

## **CURRICULUM VITAE – Rod A. Wing – September 2013**

University of Arizona  
School of Plant Sciences & Department of Ecology & Evolutionary Biology  
Arizona Genomics Institute, & BIO5 Institute for Collaborative Research  
Tucson, AZ 85721

### **RESEARCH/PROFESSTIONAL EXPERIENCE**

- 2012-Present Co-Chair, College of Agriculture & Life Science Dean's Research Advisory Committee (DRAC)
- 07/09- 08/10 Visiting Sabbatical Professor, Department of Molecular Biology, Max Planck Institute for Developmental Biology, Tübingen, Deutschland
- 2008-present Joint Appointment – Ecology & Evolutionary Biology, University of Arizona
- 2007-2009 Plant Biology Division Chair, Department of Plant Sciences, University of Arizona
- 2005-present Appointed Bud Antle Endowed Chair of Excellence in Agriculture & Life Sciences
- 2002-present Professor - School of Plant Sciences, Director - Arizona Genomics Institute, & Member BIO5 Institute, University of Arizona
- 1997- 2002 Director, Clemson University Genomics Institute, Clemson, SC
- 1996- 2002 Associate/Full Professor & Coker Endowed Chair of Plant Molecular Genetics, Departments of Agronomy and Biological Sciences, Clemson University, Clemson, SC
- 1997- 1998 Course Instructor – Cloning & Analysis of Large DNA Molecules, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY
- 1991-1996 Assistant/Associate Professor, Department of Soil and Crop Science, Texas A&M University, College Station, TX
- 1990-1991 Research Associate, Cornell University, NSF Plant Science Center, Ithaca, NY (Advisor: S. Tanksley)
- 1987-1990 Postdoctoral Research Associate, Plant Gene Expression Center, U.C. Berkeley-USDA/ARS, Albany, CA. (Advisor: S. McCormick)

### **EDUCATION**

- 1987 Ph.D., Genetics, University of California, Davis (Advisor: D. Ogyrdziak)
- 1980 A.B. Biochemistry, University of California, Berkeley (Advisor: J. Hosoda)

## PROFESSIONAL DEVELOPMENT

- 2012 College of Agriculture & Life Sciences – Faculty Leadership Development Program (9 course program to develop and lean leadership skills)
- 2009-2010 German Language Course (6 weeks intensive Deutsch language course at Vivat Lingua, Tübingen, Germany)
- 2008 Bisulfite sequencing of the *O. sativa* ssp. *japonica* (cv. Nipponbare) genome, Salk Institute, J. Ecker’s lab, La Jolla, CA (4 week summer mini sabbatical)
- 2007 Workshop on Molecular Evolution, Marine Biological Laboratory, Woods Hole, MA (3 week summer course)
- 2006 Analysis of transposon tagged lines in rice, UC Davis, V. Sundaresen’s lab, Davis, CA (5 week summer mini sabbatical)
- 2006 Next Generation Sequencing Methods & Analysis, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (2 week summer course)
- 2004 Successful Supervisor Series, University of Arizona, Tucson, AZ (9 week lab management course)
- 2000 Genome Sequencing and Analysis Methods, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (2 week summer course)
- 1993 Seven Habits of Highly Effective People, Texas A&M University, College Station, TX (10 week management course)

## ADVISORY/EDITORIAL BOARDS and AWARDS

- 2013 (in press) Co-Editor w/Qifa Zhang – Springer Science Book entitled “The Genetics and Genomics of Rice”
- 2013 (in press) Guest Editor w/Qifa Zhang – Current Opinion in Plant Biology – Special Issue: “Rice Functional Genomics”
- 2011-May Extraordinary Faculty Award – University of Arizona Alumni Association & College of Agriculture and Life Sciences
- 2010-2012 Scientific Advisory Board Chair - “Tomato Chr 1 and 10 Sequencing, Coordination and Bioinformatics for the International Solanaceae Genome Initiative” (PI: J. Giovannoni, NSF Plant Genome Program)
- 2010-Dec Editor – RICE – Special Issue: “*Oryza* Map Alignment Project”
- 2010-Dec Elected Fellow of the American Association for the Advancement of Science
- 2009-2010 Alexander von Humboldt Research Award – AvH Foundation, DE (60k Euro)
- 2009-present Scientific Advisory Board Member – “Construction of High Resolution Physical Maps for Large Plant Genomes” (PI: S. Kianian, NSF Plant Genome Program)
- 2009-present Scientific Advisory Board Chair – “Comparative Genomics of Phenotypic Variation in the *Compositae*” (PI: L. Rieseberg, NSF Plant Genome Program)
- 2008 Award for Research Excellence - Arizona BioIndustry Association
- 2008 Technology Innovation Award – University of Arizona, Innovation Awards
- 2008-2012 Scientific Advisory Board Chair – “A Plant Interactome Network Map” (PI: M. Vidal, NSF Plant Genome Program)
- 2007-present Editorial Board Member – RICE
- 2007-present Rice Genetics Cooperative Committee Member
- 2006 Guest Professor (5 yr. Appt.) – Huazhong Agricultural University, Wuhan, China
- 2005 First Holder, Bud Antle Endowed Chair of Excellence in Agriculture & Life Sci.
- 2005 Researcher of the Year – Univ. of Arizona, College of Agriculture & Life Sci.
- 2005-2006 Editor – Plant Molecular Biology – Special Issue: “Unlocking the Secrets of the Rice Genome”

Rod A. Wing - CV

- 2004 USS Arizona Outstanding University Achievement Honoree – Rice Genome Sequencing Project
- 2004 USDA Secretary’s Honor Award for Superior Service, Group Leader - United States Rice Genome Consortia
- 2003-2005 U.S. Representative of the International Rice Genome Sequencing Project
- 2003-present Organizing Committee – International Symposium on Rice Functional Genomics
- 2002-present Organizing Committee – International Plant and Animal Genome Conference
- 2001-2008 Scientific Advisory Board, Member – Genetix
- 2000-2001 U.S. Representative of the International Rice Genome Sequencing Project
- 1999-2007 Editorial Board–Functional and Integrative Genomics
- 1999-2005 Associate Editor – International Rice Genome Sequencing Project - News Letter
- 1997-2003 Honorary Scientist of the Rural Development Administration, Korean Rice Genome
- 1996-2002 First Holder of the Robert and Lois Coker Endowed Chair of Molecular Genetics
- 1996-2000 Associate Editor – Plant Molecular Biology
- 1996-1998 Scientific Advisory Board – TIGR – *Arabidopsis* Genome Sequencing Project

## SYNERGISTIC ACTIVITIES

1) Development of structural frameworks to understand complex genomes. Since 1994 my laboratory has specialized in the construction and distribution of deep-coverage large-insert BAC libraries for plants and the utilization of these libraries to create fingerprint/BAC end sequence based physical maps for positional cloning and genome sequencing (e.g. rice and maize genome sequencing projects). The first plant BAC library was published in December, 1994 for *Sorghum bicolor* in *Nucleic Acids Research*.

2) International Rice Genome Sequencing Project. I served as the United States representative to the IRGSP. This work involved extensive coordination with PIs and government officials from 10 nations to ensure the rice genome sequence was finished on schedule. My laboratory generated the physical map of the rice genome that was used as a framework to sequence rice, and lead the Arizona, Cold Spring Harbor, Washington University consortia that sequenced and finished the short arms of rice chromosomes 3 and 10. The rice genome was published on August 11, 2005 in *Nature*.

3) The *Oryza* Map Alignment Project (OMAP: [www.omap.org](http://www.omap.org))/*Oryza* Genome Evolution Project. My laboratory, in collaboration with S. Jackson, L. Stein, D. Ware, M. Long, C. Machado, and M. Sanderson established a large array of integrated genomics tools and resources that have been used to create a genus level research platform to investigate cereal genome evolution and crop improvement. The OMAP/OGE resources are being actively used around the world as a foundation to launch numerous research projects. One such endeavor is the International OMAP which aims to generate a comprehensive set reference genome sequences for all 18 diploid *Oryza* species by the end of 2012.

4) Maize Genome Sequencing Project. My laboratory played a leadership role in sequencing the maize genome by first generating a physical map of the maize genome, and subsequently picking a minimum tiling path or BAC clones across the genome that was sequenced by the Washington University Genome Sequencing Center. Finally we played a key role in finishing the genome by finishing approximately 25% of all sequenced BACs. The maize genome was published on November 20, 2009 in *Science*.

5) *Brassicales* Map Alignment Project (BMAP). During my Alexander von Humboldt Research Award sabbatical in Germany (2009/10), I co-organized (with Detlef Weigel & J. Chris Pires) a series of four grand challenge meetings, in the US, Europe, Asia, and Canada, with the goal of establishing Brassicaceae as the premier dicot family for experimental and theoretical biology. The immediate goal is select and target 150 key phylogenetically diverse species for the establishment of high quality reference genome and transcriptome sequences. DOE's Joint Genome Institute recently approved a Community Sequencing Program proposal to initiate the sequencing of the "Top 20 Brassicales" (PI: Wing; 1/2012).

6) Arizona Phenotyping Network (AZPN). My laboratory, in collaboration with C. Kubota (UA CEAC), K. Nolte (UA Yuma Ag Center), and M. Jenks (USDA ALARC), have teamed up to create greenhouse and field based phenotyping facilities across the state that will allow us to phenotype crops under semi-arid conditions that are important to the state and the nation. The eventual outcome will be the generation of a new breed of "green super crops" that have less of an environmental impact (i.e. less water, fertilizer, pesticides) and are higher yielding and more nutritious. This project began in January 2013.

**PEER REVIEWED PUBLICATIONS 2013-2002**

(Total 203 [141 since arriving in University of Arizona in 2002]; + 5 in review).

203) Jacquemin, J., J.S.S. Ammiraju, G. Haberer<sup>2</sup>, D.D. Billheimer, Y. Yu., L.C. Liu, L.F. Rivera, K. Mayer, M. Chen, R.A. Wing. 15 MYA of evolution in the *Oryza* genus shows extensive gene family expansion. 2013. *Molecular Plant* (In Press).

202) C. Wang, X. Shi, L. Liu, H. Li, J.S.S. Ammiraju, D.A. Kudrna, W Xiong, H. Wang, Z. Dai, Y. Zheng, J. Lai, W. Jin., J. Messing, J.L. Bennetzen, R.A. Wing, M. Luo. Genomic resources for gene discovery, functional genome annotation, and evolutionary studies of maize and its close relatives. 2013. *Genetics* (Online September 2013)

201) Ortiz M, A. Legatzki, J.W. Neilson, B. Fryslie, W.M Nelson, R.A. Wing, C.A. Soderlund, B.M. Pryor, R.M. Maier. Making a living while starving in the dark metagenomic insights into the energy dynamics of a carbonate cave. 2013. *Intl. Soc. Micro. Ecol.* 1-14.

200) Singh, R., M. Ong-Abdullah, E.T.L. Low, M.A.A. Manaf, R. Rosli, R. Nookiah, L.C.-L. Ooi, S.E. Ooi, K.L. Chan, M.A. Halim, N. Azizi, J. Nagappan, B. Bacher, N. Lakey, S.W. Smith, D. He, M. Hogan, M.A. Budiman, E.K. Lee, R. DeSalle, D. Kudrna, J.L. Goicoechea, R.A. Wing, R.K. Wilson, R.S. Fulton, J.M. Ordway, R.A. Martienssen, R. Sambanthamurthi. Oil plam genome sequence reveals divergence of interfertile species in old and new worlds. 2013. *Nature* **500**:335-339.

199) Matsubaa, Y., T.T.H. Nguyene, K. Wiegertb, V. Falaraa, E. Gonzales-Vigilb, B. Leonga, D. Kundra, W. Golserc, R.A. Wing, A. Bolgerd, B. Usadeld, A.R. Fernied, C.S. Barryb, E. Picherskya. Evolution of a Complex Locus for Terpene Biosynthesis in *Solanum*. 2013. *Plant Cell* (Online June 2013).

198) Dereeper, A., R. Guyot, C. Tranchant-Bubreuil, F. Anthony, A. de Kochko, D. Kudrna, T. Leroy, J. Poulain, M. Rondeau, X. Song, R.A. Wing, P. Lashermes. BAC-end sequence analysis provides first insights into coffee (*Coffea canephora* P.) genome composition and evolution. 2013. *Plant Mol. Biol.* (in press).

197) Zhang, C., J. Wang, N.C. Marowsky, M. Long, R.A. Wing, and C. Fan. High Occurrence of Functional New Chimeric Genes in Survey of Rice Chromosome 3 Short Arm Genome Sequences. 2013. *Genome Biol. & Evo.* (in press).

196) Jacquemin, J., D. Bhatia, K. Singh, and R.A. Wing. The International - *Oryza* Map Alignment Project: Development of a genus-wide comparative genomics platform to help solve the 9 billion-people question. 2013. *Curr. Op. Plant Biol.* **16**:147-156.

195) Koo, H.J., E.T. McDowell, X. Ma, K.A. Greer, J. Kapteyn, Z. Xie, A. Descour, H. Kim, Y. Yu, D. Kudrna, R.A. Wing, C.A. Soderlund, D.R. Gang. Ginger and turmeric expressed sequence tags identify signature genes for rhizome identity and development and the biosynthesis of curcuminoids, gingerols and terpenoids. 2013. *BMC Plant Biol.* **13**:27.

194) Chen J, Q. Huang, D. Gao, J. Wang, Y. Lang, T. Liu, B. Li, Z. Bai, J.L. Goicoechea, C. Liang, C. Chen, W. Zhang, S. Sun, Y. Liao, X. Zhang, L. Yang, C. Song, M. Wang, J. Shi, G. Liu, J. Liu, H. Zhou, W. Zhou, Q. Yu, N. An, Y. Chen, Q. Cai, B. Wang, B. Liu, J. Min, Y. Huang, H. Wu, Z. Li, Y. Zhang, Y. Yin, W. Song, J. Jiang, S.A. Jackson, R.A. Wing, J. Wang, M. Chen. (2013) Whole-genome sequencing of *Oryza brachyantha* reveals mechanisms underlying *Oryza* genome evolution. *Nature Commun* **4**: 1595

193) Maron, L.G., C.T. Guimarães, M. Kirst, P.S. Albert, J.A. Birchler, P.J. Bradbury, E.S. Buckler, A.E. Coluccio, T.V. Danilova, D. Kudrna, J.V. Magalhaes, M.A. Piñeros, M.C. Schatz, R.A. Wing, L.V.

Kochian. Aluminum tolerance in maize is associated with higher *MATE1* gene copy-number. 2013. *PNAS* **110**:5241-5246.

192) Horvath, D.P., D. Kudrna, J. Talag, J.V. Anderson, W.S. Chao, R.A. Wing, M.E. Foley, and Münevver Dogramaci. BAC library development and clone characterization for dormancy-responsive DREB4A, DAM, and FT from leafy spurge (*Euphorbia esula*) identifies differential splicing and conserved promoter motifs. 2013. *Weed Science* **61**:303-309.

191) Yang, R., D.E. Jarvis, H. Chen, M.A. Beilstein, J. Grimwood, J. Jenkins, S. Shu, S. Prochnik, M. Xin, C. Ma, J. Schmutz, R.A. Wing, T. Mitchell-Olds, K.S. Schumaker, X. Wang. The Reference Genome of the Halophytic Plant *Eutrema salsugineum*. 2013. *Frontiers in Plant Sci* **4**:46.

190) Ortiz, M., J.W. Neilson, W.M. Nelson, A. Legatzki, A. Byrne, Y. Yu, R.A. Wing, C.A. Soderlund, B.M. Pryor, L.S. Pierson, R.M. Maier. Profiling bacterial diversity and taxonomic composition on speleothem surfaces in Kartchner Caverns, AZ. 2013. *Microbial Ecology* **62**:371-383.

190) Yang, Lu, T. Liu, B Li, Y. Sui, J. Chen, J. Shi, R.A. Wing, M. Chen. Comparative Sequence Analysis of the Ghd7 Orthologous Regions Revealed Movement of Ghd7 in the Grass Genomes. 2012. *PLoS ONE* **7**: e50236. doi:10.1371/journal.pone.0050236

189) The International Barley Genome Sequencing Consortium. A physical, genetic and functional sequence assembly of the barley genome. 2012. *Nature* doi:10.1038/nature11543.

188) Thais RS Figueira, T.R.S., V. Okura, F.R. Silva, M.J. Silva, D. Kudrna, J.S.S. Ammiraju, J. Talag, R.A. Wing, and P. Arruda. A BAC library of the SP80-3280 sugarcane variety (*Saccharum* sp.) and its inferred microsynteny with the sorghum genome. 2012. *BMC Research Notes* **5**:185 (11 pages).

187) Tomato Genome Sequencing Consortium (300+ authors). The tomato genome sequence provides insights into fleshy fruit evolution. 2012. *Nature* **485**:635-641.

186) Ha, Jungmin, B. Abernathy, D. Grant, X. Wu, W. Nelson, G. Stacey, R.A. Wing, R. Shoemaker and S.A. Jackson. 2012. Integration of the draft sequence and physical map as a framework for genomic research in Soybean (*Glycine max* (L.) Merr.). 2012. *Genes, Genomes, Genetics* **2**:321-329.

185) Neilson, J.W., J. Quade, M. Ortiz, W.M. Nelson, A. Legatzki, F. Tian, M. LaComb, J.L. Betancourt, R.A. Wing, C.A. Soderlund, R.M. Maier. Life at the hyperarid margin: novel bacterial diversity in arid soils of the Atacama Desert, Chile. 2012. *Extremophiles* **16**:553-566.

184) Li, H.J., X.H. Li, J.H. Xiao, R.A. Wing, S.P. Wang. Ortholog Alleles at *Xa3/Xa26* Locus Confer Conserved Race-Specific Resistance against *Xanthomonas oryzae* in Rice. 2012. *Molecular Plant* **5**:281-290.

183) Lin, H., P. Xia, R.A. Wing, Q. Zhang, M. Luo. Dynamic intra-*japonica* subspecies variation and resource application. 2012. *Molecular Plant* **5**:218-230.

182) Gao, D., Z. Gong, R.A. Wing, J. Jiang, S.A. Jackson. Molecular and cytological characterization of centromeric retrotransposons in a wild relative of rice, *Oryza granulata*. 2011. *Tropical Plant Biol* **4**:217-227.

181) Fan, C., J. Walling, J. Zhang, J. Jiang, and R.A. Wing. Conservation and purifying selection of transcribed genes in recombination-free centromeres. 2011. *Plant Cell* **8**:2821-2830.

180) Jacquemin J, C. Chaparro, M. Laudie, A. Berger, F. Gavory, J.L. Goicoechea, R.A. Wing, R. Cooke. 2011. Long-range and targeted ectopic recombination between the two homeologous chromosomes 11 and 12 in *Oryza* species. *Mol. Biol. Evo.* **28**:3139-3150.

179) Zuccolo, A., J.E. Bowers, J.C. Estill, Z. Xiong, M. Luo, A. Sebastian, J.L. Goicoechea, K. Collura, Y. Yu, Y. Jiao, J. Duarte, H. Tang, S. Ayyampalayam, S. Rounsley, D. Kudrna, A.H. Paterson, J.C. Pires, A. Chanderbali, D.E. Soltis, S. Chamala, B. Barbazuk, P.S. Soltis, V.A. Albert, H. Ma, D. Mandoli, J. Banks, J.E. Carlson, J. Tomkins, C.W. dePamphilis, R.A. Wing, J. Leebens-Mack. 2011. A physical map for the *Amborella trichopoda* genome sheds light on the evolution of angiosperm genome structure. *Genome Biology* **12**: R48 (14 pages).

178) Paiva, J.A., E. Prat, S. Vautrin, M.D. Santos, H. San-Clemente, S. Brommonschenkel, P.G.S. Fonseca, D. Grattapaglia, X. Song, J.S.S. Ammiraju, D. Kudrna, R.A. Wing, A.T. Freitas, H. Berges, J. Grima-Pettenati. 2011. Advancing Eucalyptus genomics: identification and sequencing of lignin biosynthesis genes from deep-coverage BAC libraries. *BMC Genomics* **12**:137.

177) Tian, Z., Y. Yu, L. Feng, Y. Yu, P. SanMiguel, R.A. Wing, S.R. McCouch, J. Ma, and S.A. Jackson. 2011. Exceptional lability of a genomic complex in rice and its close relatives revealed by interspecific and intraspecific comparison and population analysis. *BMC Genomics* **12**:142.

176) Blair, M.W., N. Hurtado, C.M. Chavarro, M.C. Muñoz-Torres, M.C. Giraldo, F. Pedraza, J. Tomkins, R.A. Wing. 2011. Gene-based SSR markers for common bean (*Phaseolus vulgaris* L.) derived from root and leaf tissue ESTs: an integration of the BMC series. *BMC Plant Biol.* **11**:50.

175) Song, X., J.L. Goicoechea, J.S.S. Ammiraju, M. Luo, R. He, J. Lin, S.J. Lee, N. Sisneros, T. Watts, D.A. Kudrna, W. Golser, E. Ashley, K. Collura, M. Braidotti, Y. Yu, L.M. Matzkin, B.F. McAllister, T.A. Markow, R.A. Wing. 2011. The 19 Genomes of *Drosophila*: A BAC Library Resource for Genus-wide and Genome Scale Comparative Evolutionary Research. *Genetics* **187**:1023-1030.

174) den Camp, R.O., A. Streng, S.D. Mita, Q. Cao, E. Polone, W. Liu, J.S.S. Ammiraju, D. Kudrna, R.A. Wing, A. Untergasser, T. Bisseling, R. Geurts. LysM-Type Mycorrhizal Receptor Recruited for Rhizobium Symbiosis in Nonlegume *Parasponia*. 2011. *Science* **331**:909-912.

173) Argout, X., J. Salse, J.M. Aury, M.J. Guitinan, G. Droc, J. Gouzy, M. Allegre, C. Chaparro, T. Legavre, S.N. Maximova, M. Abrouk, F. Murat, O. Fouet, J. Poulain, M. Ruiz, Y. Roguet, M. Rodier-Goud, J.F. Barbosa-Neto, F. Sabot, D. Kudrna, J.S.S. Ammiraju, S.C. Schuster, J.E. Carlson, E. Sallet, T. Schiex, A. Dievart, M. Kramer, L. Gelley, Z. Shi, A. Bérard, C. Viot, M. Boccara, A.M. Risterucci, V. Guignon, X. Sabau, M.J. Axtell, Z. Ma, Y. Zhang, S. Brown, M. Bourge, W. Golser, X. Song, D. Clement, R. Rivallan, M. Tahi, J.M. Akaza, B. Pitollat, K. Gramacho, A. D'Hont, D. Brunel, D. Infante, I. Kebe, P. Costet, R.A. Wing, W.R. McCombie, E. Guiderdoni, F. Quetier, O. Panaud, P. Wincker, S. Bocs & C. Lanaud. 2011. The genome of *Theobroma cacao*. *Nature Genetics* **43**:101-108.

172) Lin, J., D. Kudrna, and R.A. Wing. 2011. Construction, Characterization, and Preliminary BAC-End Sequence Analysis of a Bacterial Artificial Chromosome Library of the Tea Plant (*Camellia sinensis*). *J. of Biomed. & Biotech* (doi:10.1155/2011/476723).

171) Ammiraju, J.S.S, X. Song, M. Luo, N. Sisneros, A. Angelova, D. Kudrna, H.R. Kim, Y. Yu, J.L. Goicoechea, M. Lorieux, N. Kurata, D. Brar, D. Ware, S. Jackson, and R.A. Wing. 2010. The *Oryza* BAC Resource: A genus-wide and genome scale tool for exploring rice genome evolution and leveraging useful genetic diversity from wild relatives. *Breeding Science* **60**:536-543.

170) Chen, M., F. Lu, S.A. Jackson, and R.A. Wing. 2010. Dynamic Genome Evolution of *Oryza* – A Genus-Wide Comparative Analysis. In: *Darwin's Heritage Today: Proceedings of the Darwin 200 Beijing International Conference*. M. Long, H. Gu, Z. Zhou eds, High Education Press, Beijing, Pp. 76-83.

169) Gill, N., P. SanMiguel, B.D. Dhillon, B. Aberhnathy, N. Jiang, H.R. Kim, L. Stein, D. Ware, R.A. Wing and S.A. Jackson. 2010. Dynamic *Oryza* genomes: Repetitive DNA sequences as genome modeling agents. *RICE* **3**:251-269.

- 168) Febrer, M., J.L. Goicoechea, J. Wright, N. McKenzie, X. Song, J. Lin, K. Collura, M. Wissotski, Y. Yu, J.S.S. Ammiraju, E. Wolny, D. Idziak, A. Betekhtin, D. Kudrna, R. Hasterok, R.A. Wing, and M.W. Bevan. 2010. An integrated physical, genetic and cytogenetic map of *Brachypodium distachyon*, a model system for grass research. *PLoS ONE* 5(10): e13461. doi:10.1371/journal.pone.0013461.
- 167) Goicoechea, J.L., J.S.S. Ammiraju, P.R. Marri, M. Chen, S. Jackson, Y. Yu, S. Rounsley, and R.A. Wing. 2010. The Future of Rice Genomics: Sequencing the Collective *Oryza* Genome. *RICE* 3:89-97.
- 166) Lin, L., G. Pierce, J.E. Bowers, J.C. Estill, R.O. Compton, L.K. Nelson, C. Kim, C. Lemke, J. Rong, H. Tang, X. Wang, M. Braidotti, A.H. Chen, K. Collura, E. Epps, W. Golser, C Grover, K.L. Herrick, J. Ingles, S. Karunakaran, D. Kudrna, J Olive, N. Tabassum, E. Um, M. Wissotski, Y. Yu, A. Zuccolo, M. Rahman, D.G. Peterson, Rod A. Wing, J.F. Wendel, and A.H. Paterson. 2010. A Draft Physical Map of a D-genome Cotton Species (*Gossypium raimondii*). *BMC Genomics* 11:395.
- 165) Hurwitz, B. D. Kudrna, Y. Yu, A. Sebastian, A. Zuccolo, S.A. Jackson, D. Ware, R.A. Wing\*, L. Stein\*. 2010. Rice structural variation: a comparative analysis of structural variation between rice and three of its closest relatives in the genus *Oryza*. *Plant Journal* 63:990-1003. (\*co-corresponding authors).
- 164) Ammiraju, J.S.S., C. Fan, Y. Yu, X. Song, K.A. Cranston, A.C. Pontaroli, F.L., A. Sanyal, N. Jiang, T. Rambo, J. Currie, K. Collura, J. Talag, J.L. Bennetzen, M. Chen, S. Jackson and R.A. Wing. 2010. Spatio-temporal patterns of genome evolution in homeologous *Adh1* - *Adh2* regions from four allotetraploid species of the genus *Oryza*. *Plant Journal* 63:430-442.
- 163) Gill, N., B.D. Dhillon, B. Abernathy, R.A. Wing and S.A. Jackson. 2010. Use of fragmentary sequence data to identify Conserved Non-coding Sequences: an example from the genus *Oryza*. *Mol Biol Evol.* (In press).
- 162) Geraldès, A., T. Rambo, R.A. Wing, N. Ferrand, and M.W. Nachman. 2010. Extensive gene conversion drives the concerted evolution of paralogous copies of the SRY gene in European rabbits. *Mol Biol Evol.* 27:2437-2440.
- 161) Zuccolo, A., A. Sebastian, Y. Yu, S. Jackson, S. Rounsley, D. Billheimer, R.A. Wing. 2010. Assessing the extent of substitution rate variation of Retrotransposon Long Terminal Repeat sequences in *Oryza sativa* and *Oryza glaberrima*. *RICE* 3:242-250.
- 160) Dai, J. Wu, X. Li, X. Wang, C. Jantasuriyarat, D. Kudrna, R.A. Wing, B. Zhou, G.-L. Wang. 2010. Genomic structure and evolution of the *Pi2/9* Locus in wild rice species. *Theor Appl Genet.* 121:295-309.
- 159) Sanyal, A., A. Jetty, F. Lu, Y. Yu, T Rambo, J. Currie, K. Kollura, HR. Kim, J. Ma, P.S. Miguel, M. Chen\*, R.A. Wing\* and S.A. Jackson\*. 2010. Orthologous comparisons of the *Hdl* region across genera reveal *Hdl* gene lability within diploid *Oryza* species and disruptions to microsynteny in sorghum. *Mol Biol Evol* 27:2487-2506. (\*co-corresponding authors).
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## RESEARCH GRANTS AT ARIZONA AND AWARDS

- AGI/JGI Joint Genomics Collaborative. Rod Wing (PI) (5%). 9/2013 (\$500,000 Total) (DOE/JGI's Emerging Technologies Opportunity Program).
- *CPGS Oryza Genome Evolution*. Rod Wing (PI) (60%), Scott Jackson, Manyuan Long, Carlos Machado, Michael Sanderson. 9/2010 (\$9,946,315 Total) (NSF Molecular and Cellular Biology Program).
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- *Evolutionary Genomics of a Rice Centromere*. Jiming Jiang (PI), Rod Wing (33%), Scott Jackson. 2006 (\$1,458,064 Total) (NSF Plant Genome Research Program).
- *Sequencing the Maize Genome*. R. Wilson (PI), Rod Wing (40%), Doreen Ware, W.R. McCombie, Pat Schnable. 2005 (\$2,201,983 Total) (NSF Plant Genome Research Program).
- *Comparative Evolutionary Genomics of Cotton*. J. Wendel (PI), Rod Wing (25%), Alan Gingle, Andrew Paterson. 2002 (\$1,047,034 Total) (NSF Plant Genome Research Program).
- *SoyMap, an integrated map of soybean for resolution and dissection of multiple genome duplication events*. S. Jackson (PI), R. Wing (20%). 2005 (\$1,373,592 Total) (NSF Plant Genome Research Program).
- *Genome evolution in diploid and polyploid cotton*. Jonathan Wendel (PI), Rod Wing, Andrew Paterson, Adah Leshem-Ackerman (100%). 2006 (\$534,176 Total) (NSF Comparative Sequencing Program).
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- *Highly reduced genomes of coresident bacterial symbionts of xylem-feeding insects: Ecological and evolutionary implications*. Nancy Moran, Rod Wing (30%). 2006 (\$440,793 Total) (NSF).
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- *Finishing the rice genome*. W. Richard McCombie (PI), Rod Wing (45%), Cari Soderlund. 2003 (\$2,000,000 Total) (NSF Plant Genome Research Program).
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- *Techniques for efficient finishing and physical linkage of gene-enriched shotgun sequences*. Cari Soderlund (PI), Rod Wing (20%), Jeff Bennetzen. 2003 (\$4,202,799 Total) (NSF Plant Research Genome).
- *Collaborative Research: The green plant BAC library project - public resources for studying evolution, physiology and development*. Rod Wing (PI) (80%), Dina Mandoli, Jody Banks, Claude DePamphillis. 2002 (\$1,937,246.00 Total) (NSF Tree of Life Program).
- *BAC library production and distribution for Healthy People 2010*. Rod Wing (PI) (90%), Cari Soderlund, Jeff Tomkins. 2002 (\$2,800,000.00 Total) (NIH).
- *Sequencing the Maize Genome*. Jo Messing (PI), Rod Wing (45%), Cari Soderlund. 2002 (\$1,226,000 Total) (NSF Plant Genome Research Program).
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- *Genome Analysis of Pathogen-Host Recognition and Subsequent Responses in the Rice Blast Patho-System*. Ralph Dean (PI), Rod Wing (20%), Cari Soderlund. 2001 (\$996,420 Total) (NSF Plant Genome Research Program).
- *Grass Genome Biodiversity: Application of genomics tools from Sorghum and related grasses to identify and analyze variation in structure and function*. Andrew Patterson (PI), Rod Wing (50%), Cari Soderlund. 2001 (\$614,295 Total) (NSF Plant Genome Research Program).