

Name: Andrew H. Paterson

Rank: Distinguished Research Professor; Director, Plant Genome Mapping Laboratory, University of Georgia



Statement of interests: My lab studies intrinsic genetic properties that make plants different from other organisms and from one another. In particular, selected plants have become crops because of unique attributes that also make them valuable as botanical models. Crop genetics thus offers the opportunity to increase basic scientific knowledge and apply it to contemporary needs. Our priorities are to explore basic principles of genetics and evolution in the genomes of model organisms, and to accelerate assembly of the genomic frameworks that will permit such principles to be applied to the study and improvement of major crops.

Employment:

July 2002: Distinguished Research Professor, Univ. Georgia.

Jan. 1999: Professor, Univ. Georgia, Depts Crop and Soil Sci; Plant Biology; Genetics.

Sept 1998: Professor, Texas A&M, Dept Soil and Crop Sci.

July 1996, appointed holder of Christine Richardson Endowed Professorship.

Sept 1995: Associate Professor with tenure, Dept Soil and Crop Sci., Texas A&M.

March 1991. Assistant Professor, Dept Soil and Crop Sci., Texas A&M.

Member, Graduate Fields of Genetics, and Plant Physiology/Biotechnology.

Nov. 1989. Adjunct Assistant Prof. of Plant Molecular Biology, Univ. Delaware.

1989-1991: Principal investigator, Ag. Biotechnology, E.I. DuPont de Nemours,

1987-89: Postdoctoral associate, Cornell University (Lab of S. Tanksley).

Education:

Ph.D., Cornell University, 1988; Plant Genetics (minors: Genetics, Plant Physiology).

M.S., Cornell University, 1985; Plant Breeding (minor: Agronomy).

B.S., Univ. of Delaware, 1982; Agriculture (Summa Cum Laude).

Selected Honors, Awards, Organization Appointments:

2006: DOE Joint Genome Institute Community Sequencing Program User Committee

2006: D. W. Brooks Program (UGA): Chair, Research Award Selection Committee and Member, Executive Committee

2006: Chair, Sorghum Genomics Executive Committee

2006: Who's Who in Agriculture Higher Education (AcademicKeys)

2005-6: Chair, Comparative genomics workgroup, International Cotton Genome Initiative.

2005: Principal investigator, Cotton Coordinated Agricultural Project Planning Grant.

2005: D. W. Brooks Award for Excellence in Research, Univ. Georgia.

2004-date: Peanut Genomics Steering Committee: Leader, Genome Structural Analysis.

2004-date: Steering Committee, Sorghum Genomics Executive Committee.

2003-4: Chair, Bioinformatics workgroup, International Cotton Genome Initiative.

2003-4: Co-chair, Comparative genomics workgroup, International Cotton Genome Initiative.

2002-date: Co-Director, *Genes for Georgia* initiative (<http://plantgenome.agtec.uga.edu/g4g/>)

2002-date: Council for Biotechnology Information (CBI) Community Action Network.

2001-2: ESCOP/ACOP Leadership Program (NASULGC).

2001-date: Steering committee, International Cotton Genome Initiative.

2000-2005: Director, IFAFS Virtual Center, *Reducing the Genetic Vulnerability of Cotton*
1999-2002: Director, AGTEC Plant Initiative (Univ. Georgia)
1998-date: Director, NSF-Comparative Grass Genomics Center (cggc.agtec.uga.edu)

Grants and Contracts: Dr Paterson has secured \$24.6 million, including \$17.1 million as Principal Investigator (42% of which supported his colleagues), and \$7.5 million as co-investigator on awards totaling \$38.1 million to his colleagues. He has secured two competitive training grants of \$108,000 (PI) and \$1.6 million (co-PI), one regional economic development grant (\$600,000), and has helped 31 scholars to secure \$1.14 million to study in his lab. He is the PI on a non-cash award (est. \$8 million) from the US Dept of Energy Joint Genome Institute 'Community Sequencing Program' to sequence the 736 Mb sorghum genome, and a non-cash award (est. \$1 million) to conduct pilot-scale (500 Mb) sequencing of *Gossypium raimondii*, toward the formulation of an efficient strategy to sequence its entire genome.

Mentoring. Dr Paterson has mentored 43 postdoctoral scientists (currently 6), 39 graduate students (currently 6 Ph.D.), and 78 undergraduates (presently 4).

Professional service: Associate editor (current): Genetics (93 decisions), TAG (1 Jan 2006). Past: Plant Physiology (36 decisions), Crop Sci. (ca. 20 decisions), JPACD, Brazilian J. Genetics, JQTL. Ad hoc reviewer: Nature, Nature Genetics, Nature Reviews Genetics, Science, Cell, PNAS-USA, Genome Research, Plant Cell, Trends in Evol. & Ecol., Trends in Genetics, Trends in Plant Sci., Mol. Biol. Evol., Genetics, Plant Phys., Evolution, New Phytologist, TAG, Biotechnology, Am. J. Botany, MPMI, Physiologia Plantarum, J. Hered., Genome, Crop Sci., Can. J. Forestry, Plant Sci., Molecular Breeding, Aust. J. Plant Sci., J. Genet. Breeding, Tree Physiol., Forest Ecol. & Mgmt. Ad hoc grant reviewer or panelist* for NIH (NIAAA*, NIGMS), NSF (Eukaryotic Genetics, Integrative Bio., Plant Genome, SBIR*), USDA (Biotech. Risk Assessment*, Plt Genome*, Plt Gen. Mech., Weed Sci. Nematology, Ent./Plant Path), USAID*, Consortium for Plant Biotech. Research, Texas Higher Education Coordinating Board (ARP), Southwest Consortium on Plant Genetics and Water Resources, Civilian Research and Development Foundation, NSERC (Canada), BARD (Israel), Genoscope (France), ICGEB, Israel Science Foundation, Marsden Fund, CGIAR* (Multinational). Scientific Advisory Board: SUCEST, Rockefeller Foundation (drought stress initiative), NSF YIA project.

Societies and Appointments: AAAS, American Society of Plant Biologists, Genetics Society of America, Crop Science Society of America, Sorghum Improvement Conference of North America, Professional Assn for Cactus Development, ASHG/GSA K-12 Genetics mentor network. Member, Sorghum Genomics Executive Committee. Steering committee member for the US Peanut Genome Initiative and the Int'l Cotton Genome Initiative (ICGI). Chair, comparative genomics workgroup, ICGI.

Refereed Publications: 173 (13 submitted, 16 in prep). As of August 2006, 9 of his papers had been recommended by the Faculty of 1000 (see *), and his work had been cited 6,727 times (per Web of Science). **Books:** 2 (1 pending). **Chapters:** 40 (4 pending). **Popular press articles:** 6 (1 pending). **Patent applications:** 6. **Invited lectures, seminars, or symposia presentations:** 134.

Refereed Publication list, 1999-date (of 173 total).

1999

- 54) Wright, R., P. Thaxton, A. H. Paterson, K. El-Zik. 1999. Molecular mapping of genes affecting pubescence of cotton. *J. Heredity*, 90:215-219.
- 55) Brubaker, C. L., A. H. Paterson, and J. F. Wendel. 1999. Comparative genetic mapping of allotetraploid cotton and its diploid progenitors. *Genome*, 42:184-203.
- 56) Li, Z., L. Luo, H. Mei, A. H. Paterson, X. H. Zhao, D. B. Zhong, Y. P. Wang, X. Q. Yu, L. Zhu, R. Tabien, J. W. Stansel, C. S. Ying. 1999. A defeated rice resistance gene acts as a QTL against a virulent strain of *Xanthomonas oryzae* pv. *oryzae*. *Mol. Gen. Genet.* 261:58-63.
- 57) Lin, YR, L Zhu, S Ren, J Yang, KF Schertz, AH Paterson. 1999. A *Sorghum propinquum* BAC library, suitable for cloning genes associated with loss-of-function mutations during crop domestication. *Molecular Breeding*, 5:511-520.
- 58) Wang, D., J. Zhu, Z. Li, A. H. Paterson. 1999. A mixed model approach for mapping QTLs with epistatic effects. *Theor. Appl. Genet.*, 99:1255-1264.
- 59) Lan, T-H., C. Cook, and A. H. Paterson. 1999. Identification of a RAPD marker linked to a male-fertility restoration gene in cotton (*Gossypium hirsutum* L.). *J. Agr. Genomics*, Volume 4. <http://www.ncgr.org/ag/jag/papers99/paper299/indexp299.html>.
- 60) Paterson, A. H., Yann-rong Lin, Rei-guang Ming, Keith F. Schertz. 1999. Comparative Crop Genome Analysis: Accelerated "Conversion" of Tropical Sorghums, and Other Opportunities. *Proc. Corn and Sorghum Res. Conf*, pgs 81-89.
- 61) Saranga, Y., I. Flash, A. H. Paterson, D. Yakir. 1999. Carbon isotope ratio in cotton varies with growth stage and plant organ. *Plant Science* 142:47-56.
- 62) Wang, X., P. Felker, A. H. Paterson. 1999. Environmental influences on cactus pear fruit yield, quality and cold-hardiness, and development of hybrids with improved cold hardiness. *Journal of the Professional Association for Cactus Development*, 1997, Vol.2, pp.48-59.
- 63) Choi, K., M.D. Burow, G. Church, G. Burow, A. H. Paterson, C. E. Simpson, J. L. Starr. 1999. Genetics and mechanisms of resistance to *Meloidogyne arenaria* in Peanut. *Journal of Nematology* 31:283-290.
- 64) Wang, X., M. D. Burow, P. Felker, A. H. Paterson. 1998. Comparison of RAPD marker patterns to morphological and physiological data in the classification of *Opuntia* accessions. *Journal of the Professional Association for Cactus Development* vol. 3: 3-14.
- 65) Li, ZK, AH Paterson, SRM Pinson, JW Stansel. 1999. RFLP facilitated analysis of tiller and leaf angles in rice (*Oryza sativa* L.). *Euphytica* 109: 79-84.

2000

- 66) Jiang, C., R. Wright, S-S. Woo, T. A. Delmonte, A. H. Paterson. 2000. QTL analysis of Leaf Morphology in Tetraploid *Gossypium* (Cotton). *Theor. Appl. Genet.* 100:409-418.
- 67) C. Jiang, P. Chee, X. Draye, P. Morrell, C. W. Smith, A. H. Paterson. 2000. Multi-locus interactions restrict gene flow in advanced-generation interspecific populations of polyploid *Gossypium* (cotton). *Evolution* 54:798-814.
- 68) Lan, TH, TA Delmonte, KP Reischmann, J Hyman, S Kowalski, J. McFerson, S Kresovich, AH Paterson. 2000. EST-enriched comparative map of *Brassica oleracea* and *Arabidopsis thaliana*. *Genome Research*, 10:776-788.
- 69) Lan, TH, AH Paterson. 2000. Comparative evolution of QTLs sculpting the curd of *Brassica oleracea*. *Genetics* 155:1927-1954.
- 70) Lin, YR, X Draye, X Qian, S Ren, L Zhu, J Tomkins, RA Wing, Z Li, AH Paterson. 2000. Fine-scale mapping and sequence-ready contig assembly in highly-duplicated genomes, using the BAC-RF method. *Nucleic Acids Research* 28 (7): e23. http://www3.oup.co.uk/nar/methods/Volume_28/Issue_07/gnd023_gml.abs.html.
- 71) Paterson, AH, JE Bowers, MD Burow, X Draye, CG Elsik , C Jiang , CS Katsar , T Lan , Y Lin , R Ming , RJ Wright. 2000. Comparative genomics of plant chromosomes. *Plant Cell* 12:1523-1539.
- 72) Tabien, R., Z. Li, A. H. Paterson, M. A. Marchetti, J. W. Stansel, S. R. M. Pinson. 2000. Mapping of four major rice blast resistance genes from 'Lemont' and 'Teqing' and evaluation of their combinatorial effect for field resistance. *Theor.. Appl. Genet.*, 101:1215-1225.
- 73) Peterson DG, Tomkins JP, Frisch DA, Wing RA, Paterson AH (2000). Construction of plant bacterial artificial chromosome (BAC) libraries: An illustrated guide. *J. Agric. Genomics*, 5: www.ncgr.org/research/jag.
- 74) Vinh, N. T., M. D. Burow, H. T. Nguyen, L. T. Binh, D. L. Thanh, A. H. Paterson. 2001. Molecular mapping of genes conferring aluminum tolerance in *Oryza sativa*. *Theor. Appl. Genet.*, 102:1002-1010.
- 75) Ming, R., C.A. Abbey, F.T. Zee, P.H. Moore, and A.H. Paterson. 2001. A papaya BAC library as a foundation for molecular dissection of tropical fruit genomes. *Theor. Appl. Genet* 102: 892-899.
- 76) Church, G. T., C. E. Simpson, M. D. Burow, A. H. Paterson, J. L. Starr. 2000. Use of RFLP markers for identification of individuals homozygous for resistance to *Meloidogyne arenaria* in peanut. *Nematology* 2:575-580.

2001

- 77) X. Draye, Y. Lin, X. Qian, J. E. Bowers, G. Burow, P. Morrell, D. Peterson, G. G. Presting, S. Ren, R. A. Wing, A. H. Paterson. Toward integration of comparative genetic, physical, diversity, and cytomolecular maps for grasses and grains, using the Sorghum genome as a foundation. *Plant Physiol.*, 125:1325-1334.

- 78) Tabien, R., Z. Li, A. H. Paterson, M. A. Marchetti, J. W. Stansel, S. R. M. Pinson. 2000. Mapping of four major rice blast resistance genes from 'Lemont' and 'Teqing' and evaluation of their combinatorial effect for field resistance. *Theor. Appl. Genet.*, 101:1215-1225.
- 79) Paterson, AH, TH Lan, R Amasino, TC Osborn, CF Quiros. 2001. Brassica genomics – a complement to, and early beneficiary of, the Arabidopsis sequence. *Genome Biology* 2:1011.1-1011.4.
- *80) Li, Z., L. Luo, H. Mei, Q. Shu, D. Wang, R. Tabien, D. Zhong, C. Ying, J. Stansel, G.S. Khush, A. H. Paterson. 2001. Overdominant epistatic loci are the primary genetic basis of inbreeding depression and heterosis in Rice: I. Biomass and Grain Yield. *Genetics* 158:1737-1753.
- 81) Li, Z., L. Luo, H. Mei, Q. Shu, D. Wang, R. Tabien, D. Zhong, C. Ying, J. Stansel, G.S. Khush, A. H. Paterson. 2001. Genetic basis of inbreeding depression and heterosis in Rice: II. Grain yield components. *Genetics*, 158:1755-1771.
- 82) Lan, TH, and A.H. Paterson. 2001. Comparative mapping of QTLs determining the plant size of Brassica oleracea. *Theor. Appl. Genet.*, 103: 383-397.
- 83) Burow, M.D., C. E. Simpson, J. L. Starr, A. H. Paterson. 2001. Transmission genetics of chromatin from a synthetic amphiploid in cultivated peanut (*Arachis hypogaea* L.): Broadening the gene pool of a monophyletic polyploid species. *Genetics* 159: 823-837.
- 84) Aslam, M., C. Jiang, R. Wright, A. H. Paterson. 1999. Identification of Molecular Markers Linked to Leaf Curl Virus Disease Resistance in Cotton. *Pakistan Journal of Biological Sciences*, 2 (1): 124-126.
- 85) Ming, R., S-C. Liu, J. E. Irvine, A. H. Paterson. 2001. Comparative QTL Analysis in a Complex Autopolyploid: Candidate Genes for Determinants of Sugar Content in Sugarcane. *Genome Research* 11:2075-2084.
- 86) Nguyen VT, Thanh LD, Paterson AH, Binh LT, Nguyen HT. 2000. Rapid screening method for aluminum tolerance in rice in nutrient solutions. *J. Genetics and Appl.* 2:5-11.
- 87) J. P. Tomkins, D. Peterson, T. Yang, D. Main, T.A. Wilkins, A.H. Paterson, and R.A. Wing. Development of Genomic Resources for Cotton (*Gossypium hirsutum*): BAC library construction, preliminary STC analysis, and Identification of Clones Associated With Fiber Development. *Molecular Breeding* 8:255-261.
- 88) Saranga, Y., M. Menz, C. Jiang, R. Wright, D. Yakir, A. H. Paterson. 2001. Genomic dissection of genotype x environment adaptation conferring adaptation of cotton to arid conditions. *Genome Research* 11:1988-1995.

2002

- 89) Cox, TS, M Bender, C Picone, DL Van Tassel, JB Holland, CE Brummer, BE Zoeller, AH Paterson, W Jackson. 2002. Breeding perennial grain crops. *Critical Reviews in Plant Sciences* 21:59-91.
- 90) Katsar, C.S., A.H. Paterson, G.L. Teetes, G. Peterson. 2002. Molecular analysis of sorghum resistance to the greenbug, *Schizaphis graminum*. *J. Econ. Entom.* 95:448-457.
- 91) Paterson, AH. 2002. What has QTL mapping taught us about plant domestication? *New Phytol.* 154: 591-608.
- 92) Jessup, R., B. L. Burson, G. Burow, Y-W. Wang, C. Chang, Z. Li, A. H. Paterson, M. A. Hussey. 2002. Disomic inheritance, suppressed recombination, and allelic interactions govern apospory in buffelgrass, as revealed by genome mapping. *Crop Science* 42:1688-1694.
- 93) Ming, R., S-C. Liu, J. E. Bowers, P. H. Moore, J. E. Irvine, A. H. Paterson. 2002. Construction of a *Saccharum* genetic map from two interspecific crosses between *S. officinarum* and *S. spontaneum*. *Crop Science*, 42:570-583.
- 94) Tabien, R., Z. Li, A. H. Paterson, M. A. Marchetti, J. W. Stansel, S. R. M. Pinson. 2002. Mapping QTLs for field resistance to the rice blast pathogen and evaluating their individual and combined utility in improved varieties. *TAG* 105:313-324.
- 95) Ming, R., J. E. Irvine, Y-W. Wang, X. Draye, A. H. Paterson. 2002. Molecular dissection of complex traits in autopolyploids: Mapping QTLs influencing sugar yield and related traits in sugarcane. *Theor. Appl. Genet.*, 105:332-345.
- 96) Schloss, S.J., S.E. Mitchell, G. White, R. Kukatla, J.E. Bowers, A.H. Paterson, S. Kresovich. 2002. Characterization of RFLP probe sequences for gene discovery and SSR development in *Sorghum bicolor* (L.) Moench. *Theor. Appl. Genet.*, 105: 912-920.
- 97) Osterlund, M. T. and A.H. Paterson. 2002. Applied plant genomics: the secret is integration. *Curr. Opin. Plant Biol.* 5:141-145.
- 98) Kulkarni, V., B. M. Khadi, A. M. Badigannavar, A. H. Paterson. 2001. Molecular marker technologies in cotton – a review. *J. Indian Soc. Cotton Improv.* 26:51-60.
- 99) Daniel G. Peterson, Stefan R. Schulze, Erica B. Sciara, Scott A. Lee, John E. Bowers, Alexander Nagel, Ning Jiang, Deanne C. Tibbitts, Susan R. Wessler, and Andrew H. Paterson. 2002. Integration of Cot Analysis, DNA Cloning, and High-Throughput Sequencing Facilitates Genome Characterization and Gene Discovery. *Genome Research*, 12: 795-807.
- 100) Paterson, A. H., Saranga, Y., M. Menz, C. Jiang, R. Wright. 2002. QTL Analysis of Genotype x Environment Interactions Affecting Cotton Fiber Quality. *Theor. Appl. Genet.*, 106:384-396. Online version is s00122-002-1025-y.ch000.html.

- 101) V.T. Nguyen, B.D. Nguyen, S. Sarkarung, C. Martinez, A.H. Paterson, H.T. Nguyen. 2002. Mapping Genes Controlling Al Tolerance in Rice: Comparing Different Genetic Backgrounds. *Mol Gen. Genet.*, 267: 772-780.
- 102) Ming, R., J. E. Irvine, T. A. DelMonte, A. H. Paterson. 2002. Comparative analysis of QTLs affecting plant height and flowering time among closely-related diploid and polyploid genomes. *Genome* 5:794-803.
- 103) Daniel G. Peterson, Susan R. Wessler, and Andrew H. Paterson. 2002. Efficient capture of sequence complexity using Cot-based cloning and sequencing. *Trends in Genetics* 18:547-550.
- 104) Karen Cone, Michael McMullen, Irie Vroh Bi, Georgia Davis, Young-Sun Yim, Jack Gardiner, Mary Polacco, Hector Sanchez-Villeda, Zhiwei Fang, Steven Schroeder, Seth Havermann, John E. Bowers, Andrew H. Paterson, Cari Soderlund, Rod Wing, and Edward Coe. 2002. Genetic, physical and informatics resources for maize: On the road to an integrated map. *Plant Phys.* 130:1598-1605.

2003

- 105) Jessup, R., B. L. Burson, G. Burow, Y-W. Wang, C. Chang, Z. Li, A. H. Paterson, M. A. Hussey. 2003. Segmental allotetraploidy and allelic interactions in buffelgrass, (*Pennisetum ciliare* (L.) Link syn. *Cenchrus ciliaris* L.) as revealed by genome mapping. *Genome* 46:304-313.
- 106) D. S. Senchina, I. Alvarez, R. C. Cronn, B. Liu, A. H. Paterson, J. Rong, R. D. Noyes, R. A. Wing, T. A. Wilkins, and J. F. Wendel. 2003. Rate variation among nuclear genes and the age of polyploidy in *Gossypium*. *Mol. Biol. Evol* 20:633-643.
- *107) Bowers, John E., Brad A. Chapman, Jun-kang Rong, Andrew H. Paterson. 2003. Unravelling angiosperm chromosome evolution by phylogenetic analysis of chromosomal duplication events. *Nature* 422:433-438.
- 108) Hu, F. Y, D. Y. Tao, E. Sacks, P. Xu, J. Li , Y. Yang , K. McNally, G. S. Khush, A. H. Paterson, Z. K. Li. 2003. Convergent Evolution of Perenniality in Grasses. *Proc. Nat. Acad Sci. USA* 100:4050-4054.
- 109) John E. Bowers, Colette Abbey, Sharon Anderson, Charlene Chang, Xavier Draye, Alison H. Lattu, Russell Jessup, Cornelia Lemke, Jennifer Lennington, Zhikang Li, Yannrong Lin, Sin-Chieh Liu, Lijun Luo, Barry S. Marler, Reiguang Ming, Sharon E. Mitchell, Dou Qiang, Kim Reischmann, Stefan R. Schulze, D. Neil Skinner, Yue-wen Wang, Stephen Kresovich, Keith F. Schertz, Andrew H. Paterson. 2003. A high-density genetic recombination map of sequence-tagged sites for *Sorghum*, as a framework for comparative structural and evolutionary genomics of tropical grains and grasses. *Genetics*, 165:367-386.
- 110) Rod A. Wing, Yeisoo Yu, Teri Rambo, Jennifer Currie, Christopher Saski, Hye Ran Kim, Kristi Collura, Shelly Thompson, Jessica Simmons, Tae-Jin Yang, Gyoungju N. Park, Ami J. Patel, Long Mao, Scheen Thurmond, David Henry, Ryan Oates, Michael Palmer, Gina Pries, Jennifer Gibson, Heidi Anderson, Manjiri Paradkar, Lindsay Crane, Jeff Dale, Megan B.-Carver, Todd Wood, David Frisch, Friedrich Engler, Cari Soderlund, Joachim Messing, Rentao Song, Galina Fuks, Victor Llaca, Steve Kovchak, Steve Young, Mitrick A. Johns, Long Mao, Huaqin Pan, Ralph A. Dean, John E. Bowers, Andrew H.

Paterson, Zhukuan Cheng, Jiming Jiang, Qiaoping Yuan, Shu Ouyang, Jia Liu, Kristine M. Jones, Kristen Gansberger, Kelly Moffat, Jessica Hill, Tamara Tsitrin, Larry Overton, Jyati Bera, Mary Kim, Shaohua Jin, Luke Tallon, Anne Ciecko, Grace Pai, Susan Van Aken, Terry Utterback, Steve Reidmuller, Jon Bormann, Tamara Feldblyum, Joseph Hsiao, Victoria Zismann, Stacey Blunt, Aymeric de Vazeilles, Tristan Shaffer, Hean Koo, Bernard Suh, Qi Yang, Jeremy Peterson, Mihaela Perteu, Natalia Volfovsky, Jennifer Wortman, Owen White, Steven L. Salzberg, Claire M. Fraser, and C. Robin Buell. 2003. Sequence, annotation, and comparative analyses of rice chromosome 10. *Science*, 300:1566-1569.

- 111) M. Yang, Y. Si, M. Burow, J. Irvine, E. Mirkov, A.H. Paterson. 2003. A rapid and direct approach to find promoters for driving high-level gene expression in sugarcane. *Crop Science*, 43:1805-1813.
- 112) S.L. Dwivedi, J.H. Crouch, S.N. Nigam, M.E. Ferguson, and A.H. Paterson. 2003. Molecular Breeding of Groundnut for Enhanced Productivity and Food Security in the Semi-Arid Tropics: Opportunities and Challenges. *Adv. Agron.* 80:153-221.
- 113) H. -W. Mei, L. -J. Luo, C. S. Ying, Y. -P. Wang, X. -Q. Yu, L. -B. Guo, D. -B. Zhong, A. H. Paterson, Z. -K Li. 2003 Gene actions of QTLs affecting several agronomic traits resolved in a recombinant inbred rice population and two testcross populations. *Theor. Appl. Genet.*, 107: 89-101.
- 114) Paterson, A.H., J. E. Bowers, J. C. Estill, B. A. Chapman, D. G. Peterson. 2003. Structure and evolution of cereal genomes. *Current Opinions in Genetics and Development*, 13:644-650.
- 115) Simpson, CE, JL Starr, GT Church, MD Burow, AH Paterson. 2003. Registration of 'NemaTAM' peanut. *Crop Sci.* 43:1561.

2004

- 116) H-M. Ma, S. Schulze, S. Lee, M. Yang, E. Mirkov, J.E. Irvine, P. Moore, A.H. Paterson 2004. An EST survey of the sugarcane transcriptome. *Theor. Appl. Genet.* 108:851-863.
- *117) H. Ma., P. H. Moore, Z. Liu, M. S. Kim, Q. Yu, M.M.M. Fitch, T. Sekioka, A. H. Paterson, R. Ming. 2004. High-density linkage mapping revealed suppression of recombination at the sex determination locus in papaya. *Genetics* 166:419-436.
- 118) Fukao, T., A. H. Paterson, M. A. Hussey, Y. Yamasue, R. A. Kennedy, M. E. Rumpho. 2004. Construction of a comparative RFLP map of *Echinochloa crus-galli* using buffelgrass and other grass probes, and QTL analysis of flooding tolerance and other traits. *Theor. Appl. Genet.* 108:993-1001.
- 119) Saranga, Y., M. Menz, C. Jiang, R. Wright, D. Yakir, A. H. Paterson. 2004. Genetic and physiological dissection of adaptations associated with cotton productivity under arid conditions. *Plant, Cell, and Environment* 27:263-277.
- 120) [Junkang Rong](#), [Colette Abbey](#), [John E. Bowers](#), [Curt L. Brubaker](#), [Charlene Chang](#), Peng W. Chee, Terrye A. Delmonte, Xiaoling Ding, Juan J. Garza, Barry S. Marler, Chan-hwa Park, Gary J. Pierce, [Katy M. Rainey](#), Vipin K. Rastogi, [Stefan R. Schulze](#), Norma L. Trolinder, Jonathan F. Wendel, Thea A. Wilkins, [T. Dawn Williams-Coplin](#),

- Rod A. Wing, Robert J. Wright, Xinping Zhao, Linghua Zhu, [Andrew H. Paterson](#) 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.
- 121) Chapman, B. A., J. E. Bowers, S. R. Schulze, A. H. Paterson. 2004. A comparative phylogenetic approach for dating whole-genome duplication events. *Bioinformatics* 20:180-185.
- *122) Martha T. Hamblin, Sharon E. Mitchell, Gemma M. White, Javier Gallego, Rakesh Kukatla, Rod A. Wing, Andrew H. Paterson, and Stephen Kresovich. 2004. Comparative population genetics of the panicoid grasses: Sequence polymorphism, linkage disequilibrium, and selection in a diverse sample of *Sorghum bicolor*. *Genetics*, 167:471-483.
- *123) Zhiyong Liu, Paul H. Moore, Hao Ma, Christine M. Ackerman, Makandar Ragiba, Heather M. Pearl, Minna S. Kim, Joseph W. Charlton, Qingyi Yu, John I. Stiles, Francis T. Zee, Andrew H. Paterson, and Ray Ming. 2004. A Primitive Y Chromosome in Papaya Marks Incipient Sex Chromosome Evolution. *Nature* 427:348-352.
- 124) M.E. Ferguson, M. Burow, S. R. Schulze, P. Bramel, A. Paterson, S. Kresovich, S. Mitchell. 2004. Microsatellite Identification and Characterization in Peanut (*A. hypogaea* L.). *Theor. Appl. Genet.* 108:1064-1070.
- 125) Chee, P., J. Rong, A. H. Paterson. 2004. EST-derived PCR markers for functional gene homologues in cotton. *Genome* 47:449-462.
- 126) Paterson, A. H. J. E. Bowers, B. A. Chapman, D. G. Peterson, J. Rong, T. M. Wicker. 2004. Comparative genome analysis of monocots and dicots, toward characterization of angiosperm diversity. *Current Opinions in Biotechnology* 15:120-125.
- 127) Paterson, A.H., R. K. Boman, S. M. Brown, P. W. Chee, J. R. Gannaway, A. R. Gingle, O. L. May, C. W. Smith. 2004. Reducing the genetic vulnerability of cotton. *Crop Sci.*, 44:1900-1901.
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Patent applications: 6

Filed 11 April 2001 (Texas A&M): Processing of Transgenic Sugarcane for the Recovery of High Value Proteins. TAMUS1436. T. Erik Mirkov, A. Barrilleaux, A. H. Paterson, M. Yang, J. E. Irvine.

Provisional filed 13 Nov 2001 (Univ. Georgia): Cot-based DNA sequencing. D. G. Peterson, A. H. Paterson, and S. R. Wessler. Final application filed 13 Nov 2002 (Univ. Georgia): Cot-based DNA sequencing. D. G. Peterson, A. H. Paterson, and S. R. Wessler.

Provisional filed 10 March 2005 (Univ. Georgia): Analysis of the Ultra-rapid Cot fraction. Thomas Wicker, Jon Robertson, Frank A. Feltus, Stefan R. Schulze, Robert Ivarie, Andrew H. Paterson.

Provisional filed 10 March 2005 (Univ. Georgia): Sequenced DNA from UR fraction obtained from chicken. Robert Ivarie, Thomas Wicker, Jon Robertson, Frank A. Feltus, Stefan R. Schulze, Andrew H. Paterson.

Provisional filed 10 March 2005 (Univ. Georgia): Sequenced DNA from UR fraction obtained from rice. Andrew H. Paterson, Thomas Wicker, Jon Robertson, Frank A. Feltus, Stefan R. Schulze, Robert Ivarie.

Provisional filed 10 March 2005 (Univ. Georgia): Sequenced DNA from UR fraction obtained from human. Frank A. Feltus, Thomas Wicker, Jon Robertson, Stefan R. Schulze, Robert Ivarie, Andrew H. Paterson.

Invited lectures, seminars, or symposia presentations: 1999 to date, of 134 total.

Comparative analysis of plant gene and chromosome organization.
Japan Rice Genome Workshop, February 1999.
UGA Plant Center retreat, May 1999
IPK, Gatersleben Germany, June 1999.

Annual Cotton Genome Workshop (in conjunction with Plant Genome Meeting):
QTL mapping of fiber quality and other traits in cotton. January 1999.
Progress toward a physical map of the cotton genome. January 2000.
Status of the cotton molecular map. January 2001.

Sorghum Molecular Genetics: Opportunities, Risks, and Rewards.
National Grain Sorghum Producers Convention, February 1999.

Biotechnology in Crop Improvement. Ag Showcase, 1999. Fort Valley State University,
Fort Valley, GA.

Linking Genomics and Genebanks: Agronomic Questions: CSSA, November 1999 (Salt
Lake).

Biotechnology in Crop Improvement. Certified Crop Advisor Agronomic Seminar.
Macon, GA. January, 2000.

QTL mapping of sugar content in sugarcane. Invited talk, Australian Sugarcane
Biotechnology Workshop, May 2000.

Comparative organization and function of plant chromosomes. ASPP annual meeting,
invited talk, July 2000.

Adoption of Biotechnology. Meeting on the "Future of American Agriculture", Univ. GA,
Athens, August 2000.

Biotechnology in Crop Improvement. Georgia Agri-Leaders Forum. September, 2000.

Comparative organization and function of plant chromosomes. DCAF meeting on
Molecular Evolution (Nadeau and Sankoff; Quebec, Canada), September 2000.

Comparative organization and function of plant genomes. Meeting on *Evolution: From
Molecules to Ecosystems*. Valencia, Spain, November, 2000.

Genomics in Plant Breeding. Invited talk, International Center for Advanced
Mediterranean Agronomic Studies, Zaragoza SPAIN, November, 2000.

The sorghum genome as an anchor for integrating comparative genetic, physical, and QTL
information for C4 grasses. CSSA meeting (Minneapolis). November, 2000.

New opportunities through convergence of genomics, genetics, and genebanks. CSSA
meeting (Minneapolis). November, 2000.

Molecular mapping of drought response in cotton. Beltwide Cotton Meeting, Anaheim
CA, January 2001.

Progress in molecular dissection of disease resistance in cotton. Beltwide Cotton
Meeting, Anaheim CA, January 2001.

Progress in molecular mapping of the cotton genome.

Plant and Animal Genome Conference, San Diego CA January 2001.

International Cotton Genome workshop, Montpellier France, June 2001

Progress in molecular mapping of the sorghum genome. USAID workshop, CIMMYT, Mexico. April 2001.

Comparative mapping of sorghum and buffelgrass. Plant and Animal Genome Conference, San Diego CA January 2001.

Biotechnology in Crop Improvement.

Georgia-Alabama Agricultural Consultants Tour. 22 February 2001.

Georgia Association of Plant Pathologists. Stone Mountain, Georgia, March 2001.

Genomics of drought response. International Rice Research Institute, May 2001.

Biotechnology in Crop Improvement. Biotechnology In-service Workshop for High School Teachers, UGA, July 2001.

Molecular mapping of drought response in cotton. Rockefeller Foundation meeting on drought response of major crops, Danforth Center, St Louis, November 2001.

Hybridization-based physical mapping of the Brassica genome. Crucifer Genetics workshop, Davis CA, March 2002.

Cotton genome organization and mapping. Invited lecture, Nanjing Agricultural University. June 2002.

Progress in integrated genetic/physical mapping of the cotton genome. ICGI workshop, Nanjing, PR China. June 2002.

Crop productivity and Wright's adaptive landscape: Is cotton near an adaptive peak? CSSA symposium on "Genetic diversity and gene banks," Indianapolis IN, Nov 10- 14 2002.

Reducing the genetic vulnerability of cotton. CSSA symposium on 'A CRITICAL LOOK AT GENOMICS: WILL IT BE USEFUL TO CROP BREEDING,' Indianapolis IN, Nov 10-14 2002.

Toward a gene map for sugarcane. International Plant and Animal Genome Meeting, 11-15 Jan 2003.

Duplication, deletion, substitution and repetition in comparative biology. From the green revolution to the gene revolution, Bologna Italy, 25-30 May 2003.

Sugarcane genomics and breeding. Arnel Hallauer Symposium, CIMMYT, 17 to 22 August 2003.

Unraveling the history of plant chromosome evolution.

"Plant Genomic European Meeting," University of York, UK. Sept 3, 2003.

EUCARPIA meeting, Integrated Quantitative and Molecular Genetics in Plant Breeding, La Coruna Spain, 3-5 Sept 2003.

Genetics Society of Spain Annual Meeting, Madrid, 8-9 Sept 2003.

Univ. Georgia Plant Center Annual Retreat, 31 Oct 2003.

A turfgrass genome project: Integration of Cynodon chromosomes with molecular maps of the cereals. US Golf Association, Green Section Workshop. Stillwater, OK, 16 Sept 2003.

Integrative genetic and physical mapping of Brassica, Arabidopsis, and Carica. International Plant and Animal Genome meeting, January 2004.

Progress toward a gene map for sugarcane. International Plant and Animal Genome meeting, January 2004.

Prospects for cloning the determinants of genetic variation in cotton fiber quality. International Plant and Animal Genome meeting, January 2004.

Comparative analysis of functional and anonymous genetic diversity in pearl millet and sorghum. International Plant and Animal Genome meeting, January 2004.

'Grantsmanship.' Consortium for Plant Biotechnology Research Annual Meeting of PIs, Washington DC, 25 Feb 2004.

EST sequencing in bermuda grass. US Golf Association, Green Section Workshop. 20 May 2004. Atlanta GA.

Ancient polyploidy in angiosperm genomes. FGP/FIBR workshop on polyploidy, Seattle WA, 8 July 2004.

An integrated approach to sequencing the cotton genome. International Cotton Genome Initiative meeting, October 2004.

Comparative genomics of cotton and Arabidopsis. International Cotton Genome Initiative meeting, October 2004.

On-line cotton resources at the Univ. Georgia. International Cotton Genome Initiative meeting, October 2004.

Evolutionary history of the angiosperms and its implications for Brassica. Joint meeting of the 14th Crucifer Genetics Workshop and 4th ISHS Symposium on Brassicas, Daejeon, South Korea, October 2004.

Status of physical mapping in sorghum. Sorghum Genomics Workshop, St Louis, MO. 9 Nov 2004.

Comparative genomics of the angiosperms.
Dept Plant and Soil Science, Texas Tech University, Lubbock TX. 11 Nov 2004.
Michigan State University/PRL. 28 March 2005.
University of Alabama-Birmingham. 8 April 2005.

Update on sorghum genomic tools and resources. National Grain Sorghum Producers, Lubbock TX. 11 Nov 2004.

Update on sorghum genomic tools and resources. Syngenta Cereal Annotation Workshop. Tucson AZ 13 Nov 2004.

Ancient polyploidy in angiosperm genomes. Banbury workshop on polyploidy, 10-13 Apr 2005.

Comparative genomics of the angiosperms, Wenner-Gren Foundation meeting on Phenotypic Diversity and Evolution, Sweden. June 2005.

Comparative genomics of Brassica and Arabidopsis. International Arabidopsis Workshop, Madison WI 17 June 2005.

Rhizomatousness and Its Consequences for the Sorghum Genus. International Plant and Animal Genome Meeting, Weed Biology workshop, San Diego, January 2006.

Sequencing Of The Sorghum Genome. International Plant and Animal Genome Meeting, Weed Biology workshop, San Diego, January 2006.

Are there rules determining the fates of polyploids? International Plant and Animal Genome Meeting, Polyploidy workshop, San Diego, January 2006.

SNP discovery in polyploid cotton. CPBR, 1 March 2006, Washington DC.

Peanut genomics. INDO-US Forum on Application of Genomics Tools to Chickpea, Pigeon Pea and Peanut Improvement. 7 March 2006, Patancheru India.

Ancient polyploidy in angiosperm genomes. Univ FL, Gainesville, April, 2006.

Comparative genomics of the angiosperms, Plant Genomics in China VII. August, 2006.

The sorghum genome as a nucleation point for comparative genomics of tropical cereals. Tropical Crops Biotechnology Conference, Cairns AU, August 2006.

Grand total: Grants, Contracts & Gifts: \$23.63 million

Grants and Contracts as Principal Investigator: \$17.09 million

Molecular mapping of the cotton genome, using DNA markers; USDA, 9/91- 8/94, \$200,000.

High-resolution mapping of agriculturally important genes, Texas Research Enhancement Program, September 1991-August 1993, \$170,000.

DNA markers for agriculturally important genes in cotton, Texas Higher Education Coordinating Board, January 1992-December 1993, \$230,000.

DNA markers for height and maturity in sorghum, USDA, 9/92 - 8/94, \$99,500.

QTL mapping of sugar content in sugarcane; International Consortium for Sugarcane Biotechnology, July 1994-June 1997, \$303,000.

QTL mapping of Sorghum bicolor x S. prostratum; Pioneer Hibred Competitive Grants Program, January 1993-December 1995, \$60,000.

Molecular mapping of genes for resistance to bacterial blight in cotton; Texas Agricultural Experiment Station (Research Enhancement Prog.), September 1993-August 1995, \$78,000.

DNA fingerprinting of Texas high-plains cottons; private firm (anonymity requested), \$5,000.

Molecular dissection of quantitative inheritance; Texas Higher Education Coordinating Board Advanced Research Program), January 1994-December 1995, \$169,000.

Risk of gene flow from sorghum to johnsongrass; USDA, 9/95-8/98, \$180,000.

Improving productivity of cotton under semi-arid environments. BARD, 9/95-8/98, \$330,000 (my share \$132,000).

Simplified technology for DNA marker-assisted cotton improvement. Cotton Inc. \$58,000.

High-yielding cottons with superior fiber quality. Texas Higher Education Coordinating Board (Advanced Technology Program), 1/96-12/97, \$198,000.

International Atomic Energy Agency training contract, Pakistan. \$14,000, 4/96-10/96.

Asian Development Board training contract, Pakistan. \$14,000, 4/96-10/96.

Maharastra Hybrid Seed, Ltd. training contract, India. \$20,000, 5/96-11/96.

Differential gene expression in response to greenbug predation, by resistant and susceptible sorghum genotypes. Interdisciplinary Research Initiatives Program, 1996-7, \$23,640.

Cloning of Sh1, a gene responsible for shattering of the cereal inflorescence. USDA, 9/96 - 8/99. \$210,000.

Cloning and characterization of rhizome-specific genes. USDA, 9/96 - 8/99. \$135,000.

DNA marker-accelerated conversion of exotic sorghum and maize germplasm; Pioneer Hibred Competitive Grants Program, November 1996-September 1999, \$70,000.

(Renewal) Genetic and molecular analysis of expressed-sequence tags implicated in sugarcane growth and productivity. ICSB, \$294,000, 1 July 1997-31 June 2000.

(Renewal) Toward a unified map of cotton and Arabidopsis. USDA, 1 Sept 1997 - 31 Aug 2000. \$250,000.

Mapping of microsatellite markers in cotton. Private firm, 10/97-9/98, \$26,602.

Gift in support of molecular genetics research, Maharastra Hybrid Seed, Ltd. \$25,000.

Novel cottons that reduce genetic vulnerability, Texas Higher Education Coordinating Board, (Advanced Technology Program), 1/98-12/99, \$188,000.

Pyramiding genes for cotton fiber quality, TxCOT, \$60,000. 1998-99.

QBOT for high-speed physical mapping of crop genomes. \$150,000, TAMU Provost's Initiative.

Equipment for rapid DNA fragment analysis. \$50,000, FRDP initiative, TAMU College of Ag.

A Turfgrass Genome Project, \$125,000, US Golf Association. 1/1/98 - 12/31/02.

Comparative physical mapping of *B. napus*, *B. juncea*, *A. thaliana*. \$108,000, DNA Landmarks. 1998-9.

Cross-linked Physical Maps of Sorghum and Rice. \$3.2 million (my share \$780,000), NSF. 10/1/98-9-30/01

Toward a new adaptive peak for Georgia cotton. GA Cotton Commission, \$60,000, 7/1/00-12/31/01.

The role of transposable elements in polyploid cotton evolution. (Paterson and Wessler). \$140,000, USDA, 9/1/00-8/31/02.

Molecular dissection of plant height, flowering, and apomixis (Paterson, G. Burow, and M. Hussey). \$290,000, USDA, 9/1/00-8/31/03.

Mapping of resistance-gene analogs in peanut. GA Peanut Commission, \$5,000, 1-12/00.

Reducing the genetic vulnerability of cotton. USDA-IFAFS. PI, with 7 co-PIs. \$1,000,000. 9/00-8/04.

Development of molecular markers for analysis of groundnut rosette virus, USAID,, \$90,000. 1/00-12/01.

(Renewal) Toward a gene map for sugarcane. ICSB. \$306,000, 7/01-6/04.

(Renewal) Cloning of Sh1, a gene responsible for shattering of the cereal inflorescence. USDA, 9/01 - 8/03. \$180,000.

(Renewal) Cloning and characterization of rhizome-specific genes. USDA, 9/01 - 8/03. \$250,000.

(Renewal) Grass Genomic Biodiversity. NSF, 9/01-8/05. \$3.97 million (my lab's share, \$1.2 million).

SNP discovery in cotton. Private firm, 1/1/02-12/31/03. \$280,000 plus \$44,000 supplement from the Consortium for Plant Biotechnology Research.

Grant in support of postdoctoral training of H. Singh. RF, \$99,000, 6/02-5/04.
 Chromosomal and subgenomic distribution of diversity in cotton. USDA \$140,000, 9/02-8/04.
 BAC resources for comparative biology in angiosperms. NSF \$400,000, 7/02-6/04.
 Molecular characterization of QTLs affecting earliness and fiber characteristics of Egyptian cotton. US-Egypt \$23,500. 9/02-8/04.
 Organization of cotton genomic diversity. USDA-NRI. \$140,000. 9/02-8/04.
 Toward a new adaptive peak for Georgia cotton. GA Cotton Comm. \$43,000. 1/03-12/03.
 Toward standards for bermudagrass DNA fingerprinting. GA Seed Devt. Comm. 7/01-6/05. \$150,000.
 Comparative analysis of functional and anonymous diversity in pearl millet and sorghum. USAID. \$100,000. 3/03-9/04.
 SNP discovery in cotton. CPBR. \$200,000. 10/03-9/05.
 SNP discovery in peanut. CPBR \$20,000 plus \$2,000 match from the Peanut Fndn. 10/03-9/04.
 Comparative analysis of functional and anonymous diversity in pearl millet and sorghum. USAID. \$150,000. 3/04-9/05.
 FIBR planning grant - -why are so many plants polyploids? NSF. \$50,000. 1/04-12/04.
 USDA CAP Conference proposal for cotton. USDA. \$12,000. 9/04-8/05.
 Sample sequence strategy for cotton. US-Egypt Bilateral Program. \$30,000. 10/04-9/06.
 Peanut resistance genes. GA Peanut Comm. \$7,000. 1-12/05.
 Physical mapping of sugarcane. ICSB. \$199,500. 7/05-6/08.
 Peanut resistance genes. GA Peanut Comm. \$7,000. 1-12/06.
 Unraveling angiosperm chromosome evolution. NSF, \$489,000. 8/05-7/08.
 Bermudagrass ESTs. USGA. \$90,000. 2/06-1/09.
 Physical mapping of the sugarcane euchromatin. CPBR. \$320,000. 1/06-12/07

Grants/Contracts (as Co-Investigator): \$7.49 million (total awards \$38.07 million).

Map-based cloning in Cotton: A model system for polyploids. (R. Wing and A. Paterson); USDA, September 1993-August 1996, \$250,000.
 Molecular mapping and map-based cloning of greenbug resistance in sorghum. Texas Agricultural Experiment Station (REP program), 9/93-8/95, \$75,000.
 Molecular mapping of nematode resistance in peanut. Texas Agricultural Experiment Station (Research Enhancement Program), 9/93-8/95, \$75,000.
 YAC libraries for rice. Rockefeller Found'n, 9/93-8/94, \$60,000.
 QTL mapping of genes for heterosis in rice. (Z. Li, J. Stansel, A. H. P.); Rockefeller Found'n, Oct. '94-Sept. '96, \$109,000.
 A multigenic system for nematode resistance in peanut. (J. Starr, M. Burow, A. Paterson, C. Simpson). USDA Nematology, 9/95-8/97, \$100,000.
 Molecular mapping of genes for resistance to greenbug in sorghum. (G. Peterson, A. Paterson, G. Teetes). Pioneer Hibred Competitive Grant, 1993-5, \$60,000.
 Pyramiding genes for resistance to rice blast. Texas Higher Education Coordinating Board (Advanced Technology Program), 1/96-12/97, \$93,000.
 Capturing high water-use efficiency in cold hardy fruit cacti. (P. Felker, Y. Mizrahi, A. Paterson). International Arid Lands Consortium, 1/96-12/97. \$75,000.
 AB-QTL mapping of peanut (Simpson, Starr, Paterson). USDA, \$123,000, 9/97-8/00.
 Novel genes for improvement of Texas peanut. J. Starr and C. E. Simpson. Texas Higher Education Coordinating Board (Advanced Technology Program), 1/98-12/99, \$158,000.

Toward cloning of greenbug resistance. \$70,000, TxGRAIN (Teetes and Paterson). 1998-9.

Molecular dissection of apomixis. \$98,000, TxGRAIN (Hussey & Paterson). 1998-9.

Isolation of genes for resistance to fall armyworm in Zoysia, \$78,000, TxGRAIN (Engelke, Reinert, Paterson). 1998-9.

Rice as a conduit for molecular analysis of grasses and grains. Paterson and Stansel. Texas Higher Education Coordinating Board (Advanced Technology Program), 1/98-12/99, \$129,000.

Comprehensive Genetic, Physical and Database Resources for Maize. \$11 million (\$516,000 my share), NSF. 10/98-9/01.

Structure and Function of the Cotton Genome. \$3.8 million (\$780,000, my share), NSF. 10/98-9/01.

Toward a peanut genome project, \$25,000, Peanut Foundation (Burow, Paterson, Starr, Simpson). 1-12/00.

Genomic Tools and Resources for Brassica oleracea. USDA-IFAFS. \$460,000. 9/00-8/04.

Genes for Georgia. NSF, \$600,000 (\$300,000 my share). 4/1/02-3/30/04.

Comparative evolutionary genomics of cotton. NSF. \$4.2 million (\$1.2 million). 9/1/02-8/31/07.

Expression profiling of response to water deficit in rice. Rockefeller Foundation. \$23,625. 1-8/2004.

Sequencing the genome of Azospirillum. NSF. \$800,000 (my share \$642,558). 10/04-9/06.

Sequence of the sex-determining region of papaya. NSF. \$3 million (my share \$1.2 million). 10/04-9/08.

Sequencing of maize chromosome 10 of MO17. NSF. \$3 million (my share \$125,000). 11/05-10/07.

Legume comparative genomics. NSF. \$5 million (my share \$100,000). 9/06-8/11.

Viral genome sequencing. USDA. \$576,000 (my share \$135,000). 11/06-10/09.

Brassica genomics resources. NSF. \$1.4 million (my share, \$490,000). 1/07-12/08.

Cotton comparative genomics. NSF. \$1.7 million (my share, \$530,000). 1/07-12/08.

Training Grants (as Principal Investigator): \$1.62 million

National Needs Fellowships in Plant Biotechnology, USDA, 9/95-8/00, \$108,000.

National Science Foundation GK-12: The science behind our food. 9/03-8/06. \$1.6 million.

Awards supporting Visiting Scholars: Total \$1,104,500.

THECB Minority Student Research Award, Juan Garza, \$3,500

Texas A&M Regents Fellowship, Varma Penmetsa, Jan-Aug. 1993, \$8,000.

Rockefeller Foundation Biotechnology Fellowship, Prof. J. Yang, 1993-1996, \$37,000.

Texas A&M Plant Breeding and Plant Genetics Fellowship, Tien-hung Lan, 1993, \$3,000.

Texas A&M Regents Fellowship, Leyuan Liu, Jan-Aug. 1994, \$12,000.

Chinese Academy of Sciences: Qiang Dou; Nov. 1994-Oct. 1995 \$10,000.

Rockefeller Foundation Exchange Program: Dr Zhikang Li, 1994-1997, \$25,000

United Nations Development Program, Shen Yuezheng, Apr-Oct 1995, \$6,000.

Rockefeller Foundation Graduate Research Program, Lijun Luo, 1995-7, \$10,000.

Rockefeller Foundation Biotechnology Fellowship, Prof. Ping Wu, 1996-1998, \$40,000.

Rockefeller Foundation Graduate Research Program, Nguyen Ti Vinh, 1997-8. \$12,000.

Texas A&M Tom Swift Fellowship, Tien-hung Lan, 1996-7, \$15,000.

Rockefeller Foundation Graduate Research Program, Wang Daolong, 1997-8. \$12,000.

Belgian-American Exchange Foundation, Dr Xavier Draye, 1997-8, \$30,000.

Mahyco Fellowship, Dr Debashis Rana, 1997-8, \$25,500.

Japan Science Foundation, Dr Hisato Okuizumi, 1998-9, \$30,000.
USDA-NRI Postdoctoral Fellowship, Daniel Peterson, 1999-01, \$90,000.
Rockefeller Foundation Graduate Research Program, Xiaoyin Qian, 1998-9. \$12,000.
HHMI Fellowship to B. Chapman, 1999-2004. \$165,000.
ICRISAT: Dr. M. Ferguson.
Korean Science Foundation: Dr C. Park.
BOYSCAST Fellowship, Dr V. Waghmare (India).
CPBR award to Fort Valley State, \$20,000.
NIH Postdoctoral Fellowship to M. Osterlund, \$100,000.
fellowship to Avishag Levi, \$5000.
RF award to Dr Hari Singh, \$99,000.
ISPMB award for T. Silva. \$12,000.
DBT fellowship to H. Lohithaswa. \$24,000.
DBT fellowship to M. K. Reddy. \$12,000.
NSF fellowship to M. Torres. \$120,000.
Fulbright fellowship to R. Navajas Perez. \$100,000.

Hatch funds: Total \$57,000

1991-1996: \$5,000 per year. 1997: \$4,000. 1998: \$5,000. 1999: \$5,000. 2000: \$4,000.
2001: \$4,000. 2002: \$3,000. 2003: \$2,000.

Teaching Performance

University of Georgia (1999-present)

My current appointment at UGA includes only 7% teaching (93% research). I was forgiven teaching until the final location of my lab was prepared by UGA – this happened in early 2003. In the fall of 2003, together with R. Kuzoff (Plant Bio.) and M. Deom (Plant Path.), I team-taught a new course cross-listed as PBIO8800 and GENE8830 entitled ‘Genome Evolution across the Tree of Life.’ A total of 12 students enrolled for credit (several more audited, as well as several postdocs). On a scale of 1-4 (Excellent, Good, Average, Poor), students rated my personal teaching performance at 1.82 (slightly above ‘Good’) and the overall course at 1.78.

The course was offered again in Fall 2004, as PBIO/GENE 4510/6510, with 10 students. On a scale of 1-5 (Excellent, Good, Average, Poor, Terrible), students rated my personal teaching performance at 1.93 (slightly above ‘Good’) for 6510 and 1.65 for 4510.

Due to a clerical error beyond Dr Paterson’s control, the course announcement was posted very late in 2006 and only one student registered, hence the course was not offered.

In addition I have given 3-5 guest lectures per year in other’s courses.

I presently have 8 chaired and one co-chaired graduate students, and sit on 4 additional graduate student committees. I oversee many research credits for these students.

At UGA, I have participated as co-PI in submission of three training grants. One of these was funded, a NSF GK-12 project on “*The Science Behind Our Food*,” at \$1.6 million.

Texas A&M (1991-1998)

My former appointment at Texas A&M University included 35% teaching. This has been allocated to team-teaching two 3-credit courses, participation in other courses here at Texas A&M and elsewhere, advisement of a total of 22 graduate students (6 as chairman), lab training of 24 undergraduate students (whose wages were funded from my competitive grants). In collaboration with another faculty member, I created two new courses, a 3-hour lecture and 3-hour lab each entitled "Analysis of Complex Genomes". The courses are listed in Genetics, with cross-listing in Plant Physiology, and Agronomy, with students enrolling under each discipline. The courses are open to undergraduates, but to date none have enrolled. I am formally responsible for the lecture course. When my team-teacher departed in 1996, the lab course was put on hold pending hiring of a qualified replacement (still pending). Over the 5 year history of these courses, a total of 97 students have achieved an average GPA of 3.47. My average score for student evaluation of my teaching performance has been 4.52 (with 5.0 = highest possible). Summary statistics from these courses are as follows:

<u>Year</u>	<u>Course</u>	<u>Grade distribution</u>			<u>Class</u>	<u>Student evaluations</u>	
		<u>#stdts.</u>	<u>A</u>	<u>B</u>		<u>C</u>	<u>GPA</u>
1993	AGRO654	25	11	13	1	3.40	4.37
1993	AGRO655	9	9	0	0	4.00	4.81
1994	AGRO654	14	5	9	0	3.36	4.79
1994	AGRO655	6	3	3	0	3.50	4.46
1995	AGRO654	18	6	10	2	3.22	4.30
1996	AGRO654	12	6	6	0	3.50	4.37
1997	AGRO654	13	5	7	1	3.31	4.53
1998	AGRO654	10	4	5	1	3.30	
Overall total/average		97	49	53	5	3.45 / 4.00	4.52 / 5.00

AGRO654 now uses a textbook entitled "Genome Mapping in Plants", which I wrote (9 chapters) and edited (13 additional chapters) to fill the need for a suitable text for this and related courses. In addition, I have edited a book on "Molecular Dissection of Complex Traits", which is intended to become a general reference for this field of growing importance.

In the past 6 years, I have given guest lectures in courses taught by D. Stelly (SCS), D. Smith (SCS), W. Smith (SCS), B. Taylor (BIOL), O. Smith (SCSC), D. Jarvis (ENTO), C. Miller (HORT), D. Vietor (SCSC), and C. Williams (FRSC). In addition, I have given 14 seminars on campus, and 4 seminars at TAES Centers (Beaumont, Lubbock, Weslaco, Dallas).

I have also participated in colloquia, student seminars, and advisement as an Adjunct Ass't. Prof. at Univ. Delaware (1990-92), and spoken in courses, retreats and training programs at Cornell, Rutgers, NCSU, and Univ. Pittsburgh.

Finally, I coordinated preparation and submission of 4 training grant proposals, to the National Science Foundation (2), and USDA National Needs Fellowship Program (2). One of these was funded by the USDA National Needs Fellowship Program, and another remains pending.

Postdoctoral, Research, and Visiting Scientists (43):

R. Navajas Perez – arriving October 2006

M. Torres – current.

X. Wang – current.

A. Feltus – current.

J. Bowers – current.

J. Rong – current.

C. Jang – currently Institute of Life Science & Natural Resources, Korea University, Anam-Dong, Seongbuk-Gu, Seoul 136-713, Korea

T. Kamps – unknown.

J. Leitao – Universidade do Algarve, Faculdade de Engenharia de Recursos Naturais, Portugal

H. Buhariwalla – ICRISAT.

H. Lohithaswa – University of Agricultural Sciences, Dharwad India

H. Singh – Narendra Deva University of Agriculture and Technology, India

T. Wicker – Institute of Plant Biology, University of Zurich, Switzerland

M. Osterlund – presently Department of Plant Biology, Univ. Georgia.

T. Silva – presently University of Colombo, Sri Lanka.

C. Park – presently ###.

A. Karnauh – 1/03-5/04, presently UGA.

M. Wise – presently USDA-ARS, Athens GA.

H. Ma – presently National Botanical Garden (USDA-ARS).

D. Peterson – presently Assistant Professor, Mississippi State Univ.

M. Ferguson – presently ICRISAT, Nairobi.

Y. Saranga – presently Assoc. Prof., Hebrew Univ., Jerusalem.

P. Chee – presently Asst. Prof, Univ. Georgia, Tifton.

G. Burow – presently USDA-ARS, Lubbock TX.

R. Noyes – presently Asst. Prof., Univ. Colorado, Boulder.

M. Burow – presently Asst. Prof., Texas A&M University, Lubbock.

H. Okuizumi – presently Asst. Prof., RIKEN, Tsukuba, Japan

P. Morrell – presently postdoctoral scientist, UC Irvine.

J. Ballester-Valveny – presently Research Scientist, IRTA, Cabrils Spain

V. Padmanabhan – presently Research Scientist, Pioneer Hibred International

Z. Li – presently Chief Scientist, Institute of Crop Sciences, Chinese Academy of Agricultural Sciences

Y. Si – presently Univ. Houston.

R. Ming – presently Associate Professor, Univ Ill Urbana-Champaign

C. Jiang – presently Syngenta, Belle Glade FL

D. Rana – presently John Innes Center

X. Draye – presently Assistant Professor, Louvain Univ. Belgium

A. Reinisch - presently Assistant Professor, Tarleton State University, TX.

S. Kowalski - presently Franklin Pierce Law Center.

G. Wang - presently Asst. Prof, Ohio State Univ.

X. Zhao - presently Research Scientist, U. Mich, Ann Arbor

S. Liu - presently Baylor University, Houston TX.

J. Yang - presently Professor, Fudan University, China.

D. Qiang - presently China Academy of Agricultural Sciences.

Graduate Students presently in training (6)

Haibao Tang (Ph.D.) – chair

Lifeng Lin (Ph.D.) – chair

Changsoo Kim (Ph.D.) - chair

Limei Liu (PhD) – on-campus chair.

Andrew Higginbotham (PhD) – chair.
Jeff Ross-Ibarra (PhD) – committee member, chair is Hamrick.

Degrees conferred (33):

Casey Bethel (MS) – chair, high school science teaching in Atlanta area.
Aparna Desai (MS) – on-campus chair, currently UC Davis.
Mark Mackiewicz (PhD) – committee member, currently ###.
Russell Jessup (Ph.D.) - committee member, currently USDA-ARS and TAMU.
Bayram Yuksel (Ph.D.) – chair, currently Tubitak University (Turkey).
Brad Chapman (Ph.D.) – chair, currently Codon Devices (startup company).
Ali Missaoui (Ph.D.) – committee member, chair is J. Bouton (Crop Sci, Univ. GA), currently postdoc at UGA.
Rebecca Mroczek (Ph.D.) - committee member, chair is K. Dawe (Botany/Genetics)
Takeshi Fukao (M.S.) - committee member, chair is M. Rumpho (TAMU), currently postdoc at UC Davis.
Mei-zhu Yang (M.S.) – co-chair with E. Mirkov (TAMU), currently Exelixis, San Francisco.
Tom Byrum (Ph.D.) - committee member, chair is W. Lowe (Forestry - TAMU), currently Western Gulf Forest Tree Improvement Coop.
Xiaoyin Qian (Ph.D.) – co-chair with J. Yang, Fudan Univ. P.R. China
Nguyen Thi Vinh (Ph.D.) – co-chair with Le Tran Binh, Inst. Biotechnology, Vietnam
Sharon Morton (Ph.D.) - co-chair with M. C. Engelke (TAMU), currently USDA-ARS Beltsville.
Laura Decanini (Ph.D.) – committee member with C., W. Smith (TAMU), currently USDA-ARS College Station TX.
Tien-Hung (David) Lan (Ph.D.) – chair, currently Taiwan National University.
Yann-Rong (Yvonne) Lin (Ph.D) – chair, currently Assistant Professor, Dept. of Biology, Fu-Jen Catholic University, Hsing-Chung, Taipei 242, Taiwan, R.O.C.
Robert Wright (Ph.D.) - co-chair with K. El-Zik, currently Asst Prof, Texas Tech University.
Catherine Katsar (Ph.D)- committee member, chair is G. Teetes (Ento.), currently USDA-ARS, Ft. Pierce FL.
Tzung-Fu Hsieh (Ph.D) - committee member, chair is T. Thomas (Biology)
Cathi Lehn (Ph.D) - committee member, chair is J. Taylor (An. Sci.)
Xiaodong Wu (Ph.D) - committee member, chair is J. Taylor (An. Sci.)
Danialle Stilwell (M.S.) - committee member, chair is J. Taylor (An. Sci.)
Savio Mendonsa (M.S.) - committee member, chair is B. Riley (Biology)
Lijun Luo (Ph.D.) - co-chair representing USA (Rockefeller Ph.D. Dissertation Fellow), presently director of Institute of Biotechnology, Shanghai Acad. Agr, Sciences.
Dao-long Wang (Ph.D.) - co-chair with Dr Jun-Zhu (Huazhong Univ. China: RF Fellow)
Zhongsen Li (Ph.D) - committee member, chair is T. Thomas (Biology), currently E. I. duPont
Yue-wen Wang (Ph.D) - committee member, chair is M. Hussey
Mark Jung, M.S.(Univ. Del.) - comm. member, chair J. Hawk (Pl. Br.), now E.I.DuPont
Wendy Smith, M.S. - committee member, chair was W. Smith
Joao Luis Rocha, Ph.D - committee member, chair Taylor (An. Sci.), now Pioneer Hibred
Andrew Herring, Ph.D - comm. member, chair Taylor (An. Sci.), now Texas Tech Univ.
Mahama Ouedraogo (Ph.D.) - committee member, chair is O. Smith, now Burkina Faso.
Oscar Rodriguez (Ph.D) - comm. member, chair Fredericksen (Pl. Path), now South Texas (private company).
Daniel Marchala (Ph.D.) - Graduate Committee Representative.

Undergrads/HS students: Present (8):

Ryan Buss – 9/02 to present.
Amy Chen – 6/02-12/03 (UGA Young Scholars Internship Program) and 1/06-present.
Joseph Robertson – 1/03 to present.
Chike Nwakanma – 6/03 to present.
David Petermann – 8/05- present.
Jamie Olive – 8/05 – present.
Andrew Pott – 8/05-present.
Steven Voith– 8/05-present.

Past (73):

Jennifer Avise – 6/03 to 6/06.
Kim Petermann – 5/03 to 6/05.
Elizabeth Lobello – 1/03 to 6/05.
Nandini Setia – 6/04 – 8/04
Matt Edwards – 5/04 to 6/05
Brian Blonar – 5/04 to 8/04.
Yvette Dupre – 1/04 to 5/04.
Catherine Reed – 12/03 to 5/04.
Lisa Lee – 1/04 to 3/04
Erin Keebaugh – 1/04 to 5/04
Cynthia Phelps - 1/04 to 5/04
Joana McMillan – 12/01 to 1/05
Rochelle Asher – 1/04 to 5/04
Mona Ali Shums – 6/03 to 3/04.
Erika Swinson – 2/03 to 1/04.
Gmerice Lafayette – 9/02 to 1/04.
Keimun Slaughter – 9/02 to 1/04.
Miguel Arias - 10/15/99 to 12/03
Asher Newsome – 6/03 to 9/03, 5/04-9/04.
Sean Ryan – 6/03 to 9/03.
Gene Brewer – 6/03 to 12/03.
Gary Pierce – 6/01 – 5/03, then promoted to full-time technical position in the lab.
Veronica Walker - 3/13/00-5/03.
Kristen Herrick – 9/02 to 12/02.
Elizabeth Gurley – 11/01-5/02
Brooke Schaefer – 11/01-5/02
Cassie James – 4/02-5/02, then promoted to full-time technical position in the lab.
Melissa Carter – 5/02 to 9/02.
Heather Exum – 5/02 to 9/02.
Anamaris Raybon – 6/02-8/02 (UGA SUNFIG).
Shelley Masters – 9/00-present.
Brett Jakiatis – 5/01-8/02.
Suzanne Scroggins – 5/01- 12/01.
Deanne Tibbitts - 5/17/99- 5/01.
Monique Salter - 6/9/99- 5/01.
Anna Manlapat - 6/15/99- 12/00.
Savitha Subramanian - 6/17/99 – 9/00.
Rebecca Koopman - 10/1/99 – 5/01.
Justin Wilson - 10/18/99-3/01.
Neal Skinner - 5/17/99 – 12/00.
Chrissy Brooks - 2/8/00 to 12/00.

David Amoson - 2/18/00- 5/01.
Asa Cordle - 3/6/00-5/00.
Brian Gerwe 5/99-12/99
Chrissie Case 5/99-12/99
Yvonne Ta 9/99-12/99
Kyle Johnson 1/98-12/98
Jennifer Lennington, 9/96-5/98
Alison Hoppe, 5/97-8/98
Jennifer Stivers, 6/97-8/99
Michelle Garza, 9/97-12/99
Peter Duong, 9/97-5/98
Doug Sorenson; 9/93-8/87.
Vm Smith, 1-6/97
Olga Stadelmann, 1-6/97
Joel Hyman, 2/93-5/96.
Christian deLeon, 1/95-5/95
Ryan Dalrymple, 5/94-5/96.
JoVan Currie, 5/95-9/95
Greg Warr, 5/95-12/96.
Summer Sorley, 5/95-12/95
Anurekha Ramabhadran, ca. 1994.
Renee Baggett, 2/93-5/95
Amanda Fifer 9/94-1/95
David Hamada, 4/94-8/94
Kipp Amedeo, 2/94-8/94
Stacey Foster, 5/94-8/94,
Kelly Schmitt: 1/93-12/93
Juan Garza (6/91-5/93) - supported by Supplemental ATP grant for
Minorities (Hispanic).
Caroline Vasquez-Rosado (9-12/92).
Michael Chase (6/92-1/93).
Don Sarmiento (6-9/91).

Research Interests

GENERAL OBJECTIVES: The efficiency of modern agriculture affords society the flexibility to “specialize”, and pursue intellectual, technological, and cultural activities to a degree which would not be possible if fiber, food, and feed production were less efficient. I am interested in elucidating the molecular basis of variation in complex traits associated with quality and productivity of major crops. In particular, I am interested in genes associated with evolution of productive crop plants from wild or weedy ancestors, as well as biomass accumulation and partitioning in plants. This work holds an opportunity to improve understanding of basic processes in plant biology and evolution, and to accelerate crop improvement.

The fundamental similarity in repertoire of genes of many higher plants is providing a conduit for collaborative research encompassing diverse fields, and diverse plant taxa. Many logical extensions of these goals, as well as establishment of new goals, will be fostered by opportunities to collaborate with colleagues with compatible interests in other plants and or other characteristics. Comprehensive multidisciplinary collaborations yield the sort of “complete picture” regarding a question or problem, which advances the state of knowledge. Most successful research projects I have been involved with have been collaborations with agronomists, physiologists, pathologists, entomologists, nematologists, weed scientists, molecular biologists, and many others. My experimental plans will continue to focus on multidisciplinary, collaborative approaches to challenging questions/problems, and I will look forward to adding new collaborations to existing ones.

(1) FAM. MALVACEAE; COTTON, KENAF, and relatives.

My lab has developed a detailed molecular map of the chromosomes of cotton, and is applying the map to improved understanding of chromosome evolution, characterizing historical introgression (Wang et al, 1995), and genetic mapping of 295 genes (to date) affecting both simply-inherited and complex traits which affect agricultural productivity and quality of cotton. In addition, we have cloned and sequenced 103 families of repetitive elements which collectively account for 30% of the DNA content of cultivated cotton, and are utilizing them both in evolutionary studies, and as tools to aid in “map-based cloning.”

Our near-term emphasis will be as follows:

- a) *Genome evolution in cotton.* Tetraploid cottons first appeared about 1-2 million years ago, in Central America, as a polyploid derivative of a cross between indigenous D-genome cottons, and an A-genome cotton which probably reached the New World as a result of “rafting”. While the A-genome ancestor is well-known, the D-genome ancestor is less certain. Recent results from study of genome-specific repetitive DNA elements isolated and characterized in my lab shed new light on the origins of tetraploid cotton, and more generally on molecular evolution in plants. This area will be a topic of much future research.
- b) *Identification of specific genes responsible for superior fiber quality, disease and insect resistance, and tolerance of water deficit in cotton.* These characteristics are of importance in cotton improvement, and better understanding of genetic determinants will accelerate breeding progress.
- c) *Determination of the relative gene order in cotton and other species.* “Comparative mapping” is proving a powerful tool in genome analysis — by interleaving genetic maps of related species based on common “anchor loci”, genetic and molecular information about one species can readily be extrapolated to others. Unfortunately, cotton enjoys few close relatives which are well-characterized genetically (okra and kenaf are much less-well characterized than cotton). We have determined the comparative organization of genes in tetraploid cotton (“AD-genome”) and its diploid (A and D-genome, respectively) progenitors. We have established that molecular tools made for cotton can be used effectively on kenaf and okra.
A long-term goal is to better understand correspondence between the genome of cotton and other major dicot crops and/or model systems, and is being done in two ways; (1) by sequencing mapped cotton genes, and determining their correspondence to genes mapped in other species, and (2) by mapping “heterologous” genes from other species, in cotton.

(2) FAM. POACEAE; SORGHUM, SUGARCANE, RICE, MAIZE and relatives.

My lab developed the first complete genetic map of *Sorghum* spp., and we are utilizing this map to study comparative organization of chromosomes in major Poaceae crops (sorghum, maize, rice, sugarcane, millet), to map and isolate genes associated with biomass productivity and weed dispersal (rhizomatous growth, tillering, photoperiod sensitivity), to map genes associated with fundamental morphological differences between grasses and grains (leaf morphology, seed size), and to facilitate improvement of agricultural productivity and quality of these crops.

Sorghum, is of interest not only for its positive value as a crop, but for the problems it causes as a weed of many crops. In studying genes which impart “weediness” to johnsongrass (*Sorghum halepense*), we are approaching crop improvement from a novel direction, with the objective of using molecular genetics to defeat a pest by exploiting the very characteristics which make it pestilential.

Our near-term emphasis will be as follows:

a) *Identification and cloning of genes associated with adaptation of tropical Gramineae to temperate cultivation.* We have determined that a single gene controls “short-day flowering” of many tropical grasses, and that mutations in this gene account for “day-neutral flowering” of many temperate crop plants. This gene does NOT correspond to any known regulators of plant photomorphogenesis (e.g. phytochrome), although the gene may act upon phytochrome or its regulators. We have mapped this gene to a small region of a single chromosome in the sorghum genome, and are isolating new DNA markers necessary to conduct a “chromosome walk” to the gene. Isolation of this gene which is able to impose short-day flowering on virtually all Poaceae would create a host of new opportunities for genetic engineering of grain crops, forages, energy crops, and ornamentals — specifically with regard to preventing seed production in plants cultivated for vegetative parts.

In a like manner, a discrete mutation which eliminates “shattering” (disarticulation) of the sorghum inflorescence corresponds to QTLs in maize and rice. We have mapped this locus to a region of ca. 1 cM in the sorghum genome, and are isolating new DNA markers needed to walk to the gene.

Finally, we are using a comparative approach to pursue a gene that confers apomixis to buffelgrass, *Pennisetum ciliare*.

b) *Identification and cloning of genes associated with fundamental morphological differences between grasses and grains.* We have mapped genes responsible for clonal reproduction by rhizomes, the primary basis for weediness of Johnsongrass (*Sorghum halepense*), one of the worlds most noxious weeds. In addition, we have mapped several genes associated with tillering, and ratoon growth in *Sorghum*, each traits of fundamental importance in many grass species with less well-developed genetic maps than *Sorghum*. We are pursuing several strategies to isolate and clone genes specifically expressed in rhizomes, and in particular the genes responsible for committing vegetative buds to become rhizomes (as opposed to tillers). Such genes would provide a means for targetting plant growth regulators to the rhizomes, for shutting off rhizomatous growth in weeds, and perhaps for enhancing rhizomatous growth in forage and turfgrasses where it is essential to productivity and quality.

c) *Development of a comprehensive “comparative molecular map” of the Poaceae chromosomes.* The Poaceae have “only” been diverged for about 60 million years, and still share a common repertoire of genes. Together with several collaborators, we are assembling comparative maps which describe the evolution of chromosomes in the Poaceae over the past 60-70 million years, and permit direct, rapid comparison of the locations of mutations in specific traits between diverse species such as maize, wheat, rice, and sorghum. The *Sorghum* population which we have developed enjoys an unprecedented level of DNA polymorphism thus is a central tool in assembling the comparative map.

d) *Sugarcane: Molecular analysis of complex measures of agricultural productivity and quality in autopolyploids.* We have mapped many quantitative trait loci in this autopolyploid, sugarcane, which is closely related to sorghum and cross-hybridizes with most sorghum DNA probes. We are emphasizing mapping genes which account for variation in sucrose concentration of the sugarcane stem, in a cross between genotypes with 3° Brix and 19° Brix, respectively. We have also mapped genes for flowering time, height, leaf morphology, tillering, stem diameter, and rhizome production, and these traits will be subjected to comparative analysis with sorghum. Sugarcane provides us with the opportunity to examine the evolution of several traits, by comparative analysis with sorghum, and also permits us to study genetic variation

in sugar accumulation and deposition. Ongoing goals include the completion of an EST project for sugarcane, identification of differentially-expressed genes and study of their relationship to mapped QTLs, and development of a 'gene map' comprised of Est to BAC hybridization data.

e) *Rice*. We are contributing to assembly of the physical map needed for the International Rice Genome Sequencing effort.

(3) FAM. BRASSICACEAE; BRASSICA, ARABIDOPSIS, and relatives.

The Cruciferae are a relatively recently-evolved plant family (ca. 10 million years old) which includes a remarkably wide range of morphologies (shape and size). Exemplary of this variation is the single species *Brassica oleracea*, which includes well-known vegetables such as cabbage, cauliflower, broccoli, brussels sprouts, kale, kohlrabi, and others. Picturing these diverse vegetables, one can quickly see that there is tremendous opportunity to study genetic/molecular control of plant development by taking advantage of the fact that they all intercross freely. We have made a "comparative molecular map" of Brassica and Arabidopsis, identified many QTLs that control many aspects of growth and development of the plant, and candidate genes from Arabidopsis that may account for some of the QTLs. We have also compared QTLs in different Brassica genotypes to investigate genes and genetic mechanisms associated with rapid morphological divergence in Brassica oleracea. Our ongoing efforts in this family will focus on use of comparative information from Arabidopsis to contribute to assembly of a physical map of Brassica, with special focus on the genomic regions in which we have identified QTLs of agricultural importance.

PROFESSIONAL REFERENCES

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(Footnotes)

¹Only projects for which all data collection is completed are listed as “in preparation”