet.* 133:563-577. <https://doi.org/10.1007/s00122-019-03487-x>
 17. Grover, G., M. Pan, D. Yuan, M. Arick, G. Hu, L. Brase, D. Stelly, Z. Lu, R. Schmitz, D. Peterson, J. Wendel and J. Udall. 2020. The *Gossypium longicalyx* genome as a resource for cotton breeding and evolution. *G3/2020/401050*. <https://doi.org/10.1534/g3.120.401050>
 18. Chen, Z. J., A. Sreedasyam, A. Ando, Q. Song, L. M. De Santiago, A. M. Hulse-Kemp, M. Ding, W. Ye, R. C. Kirkbride, J. Jenkins, C. Plott, J. Lovell, Y-M. Lin, R. Vaughn, B. Liu, S. Simpson, B. E. Scheffler, L. Wen, C. A. Saski, C. E. Grover, G. Hu, J. L. Conover, J. W. Carlson, S. Shu, L. B. Boston, M. Williams, D. G. Peterson, K. McGee, D. Jones, J. F. Wendel, D. M. Stelly, J. Grimwood, and J. Schmutz. 2020. Genomic diversifications of five *Gossypium* allopolyploid species and their impact on cotton improvement. *Nat Genet* 52:525–533. <https://doi.org/10.1038/s41588-020-0614-5>
 19. Saha, S., N. Bellaloui, J. N. Jenkins, J. C. McCarty and D. M. Stelly. 2020. Effect of chromosome substitutions from *Gossypium barbadense* L., *G. tomentosum* Nutt. Ex Seem and *G. mustelinum* Watt into *G. hirsutum* L. on cottonseed protein and oil content. *Euphytica* 216:1-12 (June 2020) <https://doi.org/10.1007/s10681-020-02644-4>
 20. Ellassbli, H., Abdelraheem, A., Zhu, Y., Teng, Z., Wheeler, T.A., Kuraparthy, V., Hinze, L., Stelly, D.M., Wedegaertner, T. and Zhang, J., 2021. Evaluation and genome-wide association study of

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- resistance to bacterial blight race 18 in US Upland cotton germplasm. *Molecular Genetics and Genomics*, 296(3), pp.719-729. <https://doi.org/10.1007/s00438-021-01779-w>
21. Bellaloui, N., Saha, S., Tonos, J.L., Scheffler, J.A., Jenkins, J.N., McCarty, J.C. and Stelly, D.M., 2020. Effects of interspecific chromosome substitution in upland cotton on cottonseed micronutrients. *Plants*, 9(9), p.1081. (17 pp.) <https://doi.org/10.3390/plants9091081>
 22. Reddy, K.R.; Bheemanahalli, R.; Saha, S.; Singh, K.; Lokhande, S.B.; Gajanayake, B.; Read, J.J.; Jenkins, J.N.; Raska, D.A.; Santiago, L.M.D.; Hulse-Kemp, A.M.; Vaughn, R.N.; Stelly, D.M. 2020. High-temperature and drought-resilience traits among interspecific chromosome substitution lines for genetic improvement of upland cotton. *Plants* 9:1747 (22p). <https://doi.org/10.3390/plants9121747>
 23. Bellaloui, N., S. Saha, Sukumar, J. Tonos, J. Scheffler, J. McCarty, D. M. Stelly. 2021. Effect of chromosome substitution from alien tetraploid cotton species in Upland cotton on (+) and (-) gossypol enantiomer levels in cottonseed. *J. Cotton Sci.* 25:7–20. <https://www.cotton.org/journal/2021-25/1/upload/JCS25-007.pdf>
 24. Ayubov M.S., T.M. Norov, S. Saha, T. Tseng, K. R. Reddy, J. N. Jenkins, I. Y. Abdurakhmonov and D.M. Stelly. 2021. Alteration of root and shoot morphologies by interspecific replacement of individual Upland cotton chromosome or chromosome segment pairs. *Euphytica* 217:154 (23p). <https://doi.org/10.1007/s10681-021-02771-6>

Hyperlinks and URLs to Additional Information (accuracy varies)

- [Faculty web-page](http://soilcrop.tamu.edu/people/stelly-david-m/): <http://soilcrop.tamu.edu/people/stelly-david-m/>
- [TAMU Scholars](https://scholars.library.tamu.edu/vivo/display/nfec36db0/Persons/View%20All): <https://scholars.library.tamu.edu/vivo/display/nfec36db0/Persons/View%20All>
- [ORCID](https://orcid.org/0000-0002-3468-4119): <https://orcid.org/0000-0002-3468-4119>
- [gScholar](https://scholar.google.com/citations?user=z6fIJ9kAAAAJ&hl=en): <https://scholar.google.com/citations?user=z6fIJ9kAAAAJ&hl=en>
- [Scopus](https://www.scopus.com/authid/detail.uri?authorId=7003696727): <https://www.scopus.com/authid/detail.uri?authorId=7003696727>