

**DEPARTMENT OF PLANT AND SOIL SCIENCE
TEXAS TECH UNIVERSITY
LUBBOCK, TX 79409-2122
Curriculum Vitae**

Thea A. Wilkins
Professor

Education:

- Ph.D. Michigan State University. 1990. Plant Cell and Molecular Biology
- M.S. University of Georgia. 1993. Plant Genetics/Breeding
- B.S. Georgia Southern University. 1980. Plant Biology (*Summa Cum Laude*)

Research Positions:

- 2006-present Professor, Dept. of Plant & Soil Science, Texas Tech University
- 2001- 2005 Professor, Dept. of Plant Sciences, University of California-Davis
- 2004-present Adjunct Professor, Cotton Functional Genomics, Chinese Cotton Research Institute, Anyang, Henan Province, PRC
- 2003-present Co-Director, Cotton Functional Genomics Project, National Institute for Biotechnology & Genetic Engineering, Pakistan
- 2002-2005 Director, UCD Cotton Functional Genomics Center, University of California-Davis
- 1998-2002 Director, NSF (virtual) Cotton Genome Center, University of California-Davis
- 1996-2001 Associate Professor, Dept. of Agronomy and Range Science, University of California-Davis
- 1990-1996 Assistant Professor, Dept. of Agronomy and Range Science, University of California-Davis
- 1986-1989 Research Assistant, MSU-DOE Plant Research Laboratories, Michigan State University

Professional Service:

- 2004-2007 Western Section Representative to the Executive Committee of the American Society of Plant Biologists (ASPB)
- 2004-2005 Committee to draft ICGI Constitution & By-laws
- 2003-2005 Chair, International Cotton Genome Initiative, Functional Genomics Workgroup
- 2003-2004 Chair, Western Section American Society of Plant Biologists (WASPB)
- 2000-present Member, Executive Steering Committee for the International Cotton Genome Initiative (ICGI)
- 2000-present Member, Southern Regional Research Project S-304 on Development of Genetic Resources for Cotton
- 1998-2002 Associate Editor, *Journal of Cotton Science*

1999-present Editorial Board, *Journal of Cotton Science*
 1999, 2002-04 NSF Metabolic Biochemistry Review Panel
 1990-present Member, Genetics Graduate Group, Plant Biology Graduate
 Group, UC Biotechnology Program, Plant Genomics Education
 and Research Program

Publications:

Raikhel, N.V. and **T.A. Wilkins**. 1987. Isolation and characterization of a cDNA clone encoding wheat germ agglutinin. *Proc. Natl. Acad. Sci. USA* 84:6745-6749.

Raikhel, N.V., **T.A. Wilkins**, and W.M. Ainley. 1987. Isolation of cDNA clone encoding wheat germ agglutinin. *In: "UCLA Symposia on Molecular and Cellular Biology, New Series"*, V.62, A.R. Liss, NY, pp. 153-160.

Raikhel, N.V., **T.A. Wilkins** and M.A. Mansfield. 1988. Molecular basis of post-translational modifications of wheat germ agglutinin. *Current Topics in Plant Biochemistry and Physiology*. V. 7:83-89.

Raikhel, N.V., S.Y. Bednarek, and **T.A. Wilkins**. 1988. Cell-type specific expression of a wheat germ agglutinin gene in embryos and young seedlings. *Planta* 176:406-414.

Wilkins, T.A. and N.V. Raikhel. 1989. Expression of rice lectin is governed by two temporally and spatially regulated mRNAs in developing embryos. *The Plant Cell* 1:541-549.

Galau, G.A. and **T.A. Wilkins**. 1989. Alloplasmic male sterility in AD allotetraploid *Gossypium hirsutum* upon replacement of its resident A cytoplasm with that of D species *G. harknessii*. *Theor. Appl. Genet.* 78:23-30.

Wilkins, T.A., S.Y. Bednarek and N.V. Raikhel. 1990. Role of propeptide glycan in post-translational processing and transport of barley lectin to vacuoles in transgenic tobacco. *Plant Cell* 2:301-313.

Yates, I.E., E.A. Carter, **T.A. Wilkins**, and B.W. Wood. 1990. Seasonal variation in polypeptide profiles and cellular structure of pecan leaves. *J. Amer. Soc. Hort. Sci.* 115:924-929.

S.Y. Bednarek, **T.A. Wilkins**, J.D. Dombrowski, and N.V. Raikhel. 1990. A carboxyl-terminal propeptide is necessary for correct sorting of barley lectin to vacuoles in tobacco. *Plant Cell* 2:1145-1155.

Wilkins, T.A. 1993. Vacuolar H⁺-ATPase 69-kilodalton catalytic subunit cDNA from developing cotton (*Gossypium hirsutum*) ovules. *Plant Physiol.* 102:679-680.

Wan, C-Y and **T.A. Wilkins**. 1993. Spermidine facilitates PCR amplification of target DNA. *PCR Methods and Applications*. 3:208-210.

Wan, C.-Y. and **Wilkins, T.A.** 1994. Isolation of multiple cDNAs encoding the vacuolar H⁺-ATPase subunit B from developing cotton (*Gossypium hirsutum* L.) ovules. *Plant Physiology* 106:393-394.

Wilkins, T.A., Wan, C.-Y., and Lu, C.-C. 1994. Ancient origin of the vacuolar H⁺-ATPase 69-kilodalton catalytic subunit superfamily. *Theoretical and Applied Genetics* 90:514-524.

Wan, C.-Y. and **Wilkins, T.A.** 1994. A modified hot borate method significantly enhances the yield of high quality RNA from cotton (*Gossypium hirsutum* L.). *Analytical Biochemistry* 223:7-12.

Tiwari, S. C. and **Wilkins, T.A.** 1995. Cotton (*Gossypium hirsutum*) seed trichomes expand via diffuse growing mechanism. *Can. J. Bot.* 73:746-757.

Hasenfratz, M.-P., Tsou, C.-L. and **Wilkins, T.A.** 1995. Expression of two related vacuolar H⁺-ATPase 16 kD proteolipid genes is differentially regulated in a tissue-specific manner. *Plant Physiology* 108:1395-1404.

Wilkins, T.A. and L.B. Smart. 1996. Isolation of RNA from plants. Chapter 2. *In* A Laboratory Guide to RNA: Isolation, analysis and synthesis (P. Kreig, ed.). Wiley & Sons. pp. 21-41.

Kim, W. and **T.A. Wilkins**. 1997. Isolation of a vacuolar H⁺-ATPase subunit E cDNA from developing cotton (*Gossypium hirsutum* L.) fibers (Accession No. AF009338) (PGR 97-126). *Plant Physiology* 115:314.

Vojdani, F., W. Kim and **T.A. Wilkins**. 1997. Phosphoenolpyruvate carboxylase cDNAs from developing cotton (*Gossypium hirsutum* L.) fibers (Accession No. AF008939 and AF008940) (PGR 97-135). *Plant Physiology* 115:315.

Dirk, L.M.A. and **T.A. Wilkins**. 1998. Current status in cotton molecular genetics. Part VI, Chapter 42. *In* Cotton Physiology Book II (J.McD. Stewart, D. Oösterhuis and J. Heitholt, eds). Cotton Foundation, Memphis.

Smart, L.B., F. Vojdani, M. Maeshima and **T.A. Wilkins**. 1998. Genes involved in osmoregulation during turgor-driven cell expansion of developing cotton (*Gossypium hirsutum* L.) fibers are differentially regulated. *Plant Physiol.* 116:1539-1549.

Loguercio, L.L. and **Wilkins, T.A.** 1998. Two genomic clones encoding 3-hydroxy-3-methylglutaryl-coenzyme A reductase (Accession Nos. AF038045 and AF038046) from cotton (*Gossypium hirsutum* L.). *Plant Physiol.* 116:869.

Loguercio, L.L. and **T.A. Wilkins**. 1998. Structural analysis of a hmg-coA pseudogene: insights into evolutionary processes affecting the *hmgr* gene family in cotton (*Gossypium hirsutum* L.). [Current Genetics 34:241-249](#). (pdf format)

Downie, B., L.M.A. Dirk, K.A. Hadfield, **T.A. Wilkins**, A.B. Bennett, and K.J. Bradford. 1998. A gel diffusion assay for quantification of pectin methylesterase activity. [Analytical Biochemistry 264:149-157](#). (pdf format)

Wilkins, T.A. and J.A. Jernstedt. 1999. Chapter 9. Molecular genetics of developing cotton fibers. *In* Cotton Fibers (A.M. Basra, ed.). Food Products Press, New York. pp. 231-267.

Loguercio, L.L., J.-Q. Zhang and **T.A. Wilkins**. 1999. Differential regulation of six novel *myb*-domain genes define two distinct expression patterns in allotetraploid cotton (*Gossypium hirsutum* L.). [Molecular & General Genetics 261:660-671](#). (pdf format)

Kim, W., C.-Y. Wan, and **T.A. Wilkins**. 1999. Functional complementation of yeast *vma1* cells by a plant subunit A homolog rescues the mutant phenotype and partially restores vacuolar H⁺-ATPase activity. [Plant Journal 17:501-510](#).

Loguercio, L.L., H.C. Scott, N.L. Trolinder, and **T.A. Wilkins**. 1999. Hmg-co-A reductase gene family in cotton (*Gossypium hirsutum* L.): Unique structural features and differential expression of *hmg2* are potentially associated with synthesis of specific isoprenoids in developing embryos. *Plant Cell Physiology* 40:750-761.

Schumacher, K., D. Vafeados, M. McCarthy, H. Sze, **T.A. Wilkins** and J. Chory. 1999. The Arabidopsis *det3* mutant reveals a central role for the vacuolar H⁺-ATPase in plant growth and development. [Genes & Development 13:3259-3270](#).

Wilkins T.A., Jernstedt JA. 1999. Molecular genetics of developing cotton fibers. Chapter 9. *In* Cotton Fibers (A.M. Basra, ed). Hawthorne Press, New York. pp. 231-267.

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Kim W, Wan C-Y, **Wilkins T.A.** 1999. Functional complementation of yeast *vma1*Δ cells by a plant subunit A homolog rescues the mutant phenotype and partially restores vacuolar H⁺-ATPase activity. *Plant J* 17:501-510.

Loguercio LL, Scott HC, Trolinder NL, **Wilkins T.A.** 1999. Hmg-co-A reductase gene family in cotton (*Gossypium hirsutum* L.): Unique structural features and

differential expression of *hmg2* are potentially associated with synthesis of specific isoprenoids in developing embryos. *Plant Cell Physiol* 40:750-761.

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Wilkins, T.A., K.A. Rajasekaran, and D.M. Anderson. 2000. Cotton Biotechnology. *Critical Reviews in Plant Sciences* 15:511-550.

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Tomkins JP, Peterson D, Yang T, **Wilkins T.A.**, Paterson AH, Frisch DA, Wing RA. 2001. Development of genomic resources for cotton (*Gossypium hirsutum*): BAC library construction, preliminary STC analysis, and identification of clones associated with fiber development. *Molec Breeding* 8:255-261.

Chen X., Kanokporn T, Zeng Q, **Wilkins T.A.**, Woods AJ. 2001. Characterization of the V-type H⁺-ATPase in the resurrection plant *Tortula ruralis*: Post-transcriptional gene control of the proteolipid c subunit in response to salinity. *J Expt Bot* 53:225-232.

Chen X., Kanokporn T, Zeng Q, **Wilkins T.A.**, Woods AJ. 2001. Characterization of the V-type H⁺-ATPase in the resurrection plant *Tortula ruralis*: Post-transcriptional gene control of the proteolipid c subunit in response to salinity. *J Expt Bot* 53:225-232.

Tomkins JP, Peterson DG, Yang TJ, Frisch DA, **Wilkins T.A.**, Paterson AH, Wing RA. 2001. Development of genomic resources for cotton (*Gossypium hirsutum*): BAC library development, preliminary STC analysis, and identification of clones associated with fiber development. *Molec Breed* 8:255-261.

Cedroni ML, Cronn RC, Adams KL, **Wilkins T.A.**, Wendel JF. 2003. Evolution and expression of *GhMYB* genes in diploid and polyploid cotton. *Plant Molec Biol* 51:313-325.

Senchina DS, Alvarez I, Cronn RC, Liu B, Rong J, Noyes RD, Paterson AH, Wing RA, **Wilkins TA**, Wendel JF. 2003. Rate variation among nuclear genes and the age of polyploidy in *Gossypium*. *Molec Biol Evol* 20:633-643.

Mishra R, Wang H-Y, Yadav N, **Wilkins T.A.** 2003. Development of highly regenerable elite Acala cotton (*Gossypium hirsutum* L.) – A step towards genotype-independent regeneration. *Plant Cell Tiss Org Cult* 73:21-35.

Wilkins T.A. 2003. Cotton fiber biology: Integrating genomics and development for improving fiber traits. (Plenary Paper) *World Cotton Research Conference Proceeding* 3.

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Cedroni ML, Cronn RC, Adams KL, **Wilkins T.A.**, Wendel JF. 2003. Evolution and expression of *MYB* genes in diploid and polyploid cotton. *Plant Molec Biol* 51:313-325.

Rong J, Abbey C, Bowers JE, Brubaker CL, Chang C, Chee P-W, Delmonte TA, Ding X, Garza JJ, Marler BS, Park C-H, Pierce GJ, Rainey KM, Rastogi VK, Schultze SR, Trolinder NL, Wendel JF, **Wilkins T.A.**, Williams-Coplin D, Wing RA, Wright RJ, Zhao X, Zhu L, Paterson AH. 2004. A 3347-locus genetic recombination map of sequence-tagged sites reveals features of genome organization, transmission and evolution of cotton (*Gossypium*). *Genetics* 166:389-417.

Wilkins T.A., Mishra R, Trolinder NL. 2004. *Agrobacterium*-mediated transformation and regeneration of cotton. *Journal of Food, Agriculture Environment*.

Arpat AB, Waugh M, Sullivan JP, Gonzales M, Frisch D, Main D, Wood T, Leslie A, Wing RA, **Wilkins T.A.** 2004. Functional genomics of developing cotton fibers. *Plant Molecular Biology*.

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Wilkins T.A., Mishra R, Trolinder NL. 2004. *Agrobacterium*-mediated transformation and regeneration of cotton. *J Food Agric Environ* 2:179-187.

Rong J, Abbey C, Bowers JE, Brubaker CL, Chang C, Chee P-W, Delmonte TA, Ding X, Garza JJ, Marler BS, Park C-H, Pierce GJ, Rainey KM, Rastogi VK, Schultze SR, Trolinder NL, Wendel JF, **Wilkins T.A.**, Williams-Coplin D, Wing RA, Wright RJ, Zhao X, Zhu L, Paterson AH. 2004. A 3347-locus genetic recombination map of sequence-tagged sites reveals features of genome organization, transmission and evolution of cotton (*Gossypium*). *Genetics* 166:389-417.

Rong J, Pierce GJ, Waghmare VN, Rogers CJ, Desai A, Chee PW, May OL, Gannaway JR, Wendel JF, **Wilkins T.A.**, Paterson AH. 2005. Genetic mapping and comparative analysis of seven mutants related to seedborne fiber development in cotton. *Theor Appl Genet* 111:1137-1146.

Park Y-H, Alabady MS, Sickler BA, **Wilkins T.A.**, Yu J, Stelly DM, Kohel RJ, El-Shihy OM, Cantrell RG, Ulloa M. 2005. Genetic mapping of new cotton fiber loci using EST-derived microsatellites in an interspecific recombinant inbred line (RIL) cotton population. *Molec Gen Genomics* 274:428-441.

Wilkins T.A., Arpat AB. 2005. The cotton fiber transcriptome. *Physiol Plantarum* 124:295-300.

Udall JA, Swanson JM, Haller K, Rapp RA, Sparks ME, Hatfield J, Yu Y, Wu Y, Dowd C, Arpat AB, Sickler BA, **Wilkins T.A.**, Guo J-Y, Chen X-Y, Scheffler J, Taliencio E, Turley R, McFadden H, Payton P, Allen R, Zhang D, Haigler C, Wilkerson C, Suo J, Schulze SR, Pierce ML, Essenberg M, Kim H, Llewellyn DJ, Dennis ES, Kudrna D, Wing R, Paterson AH, Soderlund C, Wendel JF. 2006. A global assembly of cotton ESTs. *Genome Res* 16:441-450.

In Preparation:

Udall J, et al. (200X) Cotton ESTs. In Preparation.

Mishra R, Alabady MS, **Wilkins TA** (200X) *Agrobacterium*-mediated cotton transformation: A rapid procedure suitable for high-throughput applications in agricultural biotechnology. In Preparation.

Alabady MS, Arpat AB, Wright R, **Wilkins TA.** (200X) Fiber alleles differentially expressed in Pima cotton are linked to major fiber quality QTL. In Preparation.

Wilkins TA, Alabady MS, Sickler B, Kim WB, Sutter E (200X) Termination of auxin-induced cell elongation in developing cotton fibers is triggered by increasing cellular concentrations of ABA that suppress auxin-regulated gene expression. In Preparation.

Sickler B, Arpat AB, **Wilkins TA.** (200X) Developmental regulation of the cotton fiber transcriptome during primary and secondary cell wall synthesis: dynamics of carbon partitioning. In Preparation.

Wilkins TA. (200X) Sustainability of GM cotton. *In* Biotechnology in Agriculture and Forestry (Pua EC, Widholm MR, eds) Springer Press. Invited Chapter: In Preparation.

Wilkins, TA. (200X) Cotton Fiber Biology. In: Cotton Genomics (A.H. Paterson, ed.), a planned series on Plant Genetics and Genomics (series editor R. Jorgenson).

Wilkins, TA. and M. Ulloa, eds. (200X) Cotton Genomics. A book in planned series on Crop Genomics (series editor C. Kole).

In Review:

Hendrix BL, Stewart JMcD, **Wilkins TA.** (200X) Gene expression in developing fibers as a model for water-deficit stress in cotton. Submitted.

Arpat AB, Hequet EF, **Wilkins TA.** (200X) Expression profiling of the cotton fiber transcriptome in *Naked Seed* mutants reveals novel genes involved in fiber cell morphogenesis. Submitted.

In Press:

Wilkins TA, Arpat AB, Sickler B. 2005. Manipulating the cotton fiber transcriptome for genetic improvement of agronomic traits. *Pflanzenschutz Nachrichten*:In Press.

Reports and Proceedings:

Wilkins, T.A. and J.B. Weaver, Jr. 1983. Transfer of the Pima Enhancer Factor into cytoplasmic male sterile lines. Proc. Beltwide Cotton Prod. Res. Conf. pp. 98-99.

Wilkins, T.A. 1992. Applications of biotechnology in enhancing resistance to plant pests. Proceedings California Plant and Soil Conference. pp. 95-98.

Wilkins, T.A. 1992. Role of proton pumps in cotton fiber development. Proceedings of the Cotton Fiber Cellulose Conference. pp. 145-152.

Kerby, T. and **T.A. Wilkins.** 1992. Factors that influence fiber length. California Cotton Review. Vol. 27. October issue.

Wilkins, T.A. and Tiwari, S.C. 1995. Cotton fiber morphogenesis: A subcellular odyssey. Proceedings Cotton Fiber Cellulose Conference. pp. 89-94.

Wilkins, T.A. 1995. Biotechnology Update: Transgenic Cotton Germplasm with Gossypol-free Seed Under Development at UC-Davis. California Cotton Review. Vol. 38. December issue.

Wilkins, T.A. 1996. Cotton Molecular Genetics Program Progress Report. Cotton Workgroup Meeting. Kearney Agricultural Research Station, Reedley.

Wilkins, T.A. 1996. Bioengineering fiber quality: Molecular determinants of fiber length and strength. Proc. Beltwide Cotton Research Conf., pp. 1679-1680.

Wilkins, T.A. 1996. Performance of Bt Cotton: Status report. California Cotton Review 41:3-4.

Wilkins, T.A. 1997. Cotton Molecular Genetics Program Progress Report. Cotton Workgroup Meeting. Kearney Agricultural Research Station, Reedley.

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Wilkins, T.A., R.B. Turley, N. Trolinder, L. Koonce, J. Dever, K. Rajasekaran, A. Zipf, and A. Nepomuceno. 1998. Cotton biotechnology: the rudiments of cotton transformation and biotechnology. Proc. Beltwide Cotton Prod. Res. Conf. pp. 96-99.

Rajguru, S.N., J.M. Stewart, and **T.A. Wilkins**. 1998. Assessment of resistance of cotton transformed with lectin genes to tobacco budworm (*Heliothis virescens*). Proc. Beltwide Cotton Prod. Res. Conf. pp. 490-492.

Wilkins, T.A. 1998. Cotton Molecular Genetics Program Progress Report. Cotton Workgroup Meeting. Kearney Agricultural Research Station, Reedley.

Wilkins TA. 2003. Cotton functional genomics. S-304 Regional Progress Report.

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Wilkins TA, Mishra R. 2003. **Notice of release**..... *Agric Expt Stn*

Patents:

Wilkins TA (2004) Cotton Transcription Factors and their Uses. U.S. Patent No. 6,828,476.

Wilkins TA (2006) Bioengineering Cotton Fiber Properties. U.S. Patent No. 7,060,874B2.

Synergistic Activities:

Integration of research and education: In keeping with the mission of the department, college and campus, my focus on crop improvement using molecular tools integrates basic and applied research with agricultural applications is tightly linked to training, education and outreach activities. I have mentored 8 graduate students, 8 postdoctoral scientists, 40 undergraduates, and 5 high school students, served as academic advisor to undergraduate and graduate students, serve on 2-3 thesis committees each year, and serve on curriculum development committees at both the graduate and undergraduate levels.

Innovations in teaching and training: My primary teaching responsibility, which incorporates cutting edge technological advances, including those from my research program, is Plant Genetics & Genomics. In the last two years, I have incorporated teaching modules in bioinformatics and functional genomics as companions to 10 extensive problem sets that utilize data from our genome research. Student evaluations for this class average 4.5/5.0. I participated in creating a Biotechnology major, and designed and served as lead instructor for two requisite lab courses (PLB161A/B) in Plant Genetics & Biotechnology. I also serve as a participating member of the campus Biotechnology Program, and am currently a trainer on two campus education grants.

Development of research tools, computation methods, and algorithms for problem-solving: We have established criteria to quality-control EST and microarray data as part of our SOPs that will serve as the standard for the cotton community. Programs were tested and evaluated to set parameters to provide high quality unigene sets subjected to functional binning. We developed software to allow normalization of filter macroarrays to eliminate 80% redundancy in EST projects (Arpat *et al.* 2004). New algorithms and software were developed for mining of our fiber dbEST for SSRs as the first step towards aiding the community in development of robust, portable PCR-based DNA markers (Park *et al.* 200X; <http://cfgc.ucdavis.edu>). Significant advances in cotton biotechnology were made with NSF funding (Mishra and Wilkins 2003; Wilkins *et al.* 2004; Mishra and Wilkins, In Prep).

Development of databases: Public databases developed under NSF support (DBI 9872630) includes a searchable EST database binned by function using GO, and a cDNA clone relational db to facilitate ordering of biological materials through the UCD Cotton Functional Genomics Center. The db has been expanded to allow posting of microarray data. We have established the foundation for linking ESTs to markers and map data (www.plantgenome.uga.edu) and other relevant sites.

Broadening participation of under-represented groups: Past and present members of my research group are equally distributed by gender, the majority of which are represented by diverse ethnic backgrounds (Asian, Indian, African, Hispanic, Vietnamese-American, Chinese-American, and Turkish).

Professional Service: I have been an Associate Editor and serve on an Editorial Board, served as an ad hoc reviewer for journals and panelist for state, campus,

commodity, federal and international funding agencies, and am the former Chair of the Western Section of the American Society of Plant Biologists (ASPB), and now serve as the WAPB representative to the ASPB Executive Committee. I am a scientific advisor on two major international programs, and have collaborative ties to the international community, including as member of the International Cotton Genome Initiative's (ICGI) Executive Steering Committee, and Chair, of ICGI's Functional Genomics Workgroup.

Funding (1993-2007): >\$9,000,000 from NSF, DOE, USDA, Cotton Incorporated, US-Egypt Technical Program, Biotechnology Program, and commodity groups, excluding numerous training and education grants

Current Funded Research:

1. Cotton Functional Genomics. \$1,195,000. 2006-2007. Texas Tech University. (PI)
2. Cotton Genomics. \$1,945,000. 2006-2008. Texas Governor's Emerging Technology Fund (ETF). (PI)
3. Discovering Nucleotide Diversity in Cotton. \$420,000. 2000-2008. USDA U.S. – Egypt Joint Research Program. (Co-PI)
4. Multidisciplinary Approach to investigate the Link between Secondary Cell Wall Biogenesis and Cotton Fiber Maturity. 2006-2007. International Cotton Research Council. (PI)
5. Equipment to Establish an Advanced Natural Fiber Structural Analysis Laboratory. International Cotton Research Center. \$60,000. 2006-2007. (Co-PI)
6. Improving West Texas Cotton. \$115,000. 2007. Texas State Support Committee. (Co-PI)
7. Multidisciplinary Approach to Study Cotton Fiber Maturity. \$35,000. 2007. Texas Food and Fiber. (PI)

Thesis Advisor and Postgraduate-Scholar Sponsored:

Graduate Students in Progress:

M.S.

W. Zhou, A. Leslie, C-L. Tsou (M.S.).

Ph.D.

A.B. Arpat (Ph.D.)

B.A. Sickler (Ph.D.)

M. Sh. Al-Abady (Ph.D.).

Prior. C.-Y. Wan, W. Kim, L.L. Loguercio (Ph.D.),

Postdoctoral Scientists (6). Current: R. Mishra, Young-Hoon Park. Prior: F. Zhou, S. Tiwari, L.B. Smart, F. Vojdani, L. Dirk