Rod. A Wing

Honors Professor, Honors College, University of Arizona

RESEARCH/PROFESSTIONAL EXPERIENCE

2014-2019	AXA Chair for Genome Biology & Evolutionary Genomics, International Rice Research Institute, Los Banos, Philippines/University of Arizona (3 month appointment/yr for 5 years)
2012-Present	Honors Professor, Honors College, University of Arizona
2012-Present	Co-Chair, College of Agriculture & Life Science Dean's Research Advisory Committee (DRAC)
07/09 - 08/10	Alexander von Humboldt Sabbatical Professor, Department of Molecular Biology, Max Planck Institute for Developmental Biology, Tübingen, Deutschland
2008- Present	Joint Appointment – Dept. of 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: Steve Tanksley)
1987-1990	Postdoctoral Research Associate, Plant Gene Expression Center, U.C. Berkeley-USDA/ARS, Albany, CA. (Advisor: Sheila McCormick)

EDUCATION

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

ADVISORY/EDITORIAL BOARDS and AWARDS

2014-Nov	Organizing Committee Chair – 12nd International Symposium on Rice Functional Genomics, Tucson, Arizona (http://www.isrfg12-tucson.org/)
2013	Co-Editor (w/Q. Zhang) – Special Issue on “Rice Functional Genomics” in Current Opinion in Plant Biology
2013	Co-Editor (w/Q. Zhang) “Genetics and Genomics of Rice” Springer
2012-present	Editorial Board Member – Molecular Plant
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)
2009-2013	Scientific Advisory Board Member – “Construction of High Resolution Physical Maps for Large Plant Genomes” (PI: S. Kianian, NSF Plant Genome Program)
2009-2014	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-present	Shennong Professor – 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”
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
2004-Nov	Organizing Committee Chair – 2nd International Symposium on Rice Functional Genomics, Tucson, Arizona
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

REVIEWED PUBLICATIONS 2010-2014
(Total 211 [149 since arriving in University of Arizona in 2002]; + 5 in review).

211) Gerring, A.D.W., F. Maumus, D. Copetti, N. Choisne, D. Zwickl, M. Zytnicki, A.R. McTaggart, S. Scalabrin, S. Vezzulli, R.A.Wing, H. Quesneville, P.Y. Teycheney. Endogenous florendoviruses are major components of plant genomes and hallmarks of virus evolution. 2014. *Nature Communications* **5**: Article number 5269.

210) Wang, M., Y. Yu, G. Haberer, P. Marri, C. Fan, J.L. Goicoechea, A. Zuccolo, X. Song, D. Kudrna, S.A. Jetty, R. Cossu , C. Maldonado, J. Chen , S. Lee, N. Sisneros, K. de Baynast , W. Golser, M. Wissotski, W. Kim , P. Sanchez, M.N. Ndjiondjop, K. Sanni , M. Long, J. Carney, O. Panaud, T. Wicker, C. Machado, M. Chen, K. Mayer, S. Rounsley, R.A. Wing. The genome of African rice (*Oryza glaberrima*): Evidence for independent domestication. 2014. *Nature Genetics* **46**:982-988.

209) Schmutz, J., P. McClean, S. Mamidi, G.A. Wu,, S.B. Cannon, J Grimwood, J. Jenkins, S. Shu, Q. Song, C. Chavarro, M. Torres-Torres, V. Geffroy, S.M. Moghaddam, D. Gao, B. Abernathy, K. Barry, M. Blair, M.A. Brick, M. Chovatia, P. Gepts, D.M Goodstein, M. Gonzales, U. Hellsten, D.L. Hyten, G. Jia, JD. Kelly, D. Kudrna, R. Lee, M.M.S. Richard, P.N. Miklas, JM. Osorno, J Rodrigues, V. Thareau, C.A. Urrea, M. Wang, Y. Yu, M. Zhang, R.A. Wing, P.B. Cregan, D.S. Rokhsar, SA. Jackson. A reference genome for common bean and genome-wide analysis of dual domestications. 2014. *Nature Genetics* **46**: 707–713.

208) Zwickl D., J. Stein, R.A. Wing, D. Ware, M. Sanderson. Disentangling methodological and biological sources of gene tree discordance on *Oryza* (Poaceae) chromosome 3. 2014. *Systematic Biology* doi: 10.1093/sysbio/syu027.

207) Pan Y., Y. Deng, H. Lin, D.A. Kudrna, R.A Wing, L. Li, Q. Zhang, M. Luo. Comparative BAC-based physical mapping of *Oryza sativa* ssp. *indica* var. 93–11 and evaluation of the two rice reference sequence assemblies. 2014. *The Plant Journal* **77**:795–805.

206) Wang, X., D.A. Kudrna, Y. Pan, H. Wang, L.L., H. Lin, J. Zhang, X. Song, J.L. Goicoechea, R.A. Wing, Q. Zhang, M. Luo. Global genomic diversity of *Oryza sativa* varieties revealed by comparative physical mapping. 2014. *Genetics* **196**:937-949.

205) *Amborella* Genome Project. The *Amborella* genome and the evolution of flowering plants. 2013. *Science* **342**:1241084.

204) Chamala, S., A.S. Chanderbali, J.P. Der, T. Lan, B. Walts, V.A. Albert, C.W. dePamphilis, J. Leebens-Mack, S. Rounsley, S. Schuster, R.A. Wing, N. Xiao, R. Moore, P.S. Soltis, D.E. Soltis, W.. Barbazuk.Assembly and validation of the complete nuclear genome sequence of the basal angiosperm *Amborella*, a non-model species. 2013 *Science* **342**:1516-1517.

203) Jacquemin, J., J.S.S. Ammiraju, G. Haberer2, 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* (10.1093/mp/sst149).

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 **195**:723-737.

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) Matsuba, 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* **25**:2022–203.

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*. **83**:177-189.

197) Zhang, C., J. Wang, N.C. Marowsky, M. Long, R.A. Wing, and C. Fan. High occurrence of functional new chimeric genes in a survey of rice chromosome 3 short arm genome sequences. 2013. *Genome Biol. & Evo.* 5:1038-1048.

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* **491**:711-716.

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. Guiltinan, 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, HR 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) Geraldes, 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 *Hd1* region across genera reveal *Hd1* 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 The UNIVERSITY of ARIZONA & AWARDS

- Generation of two platinum standard grade reference genome sequences for rice - Minghui63 and Zhenshan97. Rod Wing (PI) (5%). 1/2014 ($1,000,000 Total) (Huazhong Agricultural University Collaborative Fixed Price Agreemnt).

- 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).

- *Alexander von Humboldt Research Award.* Rod Wing (Award Winner). 2009-2010 (60,000 Euro Total) (Alexander von Humboldt Foundation, Deutschland).

- *Generation and analysis of a reference sequence for the West African cultivated rice "Oryza glaberrima" (CG14)*. Rod Wing (PI) (66%), Steve Rounsley. 2008 ($1,500,000 Total) (NSF Plant Genome Research Program).

- *Sequencing of chromosome 3 short arms from the AA, BB, CC, BBCC genomes of wild relatives of rice for comparative functional and evolutionary genomics*. Rod Wing (PI) (60%), Scott Jackson, Steven Rounsley, Lincoln Stein. 2006 ($2,735,151 Total) (NSF Comparative Sequencing Program).

- *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).

- *Kartchner Caverns: Habitat scale community structure and function in carbonate caves*. R. Maier (PI), Rod Wing (10%), Leland Pierson, Barry Pryor. 2006 ($1,820,162 Total) (NSF).

- *IGERT: Evolutionary, computational, and molecular approaches to genome structure and function*. With M. Nachman (PI), Rod Wing (10%), Mike Hammer, Nancy Moran, Vicki Chandler . 2001 ($2,699,895 Total) (NSF).

- *The Oryza Map Alignment Project*. Rod Wing (PI) (60%), Lincoln Stein, Scott Jackson. 2003 ($9,700,000 Total) (NSF Plant Genome Research Program).

- *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).

- *Acquisition of instrumentation for Omics research at the University of Arizona*. David Gang (PI), Rod Wing (33%), David Galbraith, Cari Soderlund. 2005 ($192,350 Total) (NSF MRI).

- *Sequenced insertion lines for rice functional genomics*. V. Sundaresan (PI), Rod Wing (5%). 2005 ($76,800 Total) (USDA-NRI).

- *Insertional mutagenesis tools for functional genomics of rice*. V. Sundaresan (PI), Rod Wing (5%). 2002 ($100,000 Total) (NSF Plant Genome Research Program).

- *Finishing the rice genome*. W. Richard McCombie (PI), Rod Wing (45%), Cari Soderlund. 2003 ($2,000,000 Total) (NSF Plant Genome Research Program).

- *Exploitation of the Tomato model system for comparative and functional genomics*. Steve Tanksley (PI), Rod Wing (20%), James Govanoni, Greg Martin. 2001 ($1,387,825 Total) (NSF Plant Research Genome).

- *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).

- *Sequencing of Rice Chromosomes 3 and 10*. Rod Wing (PI) (45%), Dick McCombie, Rick Wilson. 1999 ($6,200,000 Total) (NSF/USDA/DOE).

- *Comprehensive Genetic, Physical and Database Resources for Maize*. Ed Coe (PI); Rod Wing (40%), Cari Soderlund. 1998 ($1,629,246 Total) (NSF Plant Genome Research Program).

- *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).