ICAC Researcher of the Year - 2017
Nomination Package

I. Name and Address

Name: (First, middle, last):	**David Matthias Stelly, Ph.D.**
Position (s):	**Professor, Department of Soil & Crop Sciences, Texas A&M University and Texas A&M AgriLife Research**
Organization and address:	**370 Olsen Blvd. (Heep Ctr. Rm 435) Department of Soil & Crop Sciences, TAMU College Station, Texas 77843-2474 USA**
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II. Field of Research

Dr. Stelly's research goalover the past 30+ years has been to enhance Upland cotton productivity, quality and sustainability through genetic diversification, including the development of collaborations, germplasm, scientific knowledge, methods and resources that facilitate use of the newly introduced germplasm.

He is internationally renown for hisresearch efforts that integrate the fields of plant breeding, diploid and polyploid cotton cytogenetics, genetics, multiple types of "mapping",diversity analysis, evolution, wide-cross germplasm introgression, reproductive biology, cytology, cytogenomics, genomics and bioinformatics. For example, he's presented invited talks in multiple European, Middle Eastern and Asian countries, and twice served as Chair of the International Cotton Genome Initiative.

Many of his accomplishments in research, teaching and service have brought and are still bringing global benefit to global cotton improvement efforts, especially as related to genetic diversification, manipulation and improvement. Hallmark contributions include **[1]** new methods for stain-clearings that enable large-scale cytological studies of cotton female reproductive development; **[2]** Cotton Cytogenetic Collection of isogenic monosomics, acrocentrics, reciprocal translocations of Upland cotton (*Gossypium hirsutum*); **[3]** Chromosome Substitution Line series for chromosomes of *G. barbadense*, *G. tomentosum* and *G. mustelinum*, collectively constitution an isogenic platform, providing facile access to 100,000 – 200,000 alien alleles for research, quantitative genetics and breeding; **[4]** wide-cross introgression from multiple diploid and disomic tetraploid species, including development of Upland cottons with two different genetic systems for resistance to reniform nematodes, both linked to molecular markers to facilitate breeders' use of SSR- or SNP-based marker-assisted breeding (MAB); **[5]** revolutionary techniques for physical mapping and molecular cytogenetic analyses of cotton and other species (WWRH, ISH, GISH, FISH); **[6]** discovery of gametocidal and chromosome elimination properties of certain C-genome chromosomes (e.g., C1-A); **[7]** significant contributions to many collaborative genome maps, the first major one in 1994, made with RFLPs; **[8]** development and publication of the CottonSNP63K Array and associated AD-tetraploid cluster file for automated genotype calling, providing the cotton community the first and only high-quality low-overhead globally accessible SNP genotyping platform for genome-wide, high-plex SNP genotyping; **[9]** in 2015, the first two 26-linkage group (only) single bi-parental population genome-wide linkage maps in cotton, one intra-specific (~7k loci) and one inter-specific (~19k loci); **[10]** new DNA extraction methods that enable everyone to use MAB, because they are cheap, fast and non-destructively applicable to cotton seed and seedling for simplex, low- and medium-plex PCR-based genotyping (e.g. SSRs or SNPs); **[11]** the most reliable genome sequencing assemblies to date for diploid D5-genome species, *G. raimondii*, and the tetraploid cultivated Upland cotton species; **[12]** significant contributions to fiber cell functional genomics and epi-genomics research; **[13]** collaborations and training of graduates, trainees and visiting scientists from many countries, e.g., Uzbekistan, Pakistan, India, Bangladesh, China, Korea, Japan, Taiwan, Australia, Mozambique, Ivory Coast, Senegal, Brazil, Mexico, Turkey, Greece, Czech Republic, France, and Belgium.

III. Awards and Recognitions

National

No.	Year	Award/Recognition	Remarks
1	2016	**B.B. Singh Award for Outstanding Research in Crop Science**, Texas A&M University	
2	2016, 2011, 2005	**USDA Program 301 Review Panel - Member***("Plant Genetic Resources, Genomics, and Genetic Improvement")*	
3	2015	**Margaret Annette Peters Advising Award***(This award recognizes faculty / administrators who embody the spirit of caring, compassionate, and genuine concern for the welfare of individual students.)*	
4	2014-2016	**National Academy Sciences (NAS)GE Crops Review Committee –Member***(available at http://nas-sites.org/ge-crops/2016/05/17/report/ . This 600-page report provides an unbiased assessment of GE crops to date and expectations for the future. It has already become one of the most successful NAS report of all time, with >35,000 downloads to date. Summary only:http://nas-sites.org/ge-crops/2016/05/16/report-in-brief/)*	
5	2013	**Research Award for 2012**, Department of Soil & Crop Sciences, Texas A&M University, and Texas A&M AgriLife Research	
6	2009-2013	**National Association of Plant Breeders (NAPB) - Secretary, Vice-president, President and Past-President***(NAPB has become a key voice for US plant breeders, and is the ONLY such group that represents plant breeders for all plants in the USA, commercial*	

		and public.)	
7	2007-2009	**Science & Technology, Plant Breeding Coordination Committee -Chair***(PBCC helps coordinate the role of the public sector in continuing investment in plant breeding capacity and infrastructure.)*	
8	1997-2017	**Organizer or Co-organizer of one or more "Workshops" per year at the Plant and Animal Genome Conference**	

International

No.	Year	Award/Recognition	Remarks
1	2016	**"Fellow"**, Crop Science Society of America	
2	2016	**"Lifetime Achievement Award"**, University of Agricultural Sciences, Dharwad, India	
3	2014-2016	**World Cotton Research Conference-6International Organizing Committee - Member**	
4	2015-2017, 2002-2004	**International Cotton Genome Initiative (ICGI) - Chair**(2002 - becamefirst member-elected Chair of ICGI)	
5	2008, 1995	**Cotton Genetics Research Award (2)**, Joint Cotton Breeding Policy Committee	
6	2014-16:	**Calvin Sperling Biodiversity Lectureship Committee - Chair**, Crop Science Society of America (CSSA)	
7	2010-2013	**USDA international project (58-6402-0-543) on Stable Introgression of Cotton Leaf Curl Virus Resistance into Cultivated Cotton and Germplasm Enhancement – Cooperator *(joint US-PAK project aimed as overcoming a devastating new strain of CLCuV)***	
8	1994-1995	**First International Conference on Apomixis-Organizer,** held at College Station (1995) *(attended by scientists from over 20 countries, and a series of conferences resulted)*	
9	Multiple	**Invited speaker:** e.g., Singapore, Japan, Korea, China, Brazil, Pakistan, Uzbekistan, India, England, Czech Rep.	

IV. Publications

Number	Type
285	Abstracts
2	Books (one of many contributing authors)
10	Newsletters (edited)
2	Thesis or dissertation

7	Chapters
3	Proceedings (articles, reviewed by editor(s))
149	Reviewed (peer-reviewed)
2	Patents
460	Total (175 major publications; 285 abstract publications)

1. Book chapters (as main author)

Stelly, D. M., H. J. Price and T. D. McKnight. 1995. Molecular-meiotic cytogenetic analysis of cotton. *In* Classical and Molecular Cytogenetic Analysis of Cereal Genomes (eds.) B. Gill and J. Raupp. pp. 148-156.

Stelly, D. M., C. F. Crane, R. E. Hanson, T. D. McKnight and H. J. Price. 1996. Meiotic molecular cytogenetics of cotton. *In* Methods of Genome Analysis in Plants: Their Merits and Pitfalls (ed.) P. P. Jauhar. CRC Press. pp. 99-111.

Stelly, David. 2004. Aneuploid mapping in polyploids. Encyclopedia of Plant and Crop Science.Marcell Dekker, Inc.

2. Book chapters (as co author/editor)

Paterson, A.H., D.M. Stelly, and J.F. Wendel. 1996. Status of genome mapping in the Malvaceae. *In* Genome Mapping in Plants, (ed.) AH Paterson. pp. 229-242.

Triplett B.A., Kim H.J., Hinchliffe D., Sze S-H.,Thaxton P., Stelly D. and Z.J. Chen. 2006. Phytohormone regulation of cotton fiber development *in vitro*. In Biotechnology and Sustainable Agriculture 2006 and Beyond.Springer, 153-156.

Saha, S., Stelly, D.M., Raska, D.A., Wu, J., Jenkins, J.N., McCarty, Jr., J.C., Makamov, A., Gotmare, V., Abudurakhmonov, I., Campbell, B.T. 2012. Chromosome substitution lines: Concept, development and utilization in the genetic improvement of upland cotton. *In:*Abdurakhmoov, I.Y., editor. Plant Breeding. InTech. p. 107-128. http://cdn.intechweb.org/pdfs/25555.pdf

Sanamayan M.F., A.K. Makamov, S.U. Bobokhujaev, D.E. Usmonov, S.U. Bobokhujaev, D.E. Usmonov, Z.T. Buriev, S. Saha and D.M. Stelly. 2016. The utilization of translocation lines and microsatellite markers for the identification of unknown cotton monosomic lines. Chapter 8, pp. 167-183, In Cotton Research, Ed. I.Y. Abdurakhmonov.http://dx.doi.org/10.5772/64558

***3. Peer-reviewed research papers published – International only** (space-constrained):*

Dr. Stelly authored/co-authored 109 refereedpublications 1979-2010, excluding those below.

110. Saha, S. J. Wu, J.N. Jenkins, J.C. McCarty, R. Hayes and D.M. Stelly. 2010. Genetic dissection of chromosome substitution lines of cotton to discover novel *Gossypium barbadense* L. alleles for improvement of agronomic traits. Theor. Appl. Genet. 120:1193-1205. DOI 10.1007/s00122-009-1247-3
111. Wang, K., W. Guo, Z. Yang, Yan Hu, W. Zhang, B. Zhou, D. M. Stelly, Z. J. Chen, T. Zhang. 2010. Structure and size variations between 12A and 12D homoeologous chromosomes based on high-resolution cytogenetic map in allotetraploid cotton. Chromosoma 1193:255-266. DOI 10.1007/s00412-009-0254-0
112. Buriev, Z. T., S. Saha, S. E. Shermatov, J. N. Jenkins, A. Abdukarimov, D. M. Stelly and I. Y. Abdurakhmonov. 2011. Molecular evolution of the clustered *MIC-3*multigene family of

Gossypium species. Theor. Appl. Genet. 123:1359-1373. (doi:10.1007/s00122-011-1672-y)

113. Guan X., J.J. Lee, M. Pang, X. Shi, D.M. Stelly and Z. J. Chen. 2011. Activation of arabidopsis seed hair development by cotton fiber-related genes. PLoS ONE 6(7): e21301. doi:10.1371/journal.pone.0021301
114. Saha, S., J. Wu, J. N. Jenkins, J. C. McCarty, R. Hayes and D. M. Stelly. 2011. Delineation of interspecific epistasis on fiber quality traits in *Gossypium hirsutum* by ADAA analysis of intermated*G. barbadense* chromosome substitution lines. Theor. Appl. Genet. 122:1351-1361. http://ddr.nal.usda.gov/bitstream/10113/48913/1/IND44568359.pdf
115. Bartek, M. S., G. L. Hodnett, B. L. Burson, D. M. Stelly and W. L. Rooney. 2012. Pollen tube growth after intergeneric pollinations of *iap*-homozygous sorghum. Crop Science 52: 4: 1553-1560. doi:10.2135/cropsci2011.09.0474
116. Gao, W, Saha, DP Ma, Y Guo, JN Jenkins and DM Stelly. 2012. A cotton-fiber-associated cyclin-dependent kinase a gene: characterization and chromosomal location. Intl J Plant Genomics 2012, 613812, 10 pp, doi:10.1155/2012/613812
117. Jenkins, J.N., McCarty, J.C., Wu, J., Hayes, R. and Stelly, D. 2012. Genetic effects of nine *Gossypium barbadense* L. chromosome substitution lines in top crosses with five elite Upland cotton *G. hirsutum* L. cultivars. Euphytica 187(2):161-173. DOI 10.1007/s10681-011-0580-1
118. Paterson, A H., J. F. Wendel, H. Gundlach, H. Guo, J. Jenkins, D. Jin, D. Llewellyn, K. C. Showmaker, S. Shu, J. Udall, M. Yoo, R. Byers, W. Chen, A. Doron-Faigenboim, M. V. Duke, L. Gong, J. Grimwood, C. Grover, K. Grupp, G. Hu, T. Lee, J. Li, L. Lin, T. Liu, B. S. Marler, J. T. Page, A. W. Roberts, E. Romanel, W. S. Sanders, E. Szadkowski, X. Tan, H. Tang, C. Xu, J. Wang, Z. Wang, D. Zhang, L. Zhang, H. Ashfari, F. Bedon, J. E. Bowers, C. L. Brubaker, P. W. Chee, S. Das, A. R. Gingle, C. H. Haigler, D. Harker, L. V. Hoffmann, R. Hovav, D. C. Jones, C. Lemke, S. Mansoor, M. urRahman, L. N. Rainville, A. Rambani, U. K. Reddy, J. Rong, Y. Saranga, B. E. Scheffler, J. A. Scheffler, D. M. Stelly, B. A. Triplett, A. Van Deynze, M. F.S. Vaslin, V. N. Waghmare, S-A. Walford, R. J. Wright, E. A. Zaki, T. Zhang, E. S. Dennis, K. F. X. Mayer, D. G. Peterson, D. S. Rokhsar, X. Wang, J. Schmutz. 2012. Repeated polyploidization of *Gossypium* genomes and the evolution of spinnable cotton fibress. Nature 492:423-428.
119. Yu, J., Kohel, R.J., Fang, D.D., Cho, J., Van Deynze, A., Ulloa, M., Hoffman, S.M., Pepper, A.E., Stelly, D.M., Jenkins, J.N., Saha, S., Kumpatla, S.P., Shah, M.R., Hugie, W.V., Percy, R.G. 2012. A high-density simple sequence repeat and single nucleotide polymorphism genetic map of the tetraploid cotton genome. G3 Genes, Genomes, Genetics 2:43-58. doi: 10.1534/g3.111.001552 http://www.g3journal.org/content/2/1/43.abstract
120. Zhang M, Zhang Y, Huang JJ, Zhang X, Lee M-K, DM. Stelly, H-B Zhang. (2012) Genome physical mapping of polyploids: A BIBAC physical map of cultivated tetraploid cotton, *Gossypium hirsutum* L.. PLoS ONE 7(3): e33644. doi:10.1371/journal.pone.0033644
121. Lee, M-K, Y Zhang, M Zhang, M Goebel, HJ Kim, BA Triplett, DM Stelly and H-B Zhang. 2013. Construction of a plant-transformation-competent BIBAC library and genome sequence analysis of polyploid Upland cotton (*Gossypium hirsutum* L.). BMC Genomics 14:208 doi:10.1186/1471-2164-14-208 http://www.biomedcentral.com/1471-2164/14/208
122. Page, J.T., M.D. Huynh, Z.S. Liechty, K. Grupp, D. Stelly, A.M. Hulse, H. Ashrafi, A. Van Deynze, J. Wendel, and J.A. Udall. 2013. Insights into the evolution of cotton diploids and polyploids from whole-genome re-sequencing. G3: Genes, Genomes, Genetics 3:1809-1818.
123. Saha, S., D. A. Raska, D. M. Stelly, S. Manchali, O. A. Gutiérrez. 2013. Hypoaneuploid chromosome substitution F1 hybrids of *Gossypium hirsutum* L. x *G.mustelinum*Miers ex Watt.

J. Cotton Sci. 17:102-114. http://www.cotton.org/journal/2013-17/2/upload/JCS17-102.pdf

124. Saha, S, Wu, J, Jenkins, J, McCarty, J, Stelly, D.M. 2013. Interspecific chromosomal effects on agronomic traits in *Gossypium hirsutum* by AD analysis using intermated*G. barbadense* chromosome substitution lines. Theor. Appl. Genet. 126:109-117. DOI 10.1007/s00122-012-1965-9
125. Wu, Q., F. Liu, S. Li, G. Song, C. Wang, X. Zhang, Y. Wang, D. Stelly and K. Wang. 2013. Uniqueness of the *Gossypium mustelinum* genome revealed by GISH and 45S rDNA FISH. J. Integrative Plant Biology 55(7): 654-662.
126. Bell, A.A., A.F. Robinson, J. Quintana, N.D. Dighe, M.A. Menz, D.M. Stelly, X. Zheng, J.E. Jones, C. Overstreet, E. Burris, R.G. Cantrell, and R.L. Nichols. 2014. Registration of LONREN-1 and LONREN-2 germplasm lines of upland cotton resistant to reniform nematode. J. Plant Reg. 8:187-190. doi:10.3198/jpr2013.11.0069crg
127. Guan, X., M. Pang, G. Nah, X. Shi, W. Ye, D.M. Stelly, and Z.J. Chen. 2014. miR828 and miR858 regulate homoeologous MYB2 gene functions in Arabidopsis trichome and cotton fibre development. Nature Communications 5: 3050 DOI:10.1038/ncomms4050
128. Guan, Y., G. Nah, Q. Song, J.A. Udall, D.M. Stelly and Z.J. Chen. 2014. Transcriptome analysis of extant cotton progenitors revealed tetraploidization and identified genome-specific single nucleotide polymorphism in diploid and allotetraploid cotton. BMC Research Notes 7:493 http://www.biomedcentral.com/1756-0500/7/493
129. Harris-Shultz, K.R., S. Milla-Lewis, A.J. Patton, K. Kenworthy, A. Chandra, F. C. Waltz, G.L. Hodnett and D. M. Stelly. 2014. Detection of genetic and ploidy variation within vegetatively propagated zoysiagrass cultivars. J. Amer. Soc. Hort. Science 139:547-552.
130. Hulse-Kemp, A.M., H. Ashrafi, X. Zheng, F. Wang. K.A. Hoegenauer, A.B.V. Maeda, S.S. Yang, K. Stoffel, M. Matvienko, K. Clemons, J.A. Udall, A. Van Deynze, D.C. Jones, D.M. Stelly. (2014) Development and bin mapping of gene-associated interspecific SNPs for cotton (*Gossypium hirsutum* L.) introgression breeding efforts. BMC Genomics 15:945 doi:10.1186/1471-2164-15-945
131. Ashrafi, H., A. M. Hulse-Kemp, F. Wang, S. S. Yang, X. Guan D. C. Jones, M. Matvienko, K. Mockaitis, Z. J. Chen, D. M. Stelly and A. Van Deynze. 2015. A long-read transcriptome assembly of cotton (*Gossypium hirsutum* L.) and intraspecific single nucleotide polymorphism discovery. The Plant Genome 33:531-537. doi:10.1038/nbt.3207
132. Bell, A.A., A.F. Robinson, J. Quintana, S.E. Duke, J.L. Starr, D.M. Stelly, X. Zheng, S. Prom, V. Saladino, O.A. Gutiérrez, S.R. Stetina, and R.L. Nichols. 2015. Registration of BARBREN-713 germplasm line of Upland cotton resistant to reniform and root-knot nematodes. J. Plant Reg. 9(1):89-93. doi:10.3198/jpr2014.04.0021crg
133. Hulse-Kemp, A. M., H. Ashrafi, K. Stoffel, X. Zheng, C. Saski, B. E. Scheffler, D. D. Fang, Z. J. Chen, A. Van Deynze, and D. M. Stelly. 2015. BAC-end sequence-based SNP mining in allotetraploid cotton (*Gossypium*) utilizing resequencing data, phylogenetic inferences and perspectives for genetic mapping. G3 5:1095-1105. 10.1534/g3.115.017749
134. Hulse-Kemp, A. M., J. Lemm, J. Plieske, H. Ashrafi, R. Buyyarapu, D. D. Fang, J. Frelichowski, M. Giband, S. Hague, L. L. Hinze, K. J. Kochan, P. K. Riggs, J. A Scheffler, J. A. Udall, M. Ulloa, S. S. Wang, Q-H. Zhu, S. K. Bag, A. Bhardwaj, J. J. Burke, R. L. Byers, M. Claverie, M. A. Gore, D. B. Harker, Md. S. Islam, J. N. Jenkins, D. C. Jones, J-M. Lacape, D. J. Llewellyn, R. G. Percy, A.E. Pepper, J. A. Poland, K. M. Rai, S. V. Sawant, S. K. Singh, A. Spriggs, J. M. Taylor, F. Wang, S. M. Yourstone, X. Zheng, C. T. Lawley, M. W. Ganal, A. Van Deynze, I. W. Wilson, and D. M. Stelly.

2015. Development of a 63K SNP array for cotton and high-density mapping of intra- and inter-specific populations of *Gossypium* spp. G3 5:1187-1209. doi: 10.1534/g3.115.018416

135. Kim, H-J., D. J. Hinchliffe; B. A. Triplett; Z. J. Chen; D. M. Stelly; K. M. Yeater; H. S. Moon; M. K. Gilbert; G. Thyssen; R. B. Turley and D. D. Fang. 2015. Phytohormonal networks promote differentiation of fiber initials on pre-anthesis cotton ovules grown *in vitro* and *in planta*. PLoS One. 10(4): e0125046.
136. Saha, S., D. M. Stelly, A. K. Makamov, M. S. Ayubov, D. Raska, O. A. Gutiérrez, S. Manchali, J. N. Jenkins, D. Deng and I. Y. Abdurakhmonov. 2015. Molecular confirmation of *Gossypium hirsutum* chromosome substitution lines. Euphytica 205:459-473. DOI: 10.1007/s10681-015-1407-2
137. Ueckert, J., D. H. Byrne, K. Crosby, G., Hodnett and D. Stelly. 2015. The utilization of the polyploidy nature of roses. Acta Hort., 1064:73-78. The Proceedings of the Sixth International Symposium on Rose Research and Cultivation. Eds. T. Debener, M. Linde. International Society for Horticultural Science. http://www.actahort.org/books/1064/1064_9.htm
138. Zhang, M-P., Y. Rong, M-K. Lee, Y. Zhang, D. M. Stelly and H-B. Zhang. 2015. Phylogenetic analysis of *Gossypium* L. using genome-wide restriction fragment variation of repeated sequences. Mol. Gen. Genetics: 290:1859-1872. DOI: 10.1007/s00438-015-1039-1
139. Zhang, T., Y. Hu, W. Jiang, L. Fang, X. Guan, J. Chen, J. Zhang, C. Saski, B. E. Scheffler, D. M. Stelly, A. M. Hulse-Kemp, Q. Wan, B. Liu, C. Liu, S. Wang, M. Pan, Y. Wang, D. Wang, W. Ye, L. Chang, W. Zhang, Q. Song, R. Kirkbride, X. Chen, E. Dennis, D. J. Llewellyn, D. G. Peterson, P. Thaxton, D. C. Jones, Q. Wang, X. Xu, H. Zhang, H. Wu, L. Zhou, G. Mei, S. Chen, Y. Tian, D. Xiang, X. Li, J. Ding, Q. Zuo, L. Tao, Y. Liu, J. Li, Y. Lin, Y. Hui, Z. Cao, C. Cai, X. Zhu, Z. Jiang, B. Zhou, W. Guo, R. Li, and Z. J. Chen. 2015. Sequencing of allotetraploid cotton (*Gossypium hirsutum* L. acc. TM-1) provides a resource for fibre improvement. Nature Biotechnology 33:531-537. doi:10.1038/nbt.3207
140. Zheng, X., K. A. Hoegenauer, A. B. V. Maeda, F. Wang, D. M. Stelly, R. L. Nichols and D. C. Jones. 2015. Non-destructive high-throughput DNA extraction and genotyping methods for cotton seeds and seedlings. Biotechniques 58:234-243.
141. Grauke, L. J., M. A. Mendoza-Herrera, D. M. Stelly and P. E. Klein. 2016. 'Jones hybrid' hickory: a case study in *Carya*curation. SpringerPlus 5:1860.
142. Hale, A. L., R. P. Viator, G. Eggleston, G. Hodnett, D. M. Stelly, D. Boykin and D. K. Miller. 2016. Estimating broad sense heritability and investigating the mechanism of genetic transmission of cold tolerance using mannitol as a measure of post-freeze juice degradation in sugarcane and energycane (*Saccharum* spp.). J. Agric. Food Chem., 64:1657-1663. DOI: 10.1021/acs.jafc.5b03803
143. Page, J.T., Liechty, Z.S., Alexander, R.H., Clemons, K., Hulse-Kemp, A.M., Ashrafi, H., Van Deynze, A., Stelly, D.M., Udall, J.A. 2016 . DNA sequence evolution and rare homoeologous conversion in tetraploid cotton. PLoS Genet. 12(5):e1006012.
144. Ulloa, M., C. Wang, S. Saha, R. B. Hutmacher, D. M. Stelly, J. N. Jenkins, J. Burke, and P. A. Roberts. 2016. Analysis of root-knot nematode and fusarium wilt disease resistance in cotton (*Gossypium* spp.) using chromosome substitution lines from two alien species. Genetica 144: 167-179. DOI 10.1007/s10709-016-9887-0
145. Zheng, X., K. A. Hoegenauer, J. Quintana, A. A. Bell, A. M. Hulse-Kemp, R. L. Nichols, and D. M. Stelly. 2016. SNP-based MAS in cotton under depressed-recombination for *Ren*^{lon}-flanking recombinants: results and inferences on wide-cross breeding strategies. Crop Sci. 56:1526-

1539. doi:10.2135/cropsci2015.07.0436

146. 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) DOI:10.1186/s12870-017-0981-y
147. Jenkins, JN, JC McCarty, BT Campbell, RW Hayes, J Wu, S Saha, DM Stelly. "Effects of chromosomes 01, 04, 18 from three tetraploid species of *Gossypium* in topcrosses with five elite cultivars: I. Genetic effects. Crop Science ##:##-##. (IN PRESS) DOI:######################
148. Saha, S., J. Wu, J.N. Jenkins, J.C. McCarty, R.W. Hayes, D.M. Stelly, D.A. Raska and B.T. Campbell. (XXXX). Tri-species shuffling of chromosomes to study the effects on fiber traits using chromosome substitution lines. CS special issue (accepted 2017 Mar. 10)
149. 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 ##:##-##. (IN PRESS) DOI:10.2198/jpr2015.09.0020crg

V. Conferences Attended

Local

- National Association of Plant Breeding, all years (2010-2016)
- Plant Breeding Symposium, Texas A&M University (2015-2017)
- Plant Breeding Symposium, Iowa State University (2016)
- National Conference on Genetics and Cytogenetics, University of Agricultural Sciences, Dharwad (India) (2016)
- CROPS, 2015, Huntsville, Alabama, USA.

International

- International Cotton Genome Initiative, biennially, (2002/Nanjing, 2004/Hyderabad, 2006/Brazilia, 2008/Anyang, 2010/Canberra, 2012/Raleigh, 2014/Wuhan, 2016/Goiania)
- Chromosome Conference, Joetsu, Japan (1997)
- Asia Chromosome Conference-2, Daejeon (Korea) (2004)
- Crop Science Society of America, miscellaneous locations and multiple years (1976-now)
- Plant (and Animal) Genome Conference, San Diego, California, USA (22 conferences during 1993-now)
- China-U.S. Relations Conferences, 2003 (College Station) and 2007(Washington DC)
- World Cotton Research Conference-4 (2008/Lubbock), -5 (2012/Mumbai), and -6 (2016/Goiania)

VI. List three most innovative achievements that qualifies you for the ICAC award (No more than 100 words each):

1. **Isogenic Upland cotton platform for cytogenetic stock development and manipulation of *Gossypium hirsutum* L.:**Dr. Stelly created an isogenic platform of monosomic, translocation and

monotelodicentric (acrocentric) Upland cotton, as well as **interspecific "Chromosome Substitution"(CS) lines and derivatives from them (CS-RILs and CS-CS line intercrosses).**These deliver 100,000-200,000 alien alleles into a *G. hirsutum*background that is easily analyzed genetically and easily used for breeding. New SNP genotyping capabilities (below) render them very amenable to marker-based analysis and manipulation.

2.**SNP Genotyping for Cotton, Globally:** Dr. Stelly has revolutionized global cotton research capabilities by enabling global use of SNPs for large-scale AND targeted small-scale applications. He led formation of the International **"Cotton SNP Chip Consortium"** and development of the **"CottonSNP63K Array"**, which enables high quality, high-density SNP genotyping of Upland cottons that are pure *G. hirsutum* (intraspecific) or contain germplasm from other tetraploid species (interspecific). He also published **inexpensive methods for nondestructive seed/seedling DNA extraction and efficient MAS**. *These innovationsgreatly empower cotton scope and speed of research and education on global scale.*

3.**Cotton Genome Sequencing:** Dr. Stelly has been involved with the international development of cotton structural genomics from the outset. He was among the key contributors to high-quality assemblies of the D5 genome of *Gossypium raimondii*, the extant Peruvian wild diploid cotton (26 chromosomes, 1C = ~800 Mbp) in 2012, and the $(AD)_1$ genome assembly for Upland cotton reported in 2015. These advances are leading to transformations in multiple scientific and applied disciplines of cotton.

VII. Your Biographical Sketch (No more than 300 words):

Professor David M. Stelly holds joint appointments with Texas A&M University (teaching) and Texas A&M AgriLife Research (research) in the Department of Soil & Crop Sciences.

Dr. Stelly has over 30 years of professional experience and leadership in plant breeding of cotton and other diploid and polyploid crops, germplasm introgression, reproductive biology and cytology, cytogenetics, genetic and genomics. His research and breeding emphasize the improvement of our ability to use of naturally occurring germplasm for crop improvement, especially cotton improvement. Hisscientific endeavors entaila broad spectrum of wild species germplasm, introgression methods, chromosome substitution, ploidy manipulations, conventional cytogenetics and fluorescence in situ hybridization (FISH), genetic analysis, SSR and SNP marker development, genotyping, genome and trait mapping, marker assisted selection, reproductive cytology and genetics, various types of genome mapping (linkage, BAC physical, radiation hybrid), genomics, sequencing and their integration. He has (co)authored over 150 edited and refereed publications.

Dr. Stelly also contributessignificanteducational and servicesto his institution, nation and domestic scientific groups, and he participates in four graduate degree programs: (*i*) Plant Breeding, (*ii*) Genetics, (*iii*) Molecular & Environmental Plant Sciences, and (*iv*) Professional Program in Biotechnology. Examples at the national level include serving as President of the National Association of Plant Breeders (NAPB), as an external review panelist for the USDA National Program 301 (Plant Genetic Resources, Genomics and Genetic Improvement) and as a member of the National Academy of Sciences GE Crops Committee that authored a major report on the past and future of GE crops. He is highly engaged and very well known internationally among cotton researchers,presented invited talks in many countries, and is currrently the Chair of the International Cotton Genome Initiative. Recent and ongoing cytogenetics, genetics, genomics, germplasm and breeding research involvescollaboratorson 5 continents.

VIII. Final Comments, if any:

In addition to the book chapters mentioned above, Dr. Stelly contributed significantly to two other important major recent publications

Dictionary of Cotton. International Cotton Advisory Committee and Cotton Researchers Association. 2016. Washington, D.C., . p. 174. *(Contributed by Singh, A.P., Lonnies, B., Campbell, B.T., Armijo, C.B., Munk, D., Dodds, D., Stelly, D., Whitelock, D.P., Oosterhuis, D., Monga, D., Hughs, S.E., Grobien, F., Constable, G., Stewart, J., Lacape, J., Wanjura, J.D., Pepper, L.R., Wilson, L., Matusiak, M., Zimniewska, M., Giband, M., Dowd, M.K., Chaudry, M.R., Abidi, N., Wakelyn, P., Hutmacher, R., Kranthi, S., Mansoor, S., Ferrign, S., Allen, S.J., Gordon, S., Zaidi, S., Townsend, T.P.)*

National Academies of Sciences, Engineering, and Medicine, 2017. Genetically Engineered Crops: Experiences and Prospects. National Academies Press. p. 608 *(Contributed by Fred Gould, Richard M. Amasino, Dominique Brossard, C. Robin Buell, Richard A. Dixon, José B. Falck-Zepeda, Michael A. Gallo, Ken Giller, Leland Glenna, Timothy S. Griffin, Bruce R. Hamaker, Peter M. Kareiva, Daniel Magraw, Carol Mallory-Smith, Kevin Pixley, Elizabeth P. Ransom, Michael Rodemeyer, David M. Stelly, C. Neal Stewart, Robert J. Whitaker. Kara N. Laney, Janet M. Mulligan, Jenna Briscoe; Samuel Crowell, Maria Oria, Robin A. Schoen, Norman Grossblatt)*

IX. Attach your photo: