

Grand Challenge Workshop: Mechanistic Basis of Plant Adaptation

ORGANIZERS

William Beavis (Iowa State University, Department of Agronomy, Tel 515 294 7301, Email wbeavis@iastate.edu). **Research & Outreach:** It is well known that response to selection will decline without introduction of novel sources of genetic variability. It is also known that domestication has been associated with significant loss of genetic diversity in most crops. What is the extent of subsequent losses in genetic diversity during the process of adapting crops to modern production agricultural environments? We are interested in questions about genetic diversity and expected genetic gain after adaptation to production agriculture. To pursue these questions we actively recruit students with quantitative skills from underrepresented groups to participate in research using simulation modeling approaches.

Justin Borevitz (University of Chicago, Department of Ecology and Evolution, Tel 773-702-5948, Email borevitz@uchicago.edu). **Research & Outreach:** How do organisms shape their environment, and how does environmental change shape the resident organisms? The Borevitz laboratory is pursuing the adaptive genetic events enabling ecological succession, in annuals (*Arabidopsis thaliana/lyrata*) and perennials (Aquilegia, prairie grasses). We work in the Indiana Dunes National Lakeshore as a model ecosystem. Outreach includes teaching summer courses for high school bio-teachers and an undergraduate PrairieEcosystems.org course that works with community and school groups.

Edward Buckler (USDA-ARS Research Geneticist, Cornell University, Tel 607-255-4520, Email esb33@cornell.edu). **Research & Outreach:** Interested in the basis of complex traits with an emphasis on dissecting abiotic stress tolerance in maize. Our research is involved in quantitative and statistical genetics, genomics, and field genetics. We also have projects ongoing in wild and domesticated grape and switchgrass. Outreach conducted through the development of informal science exhibits.

Susan McCouch (Cornell University, Department of Plant Breeding & Genetics, Tel 607-255-0420, Email srm4@cornell.edu). **Research & Outreach:** Interested in the evolution of population sub-structure in rice and the genetic basis of ecological adaptation, grain quality and agronomic characteristics as the basis for plant improvement. Research activities include molecular genetics and genomics, population development, molecular and whole-plant phenotyping, with extensive international collaboration. Outreach activities include a field-based short course on rice research and production in the Philippines, middle school curriculum development, high school biology research and teaching and undergraduate summer internships.

David E Salt (Purdue University, Horticulture Department, Tel 765-496-2112, Email dsalt@purdue.edu). **Research & Outreach:** Interested in the genetics basis controlling the ionome and its relationship to adaptation in *Arabidopsis thaliana*, *Thlaspi* and *Astragalus* species, and translation of this information into rice for improved rice grain mineral nutrient quality. Outreach conducted through the development of informal science exhibits.

John Willis (Duke University, Biology Department, Tel. 919-660-7340, email jwillis@duke.edu). **Research & Outreach:** Interested in the genomic basis of standing complex trait variation, adaptation, and speciation in *Mimulus* species. A current focus is on the evolution of traits related to drought and edaphic adaptation. As part of a large collaborative effort, we are developing genomic resources for *Mimulus*, including a whole genome sequence for *M. guttatus*, which are greatly aiding in the mechanistic analysis of adaptation and speciation.

Designated contact person for the group: David E Salt (Tel 765-496-2112, Email dsalt@purdue.edu).

POTENTIAL PARTICIPANTS

The organizers have recently contacted more than 75 people from the broad plant adaptation community (Table 1). The response has been overwhelmingly positive, with all respondents expressing strong enthusiasm for the workshop proposal and development of the proposed cyberinfrastructure for plant adaptation research. In just a couple of days, already 35 people have confirmed an interest in attending the proposed workshop (names in *ITALICS*). If the proposed workshop is chosen by iPlant the workshop organizers will choose ~35 people to attend, selected to cover the broadest range of research disciplines

and groups within the community. Online participation at the workshop will also be encouraged to enable engagement by people unable to attend.

Table 1. People who the organizers have already contacted about attending the proposed workshop.	
Mark Aarts <Mark.Aarts@wur.nl>	Christian Lexer <c.lexer@kew.org>
Carlos Alonso-Blanco <calonso@cnb.uam.es>	Olivier Loudet <loudet@versailles.inra.fr>
Thomas Altmann <altmann@ipk-gatersleben.de>	Nick Lauter <nick.lauter@ars.usda.gov>
Anna Amtmann <A.Amtmann@bio.gla.ac.uk>	Carolyn Lawrence <triffid@iastate.edu>
Olin Anderson <olin.anderson@ars.usda.gov>	Jonathan Lynch <jpl4@psu.edu>
Philip Benfey <philip.benfey@duke.edu>	Mark Macnair <M.R.Macnair@exeter.ac.uk>
Joy Bergel <jbergels@midway.uchicago.edu>	Julin Maloof <jnmaloof@ucdavis.edu >
Roger Boerma <rboerma@uga.edu>	Greg May <gdm@ncgr.org>
Kirsten Bomblies <kirsten.bomblies@tuebingen.mpg.de>	John McKay <jkmckay@ColoState.edu>
Toby Bradshaw <toby@u.washington.edu>	Michael McLennan <mmclenna@purdue.edu>
Diane Byers <dlbyer2@ilstu.edu>	Michael McMullen <mcmullenm@missouri.edu>
Alain Charcosset <charcos@moulon.inra.fr>	Thomas Mitchell-Olds <tmo@duke.edu>
Doug Cook <drcook@ucdavis.edu>	Stephen Moose <smoose@uiuc.edu>
Joanne Chory <chory@salk.edu>	Leonie Moyle <lmoyle@indiana.edu>
Perry Cregan <perry.cregan@ars.usda.gov>	David Neale <dbneale@ucdavis.edu>
Andrew Cuming <A.Cuming@leeds.ac.uk>	Magnus Nordborg <magnus@usc.edu>
Jeff Dangl <dangl@email.unc.edu>	Mourad Ouzzani <mourad@cs.purdue.edu>
Brian Diers <bdiers@uiuc.edu>	Adam Price <a.price@abdn.ac.uk>
John Doebley <jdoebley@wisc.edu>	Michael Purugganan <mp132@nyu.edu>
Jode Edwards <jode.edwards@ars.usda.gov>	Matthieu Reymond <reymond@mpiz-koeln.mpg.de>
Lila Fishman <Lila.Fishman@mso.umt.edu>	Loren Rieseberg <lriesebe@indiana.edu>
Sherry Flint-Garcia <Sherry.Flint-Garcia@ars.usda.gov>	Torbert Rocheford <trochefo@uiuc.edu>
Brandon Gaut <bgaut@uci.edu>	Outi Savolainen <outi.savolainen@oulu.fi>
Mary Lou Guerinot <Mary.Lou.Guerinot@Dartmouth.EDU>	Philip Scarpino <pscarpin@iupui.edu>
Stacey Harmer <slharmer@ucdavis.edu>	Barbara Schaal <schaal@biology.wustl.edu>
Scott Hodges <hodges@lifesci.ucsb.edu>	Eric Schadt <eric_schadt@merck.com>
Jim Holland <james_holland@ncsu.edu>	Henk Schat <henk.schat@falw.vu.nl>
David Hyten <david.hyten@ars.usda.gov>	Doug Schemske <schem@msu.edu>
Scott Jackson <sackson@purdue.edu>	Annie Schmitt <Johanna_Schmitt@brown.edu>
Tom Jeunger <tjuenger@austin.utexas.edu>	Todd Schuble <tschuble@uchicago.edu>
Steve Kay <skay@ucsd.edu>	Randy Shoemaker <rcsshoe@iastate.edu>
John Kelly <jkk@ku.edu>	Mark Sorrels <mes12@cornell.edu>
Bob Klein <bob.klein@ars.usda.gov>	Maureen Stanton <mlstanton@ucdavis.edu>
Maarten Koornneef <Maarten.Koornneef@wur.nl>	Bill Tracy <wftracy@wisc.edu>
Ute Kramer <ute.kraemer@bioquant.uni-heidelberg.de>	Roberto Tuberosa <tuberosa@agrsci.unibo.it>
Elena Kramer <ekramer@oeb.harvard.edu>	Mark Ungerer <mcungere@ksu.edu>
Bill Kunin <W.E.Kunin@leeds.ac.uk>	Todd Vision <tjv@bio.unc.edu>
Chuck Langley <chlangley@ucdavis.edu>	Detlef Weigel <weigel@tuebingen.mpg.den>

SUMMARY

There is clear and broad agreement within the scientific community that one of the most pressing grand challenges in biology is to understand how plants adapt to their complex and often unpredictable biotic and abiotic environments. The proposed workshop will aim to pull together approximately 35 of the top researcher involved in investigating the mechanistic basis of plant adaptation from both the non-crop and crop communities, including, but not limited to, the Arabidopsis, Mimulus, maize, rice and soybean communities to address this challenge. We will draw on individuals with expertise in genomics, genetics, biochemistry, physiology and more broadly from the ecological, evolutionary and phylogenetic communities, along with participants from the GIS community, including remote sensing.

The proposed grand challenge workshop will allow this diverse group of participants to coalesce around the concept that an integrated cyberinfrastructure would improve the group's ability to more efficiently determine the fundamental genetic, biochemical and physiological mechanisms underlying plant adaptation, by improving cooperation and integration across laboratories, field sites and species. The cyberinfrastructure would also allow for better training in the integrative concepts underlying evolutionary genetics and plant adaptation, and also improve the education of the public on the significance of this work for agriculture and future sustainable utilization of natural resources.

Deliverables from the proposed workshop will be an outline of the agreed upon components of the required cyberinfrastructure, and the establishment of a proposal team to develop a Grand Challenge project for submission to the iPlant Collaborative. This team will have a designated leader to manage and guide development and submission of the proposal. Networks of expertise's in various critical discipline areas will also be developed to help the proposal team during development of the Grand Challenge project. Mechanisms will be established at the workshop to allow feedback on the Grand Challenge proposal from the broader community to be incorporated into the proposal before submission. Such mechanisms would likely include a community WIKI and BLOG sites.

BIOGRAPHICAL SKETCH: WILLIAM D. BEAVIS, Ph.D.

(a) Professional Preparation

B.S., 1978, Range Management, Humboldt State U, Arcata, CA.

M.S., 1981, Interdisciplinary Biology-Statistics, New Mexico State U, Las Cruces, NM

Ph.D., 1986, Quantitative Genetics, (Plant Breeding Major, Statistics Minor) Iowa State U, Ames, IA

(b) Professional Appointments

Professor, and GF Sprague Chair, Department of Agronomy, Iowa State University, (Sept 2007 - present)

Chief Science Officer, NCGR, Santa Fe, NM (October 2000 - Sept., 2007).

Director of Science Programs, NCGR, Santa Fe, NM (June 1999 to October 2000)

Program Leader for Complex Traits, NCGR, Santa Fe, NM (September 1998-June 1999)

Research Statistician, Pioneer Hi-Bred, Int'l, Johnston, IA (1987-1998)

Data Manager, Sorghum Breeding Department, Pioneer Hi-Bred, Int'l, Plainview, TX (1986-1987)

(c) Recent Relevant Peer Reviewed Publications

Kingsmore, SF, IE Lindquist, J Mudge, DD Gesler, **WD Beavis** (2008) Genome-wide association studies: progress and potential for drug discovery and development. *Nature Reviews* (adv online publication) doi:10.1038/nrd2519

Kingsmore, SF, IE Lindquist, J Mudge **WD Beavis** (2007) Genome-Wide Association Studies: Progress in Identifying Genetic Biomarkers in Common, Complex Diseases. *Biomarker Insights* 2007:2 1–10.

Beavis, WD, FD Schilkey, SM Baxter (2007). Translational Bioinformatics: At the Interface of Genomics and Quantitative Genetics. *Crop Science* 47(s3): 32-43

Gonzales, MD, K Gajendran, AD Farmer, E Archuleta, **WD Beavis** (2007) Leveraging model legume information to find candidate genes for soybean Sudden Death Syndrome using the Legume Information System (LIS). In Ed. Edwards D. *Methods in Molecular Biology*, Humana Press (USA), pp. 245-260

Stein, L, DD Gessler, D Rokshar, D Main, L Mueller, E Huala, C Lawrence, S Rhee, **WD Beavis** (2006) Save our Data. *The Scientist* April 24-25.

Beavis, W.D. (2005) Architectures for Integration of Data and Applications: Lessons from Integration Projects. In *The Stadler Genetics Symposium XXII*: Springer (eds. Gustafson, Shoemaker and Snape) pp. 31-46.

Munneke, B., K.A. Schlauch, **W.D. Beavis**, and R.W. Doerge (2005). Adding Confidence to Gene Expression Clustering. *Genetics* 170:2003-2011.

Gepts, P. **WD Beavis**, EC Brummer, RC Shoemaker, HT Stalker, NF Weeden, ND Young. (2005) Legumes as a Model Plant Family: Genomics for Food and Feed. Report of the Cross Legume Advances through Genomics Conference. *Plant Physiology* 137: 1228-1235.

Jansen, R.C., J.L. Jannink and **W.D. Beavis**. (2003) Mapping quantitative trait loci in plant breeding populations: use of parental haplotype sharing. *Crop Science* 43: 829-834.

Tuggle, CK, JA Green, C Fitzsimmons, R Woods, RS Prather, S Malchenko, M Bento-Soares, T Kucaba, K Crouch, C Smith, D Tack, N Robinson, B O'Leary, T Scheetz, T Casavant, D Pomp, JB Edeal, Y Zhang, MF Rothschild, K Garwood, **WD Beavis**. (2003) EST-Based Discovery in Pig: Virtual Expression Patterns and Comparative Mapping to Human. *Mammalian Genome* 14: 565-579.

(d) Synergistic Activities

Dr. Beavis is Professor of Agronomy and GF Sprague Chair in Population Genetics at Iowa State University. His academic appointment consists of 75% research and 25% teaching. His Research program is focused on the long term consequences of phenotypic and Marker Assisted Selection in crops adapted to North American Production Agriculture. His approaches consist of simulation modeling, development of statistical methods, utilization of a model plant system and genomic analyses of maize and soybean populations. In collaboration with Dr. Thomas Lubberstedt he is incorporating these approaches into a graduate course in Marker Assisted Breeding that will be delivered to students in both the traditional on-campus venue and through a web enabled distance education program. He is the instructor of record for a graduate course in statistics as part of the distance MS program in Agronomy. He continues to provide oversight of NCGR as a member of the board of directors and he provides statistical analyses of human genetics projects at the Lovelace Respiratory Research Institute (LRRI).

(e) Collaborators & Other Affiliations

Adjunct Research Scientist, Lovelace Respiratory Research Institute, Albuquerque, New Mexico (January 2004 – present)

Board of Directors, National Center for Genome Resources (NCGR), Santa Fe, NM (July 2001 to present).

Adjunct Professor, Department of Mathematics and Statistics, University of New Mexico (November, 2002 – Sept. 2007)

Adjunct Assistant Professor, Department of Biochemistry and Molecular Biology, School of Medicine, University of New Mexico (January 2003 – December 2006).

Board of Directors, New Mexico Biomedical and Biotechnology Association (January, 2002 – January, 2004).

Board of Directors, New Mexico Technology Research Collaborative (January, 2003 – 2005).

Collaborators: Susan Atlas (UNM), Susan Baxter (San Diego State University), Volker Brendel (Iowa State U), Guy Brock (U Louisville), Mark Cooper (Pioneer), Perry Cregan (USDA-ARS), John Doebley (U Wisconsin), Rebecca Doerge (Purdue U), Jode Edwards (USDA-ARS), Damian Gessler (NCGR), David Grant (USDA-ARS), Jeff Gulcher (deCode Genetics), Ritsert Jansen (U of Groeningen), Jean-Luc Jannink (USDA-ARS), Ed Kaleikau (USDA-CSREES), Stephen Kingsmore (NCGR), Thomas Lubberstedt (Iowa State University), Rick Lyons (UNM), Greg May (NCGR), Wayne Parrot (U Georgia), Ernie Retzel (NCGR), Sue Rhee (Carnegie Institute), Jean-Marcel Ribaut (CIMMYT), Daniel Pomp (Duke U), Antoni Rafalski (DuPont), Max Rothschild (Iowa State U), Mark Salkins (CIMMYT), Laura Salter (Ohio State U), Paul Scott (USDA-ARS), Karen Schlauch (George Mason U), Randy Shoemaker (USDA-ARS), Cari Soderland (U Arizona), Chris Town (TIGR), Ann-Marie Thro (USDA-CSREES), Chris Tuggle (Iowa State U), Howard Valentine (Peanut Board), Julie Wilder (LRRI),

Graduate Students

Reka Howard (2008-), Shreyartha Mukharjee(2008-), Carla Taylor (2008-), Mark Newell (2008-)

Graduate Students (committee)

Guy Brock (UNM-2004), Brian Munneke (Purdue U-2002), Kristina Strandberg (UNM-2006), Brian Scheffler (ISU-1996), Greg Doonan (2008-), Massiel Orellana (2008-), Bryce Lemke (2008-), Kendra Meade (2008-)

Post-Doctoral Oversight

Karen Schlauch (1999-2001), Brian Shiloff (2000-2003), Baohong Guo (2008-)

BIOGRAPHICAL SKETCH: Justin Borevitz

Professional Preparation

University of California, Santa Cruz	Biochemistry & Molecular Biology	BS	1997
University of California, San Diego	Biology	PhD	2002
The Salk Institute for Biological Studies	Genomics Postdoc		2002-2004

Appointments

Assistant Professor	Department of Evolution and Ecology	University of Chicago	July 2004-
Assistant Professor	Committee on Genetics	University of Chicago	November 2004 - present

Five publications most closely related to the proposal

Zhang X, Shiu S, Cal A, Borevitz JO (2008) Global analysis of genetic, epigenetic and transcriptional polymorphisms in *Arabidopsis thaliana* using whole genome tiling arrays. *PLoS Genet.* 21;4(3):e1000032.

Borevitz JO, Hazen SP, Michael TP, Morris GP, Baxter IR, Hu TT, Chen H, Werner JD, Nordborg M, Salt DE, Kay SA, Chory J, Weigel D, Jones JD, Ecker JR (2007) Genome-wide patterns of single-feature polymorphism in *Arabidopsis thaliana*. *Proc Natl Acad Sci U S A.* 17;104(29):12057-62. Epub 2007 Jul 12.

Werner JD, Borevitz JO, Uhlenhaut H, Ecker JR, Chory J, Weigel D (2005). FRIGIDA-independent variation in flowering time of natural *A. thaliana* accessions *Genetics* 170:1197-207.

Rostoks N, Borevitz JO, Hedley PE, Russell J, Mudie S, Morris J, Cardle L, Marshall DF, Waugh R (2005). Single-feature polymorphism discovery in the barley transcriptome. *Genome Biol.* 6:R54.

Borevitz JO, Liang D, Plouffe D, Chang HS, Zhu T, Weigel D, Berry CC, Winzeler E, Chory J (2003). Large-scale identification of Single-Feature Polymorphisms in Complex Genomes. *Genome Res.* 13:513-23.

Five other significant publications

Shiu SH, Borevitz JO (2008) The next generation of microarray research: applications in evolutionary and ecological genomics. *Heredity.*;100(2):141-9.

Zhang X, Richards EJ, Borevitz JO (2007) Genetic and epigenetic dissection of cis regulatory variation. *Curr Opin Plant Biol.*;10(2):142-8.

Kim S, Zhao K, Jiang R, Molitor J, Borevitz JO, Nordborg M, Marjoram P (2006). Association mapping with single-feature polymorphisms. *Genetics.* 173:1125-33.

Werner JD, Borevitz JO, Warthmann N, Trainer GT, Ecker JR, Chory J, Weigel D (2005). Quantitative trait locus mapping and DNA array hybridization identify an FLM deletion as a cause for natural flowering-time variation. *Proc Natl Acad Sci U S A.* 15;102: 2460-5.

Maloof JN, Borevitz J O, Dabi T, Lutes J, Nehring RB, Redfern JL, Trainer GT, Wilson JM, Asami T, Berry CC, Weigel D, Chory J (2001). Natural variation in light sensitivity of *Arabidopsis*. *Nat Genet.* 29:441-6.

Synergistic Activities

Developed algorithm for identification of Single Feature Polymorphisms (SFPs) from high density oligonucleotide arrays <http://naturalvariation.org/sfp>

Developed eXtreme Array Mapping, a method to map quantitative trait loci (QTL) using selective SFP genotyping on pools of lines with extreme phenotypes. <http://naturalvariation.org/xam>

Developing methods for haplotype identification from high resolution SFP data.

Assisted on the development of BQTL (Bayesian QTL mapping). <http://hacuna.ucsd.edu/bqtl>. Used BQTL to perform two dimensional QTL epistasis scans using permutation thresholds.

1998 - Present	American Society of Plant Biologists
1998 - Present	American Association for the Advancement of Science
1997	Ken Thiman Academic Excellence Award.
1998	Ethics in Science Training at UCSD
1999 - 2001	Genetics Training Grant (NIH)
2001 - 2002	Developmental Biology Training Grant (NIH)
2002 - 2004	Helen Hay Whitney Fellow
2007- Present	Co-director Woodlawn Center for Urban Ecology 2007- www.wcue.org
2008- Present	Chicago Mayors advisory board for Nature and Wilderness
2006- Present	Academic Editor PLoS ONE
2008	NSF 2020 Plant Biology Vision Panel
2006-	Rijk-Zwaan International Seed Company Scientific Advisory Board
2004,2006	NSF Plant Genome Review Panel

Collaborators & Other Affiliations

Graduate and Post Doctoral Advisors: Joanne Chory (Salk Institute), Joseph Ecker (Salk Institute)

Students and postdocs trained. Xu Zhang is a current post doc who started 10/04, Shinhan Shiu is a postdoc and will be trained from 9/05-12/05 prior to taking his position in Michigan State University. Three rotation students have completed projects developing Hidden Markov Models for SFP deletion genotyping, genotyping wild *A. thaliana* populations, and QTL mapping in seasonal environments.

Edward S. Buckler

Institute for Genomic Diversity
159 Biotechnology Bldg.
Cornell University
Ithaca, NY 14850-2703

Email: esb33@cornell.edu
Voice: (607) 255-4520
Fax: (607) 255-6249
<http://www.maizegenetics.net/>

A. Education:

University of Virginia	Biology and Archaeology	BA(w/ Honors)	1992
University of Missouri	Biological Sciences	PhD	1997
North Carolina State Univ.	Statistical Genetics	Postdoc	1997-1998

B. Appointments:

1998-Present USDA-ARS Research Geneticist
1998-2003 Assistant Professor, Department of Genetics, North Carolina State University
2003-Present Adjunct Associate Professor, Plant Breeding, Cornell University

C. Publications Related:

Thornsberry, J.M., M.M. Goodman, J. Doebley, S. Kresovich, D. Nielsen, and E. S. Buckler. 2001. *Dwarf8* polymorphisms associate with variation in flowering time. *Nature Genetics*. **28**: 286-289.

Remington, D. L., J. Thornsberry, Y. Matsuoka, L. Wilson, S. Rinehart-Whitt, J. Doebley, S. Kresovich, M. M. Goodman, and E. S. Buckler. 2001. Structure of linkage disequilibrium and phenotypic associations in the maize genome. *Proc. Nat. Acad. Sci. USA* **98**:11479-11484.

Yu, J., Pressoir, G., Briggs, W.H., Bi, I.V., Yamasaki, M., Doebley, J.F., McMullen, M.D., Gaut, B.S., Holland, J.B., Kresovich, S., and Buckler, E.S. 2006. A Unified Mixed-Model Method for Association Mapping Accounting for Multiple Levels of Relatedness. *Nature Genetics* **38**:203-208.

Flint-Garcia, S.A., A.-C. Thuillet, J.M. Yu, G. Pressoir, S.M. Romero, S.E. Mitchell, J. Doebley, S. Kresovich, M.M. Goodman, and E.S. Buckler. 2005. Maize association population: a high resolution platform for QTL dissection. *Plant Journal* **44**: 1054-1064.

Harjes, C.E., Rocheford, T., Sowinski, S., Williams, M., Kandanis, C.B., Brutnell, T., Wurtzel, E., Yan, J., and Buckler, E.S. 2008. Natural genetic variation in lycopene epsilon cyclase can enhance provitamin a biofortification of maize. *Science* (Jan 18, 2008)

Other Publications:

Whitt, S. R., Wilson, L. M., Tenaillon, M. I., Gaut, B. S. & Buckler, E. S. 2002. Genetic diversity and selection in the maize starch pathway. *Proc. Nat. Acad. Sci. USA* **99**: 12959-12962.

Wilson, L.M., Whitt, S.R., Ibanez-Carranza, A.M., Goodman, M.M., Rocheford, T.R., and Buckler, E.S. 2004. Dissection of maize kernel composition and starch production by candidate gene association. *Plant Cell* **16**: 2719-2733.

Viviane Jaenicke, E. S. Buckler, Bruce D. Smith, M. Thomas P. Gilbert, Alan Cooper, John Doebley, Svante Pääbo. 2003. Early allelic selection in maize as revealed by ancient DNA. *Science* **302**: 1206-1208.

Stich B, Yu J, Hans P. Maurer, Melchinger AE, Utz HF, Buckler ES 2007. Power to Detect Higher-Order Epistatic Interactions in a Metabolic Pathway Using Nested Association Mapping and Diallel Association Mapping *Genetics* **176**: 563-570

Bradbury, P.J., Zhang, Z., Kroon, D.E., Casstevens, T.M., Ramdoss, Y., and Buckler, E.S. 2007. TASSEL: Software for association mapping of complex traits in diverse samples. *Bioinformatics*. **23**: 2633-2635.

D. Synergistic Activities:

1. Developing database aware software and analysis approaches for association and joint linkage-association mapping. Currently, TASSEL analyses molecular diversity and carries out a wide range of association and molecular quantitative genetic analyses.
2. Involved in designing the bioinformatics architecture for sharing and storing diversity data. As a co-PI on the Gramene project, we have developed a diversity schema, middleware, and query tools to share basic diversity data (both genotypic and phenotypic).

E. Collaboration and Other Affiliations

i. Collaborators in past 48 months

S. Avraham (Cold Spring Harbor), L. Bai (Boyce Thompson Inst.), C. Bermudez Kandanis (U. Illinois), I. Bi Vroh (IITA), P. Bradbury (USDA-ARS), W. Briggs (U. of Wisconsin), T. Brutnell (Boyce Thompson Inst.), R. Caldo (Iowa State Univ.), P. Canaran (Cold Spring Harbor), P. Casati (Stanford), T. Casstevens (Cornell U.), J. Doebley (U. Wisconsin), E. Ersoz (Cornell U.), E. Ersoz, Elhan (Cornell U.), E. Esch (U. Hannover), B. Faga (Cold Spring Harbor), S. Flint-Garcia (North Carolina State U.), M. Fogleman (Cornell U.), K. Fukunaga (U. of Wisconsin), T. Fulton (Cornell U.), B. Gaut (U. California, Irvine), J. Glaubitz (U. of Wisconsin), L. Goh (Cold Spring Harbor), M. Goodman (North Carolina State U.), M. Gore (Cornell U.), C. Harjes (Monsanto), C. Hebbard (Cornell U.), J. Heer (North Carolina State U.), J. Hill (U. of Wisconsin), O. Hoekenga (USDA/Cornell U.), R. Hogers (Keygene), J. Holland (USDA/N. Carolina State U.), T. Holtsford (U. Missouri), P. Jaiswal (Cornell U.), R. Jung (Pioneer Hi-Bred), R. Jurkuta (U. of Wisconsin), M. Kirst (U. of Florida), L. Kochian (USDA/Cornell U.), S. Kresovich (Cornell U.), D. Kroon (Cornell U.), C. Liang (Cold Spring Harbor), K. Liu (North Carolina State Univ.), J. Maohringy (U. Hohenheim), R. Martienssen (Cold Spring Harbor), K. Matias (U. Florida), Y. Matsuoka (U. of Wisconsin), H. Maurer (U. Hohenheim), S. McCouch (Cornell U.), M. McMullen (Univ. of Missouri), A. Melchinger (U. Hohenheim), S. Mitchell (Cornell U.), J. Ni (Cornell U.), D. Nielsen (North Carolina State U.), W. Pawlowski (Cornell U.), J. Peleman (Keygene), H. Piepho (U. Hohenheim), G. Pressoir (Cornell U.), Y. Ramdoss (Cisco), K. Ratnapu (Cold Spring Harbor), L. Ren (Cold Spring Harbor), T. Rocheford (U. Illinois), S. Romero (Cornell U.), J. Rose (Cornell U.), S. Schmidt (Cold Spring Harbor), M. Snook (USDA-ARS), S. Sowinski (Pioneer Hi-Bred), W. Spooner (Cold Spring Harbor), P. Springer (Cold Spring Harbor), A. Stapleton (U. North Carolina, Wilmington), L. Stein (Cold Spring Harbor), N. Stevens (Cornell U.), B. Stich (U. Hohenheim), Q. Sun (Cornell U.), S. Szalma (Univ. of Missouri), J. Szymaniak (Cornell U.), G. Tanimoto (Affymetrix), A. Thuillet (U. of Wisconsin), R. Toddhunter (Cornell U.), W. Tracy (U. of Wisconsin), F. Utz (U. Hohenheim), R. Vallabhaneni (CUNY), M. van Eijk (Keygene), J. van Oeveren (Keygene), E. Verstege (Keygene), Y. Vigouroux (U. of Wisconsin), D. Vleck (USDA-ARS (Lincoln)), E. Vollbrecht (Iowa State Univ.), V. Walbot (Stanford), D. Ware (Cold Spring Harbor), S. Whitt (North Carolina State U.), M. Williams (Pioneer Hi-Bred), R. Wise (Iowa State Univ.), E. Wurtzel (CUNY), L. Yamasaki (U. of Missouri), J. Yan (CIMMYT), I. Yap (Cornell U.), H. Yates (Cornell U.), K. Youens-Clark (Cold Spring Harbor), J. Yu (Cornell U.), Z. Zhang (Cornell U.), W. Zhao (Cold Spring Harbor)

ii. Graduate and Postdoctoral Advisors

T. P. Holtsford (U. Missouri)

B. S. Weir (North Carolina State U.)

M. Purugganan (North Carolina State U.)

iii. Thesis advisor and postdoctoral sponsor

Beth K. Saft, Sherry Flint-Garcia, Jeff M. Thornsberry, David M. Remington, Larissa M. Wilson (North Carolina State U); Elhan Ersoz, Amit Gur, Michael Gore, Carlos Harjes, Allison Krill, Matias Kirst, Jason Pfeiffer, Feng Teng, Irie Vroh, Jianming Yu, Nengyi Zhang (Cornell Univ.)

I have sponsored 5 graduate students and 10 postdoctoral scholars over my 9 year career.

BIOGRAPHICAL SKETCH: Susan R. McCouch

Professor, Department of Plant Breeding & Genetics, 162 Emerson Hall
Cornell University, Ithaca, NY 14853-1901

Education:

- 1975 Smith College: B.A. in Hispanic Studies (Cum Laude)
- 1982 University of Massachusetts: M.S. in Plant Pathology
- 1990 Cornell University: Ph.D. in Plant Breeding, Genetics, and Entomology

Professional Experience:

- 2003-present Professor, Department of Plant Breeding & Genetics, Cornell University (joint appointments with Plant Biology and Int'l Ag. Programs)
- 1999-2002 Associate Professor, Assistant Professor Department of Plant Breeding & Genetics, Cornell University (joint appointment with Int'l Ag. Programs)
- 1995-2001 Assistant Professor, Department of Plant Breeding & Genetics (joint appointment Int'l Ag. Programs)
- 1990-1994 Associate Geneticist, Department of Plant Breeding, Genetics & Biochemistry, Int'l Rice Research Institute, Los Baños, Philippines; Adjunct Assistant Professor, Dept. Plant Breeding, (1992-1994) Cornell Univ, Ithaca NY

Honors and Awards

- 2007 Golden Sickle Award for rice research presented by HRH Princess Maha Chakri Sirindhorn, Bangkok, Thailand
- 2006 CALS Outstanding Faculty Award
- 2004 AAAS Fellow
- 2002/2003 Outstanding Mentor, Siemens Westinghouse Competition in Math, Science and Technology Winners (highschool students, Juliet Girard and Roshan Prabhu, \$100,000 award).
- 2002 Outstanding Educator (most influenced Merrill Presidential Scholar Wirulda Pootakham)
- 1997 M.S. Swaminathan Outstanding Research Award
- 1996 CALS Young Faculty Teaching Excellence Award

RECENT SERVICE

- 2007 National Research Council "Objectives for the National Plant Genome Initiative: 2008-2020"
- 2007 Term Chair Awards Selection Committee for New Women Faculty in the Life Sciences
- 2006-2007 Chair, Plant Science Task Force, CALS, Cornell University
- 2003-2007 University Life Sciences Advisory Council to President and Provost
- 2002-2007 Cornell Genomics Fellowship Committee
- 2003-2005 Member, Plant Science Curriculum Committee

Graduate and Undergraduate Educational Activities

Courses taught: PL BR 201; Plants, Genes, and Global Food Production; BioPl 653.1; Concepts and Techniques in Plant Molecular Biology; Guest Lectures: BioPl 357, Grass Systematics; PL BR 604, Methods of Plant Breeding; BioPl 744, Problems in Plant, Cell and Molecular Biology; Educational Innovations Developed: CoursePack, *Plants, Genes and Global Food Production* (PIBr201); Web-Based Materials: Tutorials and User Exercises available at www.gramene.org/tutorials/ and <http://www.gramene.org/documentation/faq/> and <http://www.gramene.org/workshop/index.html>.

NSF Supplemental Grant for Outreach Activities in Local Area High Schools, "Linking rice, *Arabidopsis* and the grasses to explore natural genetic variation"(2003-2005; PI: S.McCouch); NSF DBI-Research Coordination Network in Bio Sci (RCN) "The Gramene Community Curation Network" (PI: Lincoln Stein; S. McCouch, core participant); Rice:Research to Production field course at IRRI, Philippines (2007-2009)

Synergistic Activities

Associate Editor: Genetics; RICE;

Rice Genetics Cooperative, Sub-committee on Gene Nomenclature (2005- present)
Co-Organizer of the International Rice Congress 2002 and 2005, Beijing, China, September 16-20, 2002 and Manila, Philippines, September 2005
Scientific Advisory Committee for USDA-funded RiceCAPS project (2005-present)
Scientific Advisory Committee for NSF funded project on Rice Blast, Raleigh, NC. 2001-2004
Scientific Advisory Board for NSF funded projects to sequence the maize genome (Danforth Ctr, TIGR, Purdue U, Orion Genomics, Waksman Inst. and Univ. of Arizona), 2002- 2005
NSF/USDA/DOE Scientific Advisory Board for US Rice Genome Sequencing Project, 2000 – 2004
Advisory Committee for NSF funded project on Haplotype Polymorphism in Polyploid Wheats and Their Diploid Ancestors, Univ. California, Davis. 2004-2006
AAAS Electorate Nominating Committee, Section on Agriculture, Food, and Renewable Resources, 2001-2003
Co-Organizer of Plant and Animal Genome III- VII. 1995-1999

Graduate Training History:

Current Ph.D. students: 4 (major advisor) and 3 (minor advisor); Former Ph.D. students: 14 (major advisor) and 11 (minor advisor); Former M.S. students: 3 (major advisor); Postdoctoral Fellows (current and former): 30.

Representative Recent Publications:

Kovach M, Sweeney M, McCouch S (2007) New insights into the history of rice domestication. *Trends Genet* 23:579-587

Caicedo AL, Williamson SH, Hernandez RD, Boyko A, Fledel-Alon A, York TL, Polato NR, Olsen KM, Nielsen R, McCouch SR, Bustamante CD, Purugganan MD (2007) Genome-Wide Patterns of Nucleotide Polymorphism in Domesticated Rice. *PLoS Genetics* 3:e163

Sweeney MT, Thomson MJ, Cho YG, Park YJ, Williamson SH, Bustamante CD and McCouch SR (2007) Global dissemination of a single mutation conferring white pericarp in rice. *PLoS Genetics* 3(8): e133

McCouch SR, Sweeney M, Li J, Jiang H, Thomson M, Septinginsih E, Edwards J, Moncada P, Xiao J, Garris A, Tai T, Martinez C, Tohme J, Sugiono M, McClung A, Yuan L P, Ahn SN (2007) Through the genetic bottleneck: *O. rufipogon* as a source of trait-enhancing alleles for *O. sativa*. *Euphytica*, 154: 317-339

Thomson M, Edwards J, Septinginsih E, Harrington S, McCouch S (2006) Substitution mapping of *dth1.1*, a flowering time QTL associated with transgressive variation in rice, reveals a cluster of QTLs. *Genetics* 172: 2501-2514

Jaiswal P, Ni J, Yap I, Ware D, Spooner W, Youens-Clark K, Ren L, Liang C, Zhao W, Ratnapu K, Faga B, Canaran P, Fogleman M, Hebbard C, Avraham S, Schmidt S, Casstevens T, Buckler E, Stein L, McCouch S (2006) Gramene: A bird's eye view. *Nucleic Acids Research* 34: D717-D723

Iyer A and McCouch S (2004) The rice disease resistance gene *xa5* encodes a novel form of disease resistance. *MPMI* 17: 1348–1354

Jaiswal P, Avraham S, Ilic K, Kellogg E, McCouch S, Pujar A, Reiser L, Rhee S, Sachs M, Schaeffer M, Stein L, Stevens P, Leszek V, Ware D, Zapata F (2006) Plant Ontology (PO): A controlled vocabulary of plant structures and growth stages. *Comp Func Gen* 6: 388-397

McCouch S (2004) Diversifying Selection in Plant Breeding. *PLoS Biol* 2(10): e347. DOI: 10.1371/journal.pbio.0020347

Tanksley S and McCouch S (1997) Seed banks and molecular maps: unlocking genetic potential from the wild. *Science* 277: 1063-1066

BIOGRAPHICAL SKETCH: David E Salt

Professional Preparation

University College North Wales	Biochemistry	B.Sc. 1984
Hallam University	Computer Studies	M.Sc. 1985
Liverpool University	Plant Biochemistry	Ph.D. 1988
University College, London	Postdoc Biochemistry	1987-1989
University of Kentucky	Postdoc Plant Biochemistry	1989-1992
University of Guelph	Postdoc Plant Biochemistry	1992-1993

Appointments

2005 – present	Professor, Horticulture and Landscape Architecture, Purdue University.
2004 – 2007	Scientific Director, Genomics Research & Technology, Bindley Bioscience Center, Purdue University.
2004 – 2009	University Faculty Scholar, Purdue University.
2001 – 2005	Associate Professor, Horticulture and Landscape Architecture, Purdue University
2000 – 2001	Associate Professor of Biochemistry, Department of Chemistry, Northern Arizona University.
1998 - 2000	Assistant Professor, Department of Chemistry, Northern Arizona University.
1993 - 1997	Assistant Research Professor, Center for Agricultural Molecular Biology, Rutgers University, New Brunswick, NJ.

Five publications most closely related to the proposal (total of 75)

- Baxter I, Muthukumar B, Park HC, Buchner P, Lahner B, Danku J, Zhao K, Lee J, Hawkesford MJ, Guerinot ML, Salt DE (2008) Variation in molybdenum content across broadly distributed populations of *Arabidopsis thaliana* is controlled by a mitochondrial molybdenum transporter (MOT1). *PLoS Genetics*. 4(2):e1000004.
<http://www.plosgenetics.org/article/info%3Adoi%2F10.1371%2Fjournal.pgen.1000004>.
- Rus A, Baxter I, Muthukumar B, Gustin J, Lahner B, Yakubova E and Salt DE (2006) Natural variants of AtHKT1 enhance Na⁺ accumulation in two wild populations of *Arabidopsis*. *PLoS Genetics* 2(12): e210. <http://www.plosgenetics.org/article/info%3Adoi%2F10.1371%2Fjournal.pgen.0020210>.
- Baxter I, Ouzzani M, Orcun S, Kennedy B, Jandhyala SS, Salt DE (2007) Purdue Ionomics Information Management System (PIIMS): An integrated functional genomics platform. *Plant Physiology* 143: 600-611. <http://www.pubmedcentral.nih.gov/picrender.fcgi?artid=1803751&blobtype=pdf>
- Freeman JL, Persans MW, Nieman K, Albrecht C, Peer W, Pickering IJ, Salt DE (2004). Increased glutathione biosynthesis plays a role in nickel hyper tolerance in *Thlaspi* nickel hyperaccumulators. *Plant Cell* 16: 2176-2191. <http://www.plantcell.org/cgi/content/full/16/8/2176>
- Lahner B, Gong J, Mahmoudian M, Smith EL, Abid KB, Rogers EE, Guerinot ML, Harper JF, Ward JM, McIntyre L, Schroeder JI, Salt DE (2003) The genomic scale profiling of nutrient and trace elements in *Arabidopsis thaliana*. *Nature Biotechnol*, 21: 1215-1221.
<http://www.nature.com/nbt/journal/v21/n10/abs/nbt865.html;jsessionid=9EA05D6BD309BEEB5E19D33593525F87>

Five other significant publications

- Ellis DR, Gumaelius L, Indriolo E, Pickering IJ, Banks JA, Salt DE (2006) Isolation and characterization of a unique arsenate reductase from the arsenic hyperaccumulating fern *Pteris vittata*. *Plant Physiol* 141:1544-1554. <http://www.plantphysiol.org/cgi/content/full/141/4/1544>
- Ellis DR, Sors TG, Brunk DG, Albrecht C, Orser C, Lahner B, Woods KV, Harris HH, Pickering IJ, Salt DE (2004). Production of Se-methylselenocysteine in transgenic plants expressing selenocysteine methyltransferase. *BMC Plant Biology* 4. <http://www.biomedcentral.com/1471-2229/4/1>

- Pickering IJ, Wright C, Bubner B, Ellis D, Persans MW, Yu EY, George GN, Prince RC, Salt DE (2003) Chemical form and distribution of selenium and sulfur in the selenium hyperaccumulator *Astragalus bisulcatus*. *Plant Physiol* 131: 1460-1467. <http://www.plantphysiol.org/cgi/content/full/131/3/1460>
- Persans MW, Nieman K, Salt DE (2001) Functional activity and role of cation-efflux family members in Ni hyperaccumulation in *Thlaspi goesingense*. *Proc Natl Acad Sci USA* 98: 9995-10000. <http://www.pnas.org/cgi/content/full/98/17/9995>
- Pickering IJ, Prince RC, Salt DE, George GN (2000). Quantitative chemically-specific imaging of selenium transformation in plants. *Proc Natl Acad Sci USA*. 97:10717-10722. <http://www.pnas.org/cgi/content/full/97/20/10717>

Synergistic Activities

Member of the American Society of Plant Biologist (ASPB) Education and Public Affairs Committees. Informal Science exhibits at Indiana State Museum, Indiana State Fair and Indiana Farm Progress Show. Editorial board of *Plant Physiology*, *BMC Plant Biology*, *International Journal of Phytoremediation* and the *Brazilian Journal of Plant Physiology*.

Collaborators and Other Affiliations

a. Collaborators and Co-Editors

Please see the complete alphabetized list for PI available on request.

b. Graduate and Postdoctoral Advisors

Thurman D, Dunnill P, Wagner G, Rauser WE

c. Thesis Advisor

Motley P. M.Sc 9/2000. Colorado Bureau of Reclamation.

Freeman J – PhD 9/2004. Postdoc, University of Colorado.

Gustin J – PhD 12/2007. Postdoc, University of Florida.

Gun-Nam N – 5th year PhD student.

Sors T – 5th year PhD student.

Hosmani P – 1st year PhD student.

Brazelton J – 1st year PhD student.

Mandreat M – 1st year sPh.D student.

d. Post-Graduate scholar sponsor. Dr. Xianghe Yan (1996 - 1997). Senior Scientist, Celera Genomics/Applied Biosystems. Dr. Lekha Sreedhar (1996 - 1997). Lecture, University of Missouri, Kansas City. Dr. Ute Krämer (NATO Postdoctoral Fellow, 1996 - 1997). Group Leader, Max Planck Institute, Golm, Germany. Dr. Mike Persans (1998 - 2002). Assistant Professor, University of Texas Pan American. Dr Dennis Brunk (2001 – 2003). Unknown.

Dr Mehrzad Mahmoudian (2001 – 2003). Postdoc, University of Texas Pan American.

Dr Donggiun Kim (2002 – 2004). Visiting Scientist, Gyeongsang National University, Korea.

Dr Bakhtiyor Yakubov (2001 – 2006). Postdoc University of Chicago. Dr Ana Rus (2003 – 2006). Lecturer California State University at Long Beach. Dr Danielle Ellis (2001 – 2006). Genomics Core Manager, West Virginia University. Dr John Danku (2006 – present), Dr Muthukumar Balasubramaniam (2003 – present), Dr Daiyin Choa (2007 – present), Hyeong Cheol Park (2005 – present), Dr Monica Borghi (2008), Dr Ivan Baxter (2004 – present).

BIOGRAPHICAL SKETCH: John H. Willis

Department of Biology
Duke University, Box 90338
Durham, NC 27708-0338

Phone: (919) 660-7340
Fax: (919) 660-7293
Email: jwillis@duke.edu

a. PROFESSIONAL PREPARATION.

Brown University; Providence, RI Biology Major A.B. Honors, 1985
University of Chicago; Chicago, IL Ecology & Evolution Ph.D. 1991
University of Oregon; Eugene, OR Ecology & Evolution postdoc: 1991-1993

b. APPOINTMENTS.

Associate Professor of Biology (2000 - present); Duke University; Durham, NC
Associate Professor of Biology (1999 - 2000); University of Oregon; Eugene, OR
Assistant Professor of Biology (1993 - 1999); University of Oregon; Eugene, OR
Postdoctoral Research Associate (1991 - 1993); University of Oregon; Eugene, OR
Teaching Assistant (1985 - 1991); University of Chicago; Chicago, IL
Teaching Assistant (1983 - 1985); Brown University; Providence, RI

c. PUBLICATIONS.**Five publications related to the proposed project:**

- Wu, C. A., D. B. Lowry, A. M. Cooley, K. M. Wright, Y.W. Lee, and J. H. Willis. 2008. *Mimulus* is an emerging model system for the integration of ecological and genomic studies. *Heredity*, 100:220-230.
- Mitchell-Olds, T., J. H. Willis, and D. Goldstein. 2007. What evolutionary processes influence natural genetic variation for phenotypic traits? *Nature Reviews Genetics*, 8:845-856.
- Sweigart, A. L., A. Mason, J. H. Willis. 2007. Natural variation for a hybrid incompatibility between two species of *Mimulus*. *Evolution*, 61:141-151.
- Hall, M. C. and J. H. Willis. 2006. Pleiotropic quantitative trait loci contribute to population divergence in traits associated with life-history variation in *Mimulus guttatus*. *Genetics* 172:1829-1844.
- Hall, M. C. and J. H. Willis. 2006. Divergent selection on flowering time contributes to local adaptation in *Mimulus guttatus* populations. *Evolution* 60:2466-2477.

Five other publications:

- Sweigart, A. L., N. H. Martin, and J. H. Willis. 2008. Patterns of nucleotide variation and reproductive isolation between a *Mimulus* allotetraploid and its progenitor species. *Molecular Ecology*, 17:2089-2100.
- Sweigart, A. L., L. Fishman, J. H. Willis. 2006. A simple genetic incompatibility causes hybrid male sterility in *Mimulus*. *Genetics* 172:2465-2479.
- Fishman, L. and J. H. Willis. 2006. A cytonuclear incompatibility causes anther sterility in *Mimulus* hybrids. *Evolution* 60:1372-1381.
- Fishman, L., and J. H. Willis. 2005. A novel meiotic drive locus almost completely distorts segregation in *Mimulus* (Monkeyflower) hybrids. *Genetics* 169:355-373.
- Fishman, L., A. Kelly, and J. H. Willis. 2002. Minor QTLs underlie floral traits associated with mating system divergence in *Mimulus*. *Evolution* 56:2138-2155.

d. EXAMPLES OF SYNERGISTIC ACTIVITIES.

I am Director of Graduate Studies in the Department of Biology at Duke University, and Faculty Director of Duke University's Plant Teaching and Research Facility. I helped to design a major new introductory biology majors course (including labs) that places new emphasis on genetics and evolution. I am PI of the Joint Genome Institute's effort to sequence the genome of *Mimulus guttatus*. In our lab, we have developed thousands of novel genetic markers (especially microsatellites and gene-based markers) and genetic lines of *Mimulus* that are being used by other researchers. As lead-PI on an NSF FIBR grant, I am coordinating collaborative efforts to develop genomic resources for plants in the genus *Mimulus*, that are available to the entire research community <<http://www.mimulusevolution.org>>. I have actively participated in summer research programs designed to encourage the participation of groups underrepresented in science, and have sponsored summer research projects of several students from these groups. I have served on NSF panels and NIH study sections. I have been Associate Editor for *Evolution* (2001-2005) and *The American Naturalist* (2001- 2005).

e. COLLABORATORS AND OTHER AFFILIATIONS.

Collaborators (beyond those mentioned below).

Toby Bradshaw (U. Washington), Jeff Tomkins (Clemson), Anna Blenda (Clemson), Todd Vision (UNC), G. Carvallo (Chile), Tom Mitchell-Olds (Duke), David Goldstein (Duke), Stuart McDaniel (Wash. U.), Jon Shaw (Duke), Loren Rieseberg (UBC), A. Mason (Harvard), Patrick Phillips (U. Oregon), Chris Basten (NCSU), Dick Olmstead (U. Wash.), Dan Rokhsar (Berkeley/JGI), Jeremy Schmutz (Stanford).

Graduate and Postdoctoral Advisors.

Dr. Douglas W. Schemske (University of Washington), Ph.D. advisor
Dr. Deborah Charlesworth (University of Edinburgh), Ph.D. advisor
Dr. Michael Lynch (University of Oregon), post-doctoral advisor

Thesis Advisor and Postgraduate-Scholar Sponsor.

- a. Postdoctorals (7): Alan Kelly (U. of O.), John Kelly (University of Kansas), Lila Fishman (University of Montana), Leonie Moyle (Indiana U.), Andrea Case (Kent State), Amy Bouck (Pioneer Hybrid), Carrie Wu (Duke).
- b. PH.D. Students (11): Megan Hall (NYU), Noland Martin (Texas State), Jan Aagaard (U. of Wash.), Andrea Sweigart (U. Rochester), Arielle Cooley (Duke), Young Wha Lee (Duke), David Lowry (Duke), Kevin Wright (Duke), Jennifer Modliszewski (Duke), Kathleen Ferris (Duke), and Jessica Selby (Duke).

GRANT CHALLENGE WORKSHOP DESCRIPTION

Statement of the scientific problem being addressed.

There is clear and broad agreement within the scientific community that one of the most pressing grand challenges in biology is to understand how plants adapt to their complex and often unpredictable biotic and abiotic environments. Genetic variation is the foundation for understanding plant adaptation, as genotypes may differ in their response to immediate environmental challenges due to differences in cellular physiology and development. Genetically distinct populations, subspecies, and/or species have adapted to unique or extreme environments via evolution by both natural and artificial selection. Establishing what combination of existing genome-wide diversity and/or new mutations underlie plant adaptation at a mechanistic, molecular level will provide breakthroughs in our understanding of plant physiology, ecology and evolution and will allow us to explore community and ecosystem responses to global climate change. Importantly, such fundamental discoveries will greatly advance our ability to conserve and subsequently to exploit genetic diversity to produce new crops and plant communities with greater resilience to emerging changes in pathogen, water, temperature, salinity and mineral nutrient stress, and higher level environmental impacts.

The organizing team for this proposed workshop has not worked together before as a group. However, several members of the team are taking lead roles in organizing the crop plant and non crop plant communities. McCouch and Buckler have been leading the development of the QTL and diversity data for the grasses through Gramene (rice, maize, wheat, and sorghum; <http://www.gramene.org/>), Panzea (<http://www.panzea.org/>) and Rice Diversity (<http://www.ricediversity.org/>) databases. Buckler is involved in many aspects of diversity and genomics in the maize community. With the USDA-ARS, Buckler is collaborating on a national effort to characterize genetic diversity throughout the whole US germplasm collection with an initial project in grape. Beavis is collaborating with USDA-ARS and commercial scientists to evaluate the impact on genetic diversity and linkage disequilibrium from 75 years of maize breeding for the North American agricultural ecosystems. Borevitz, Bergelson, and Nordborg, have been genotyping many thousands of wild *A. thaliana* collections at low density for fine scale analysis of population structure. >1100 Divergent, non clonal lines have been selected for 250k SNP array typing. This high density set is being used for whole genome association mapping of complex traits as well as metabolic and ionomic polytraits. Borevitz, Hodges, and Kramer have developed genetic and genomic tools for the emerging model organism *Aquilegia* (columbines). This includes genome and transcriptome sequence, SNP markers, population and mapping collections, and high throughput phenotypic analysis. Willis, Bradshaw, Schemske, Vision, Fishman, and Kelly have been leading the development of evolutionary genomic resources for *Mimulus* (<http://www.mimulusevolution.org/>), an emerging model system for studies of adaptation and speciation.

Why the problem requires cutting-edge computer science, bioinformatics, computational biology, statistical or modeling tools, rather than off the shelf solutions.

Understanding how genome-wide variation relates to plant adaptation will require major advances in bioinformatics, computational biology, statistical analysis and modeling. These tools will need to be able to handle the deluge of genomic sequence data from hundreds, thousands, or even millions of plants that is about to result from advances in next generation genome sequences, and to relate it to massively detailed phenomic (diverse morphological, developmental, cellular, physiological, metabolomic, transcriptomic, and proteomic phenotypes scored in native and experimental settings), geographical, climatological, and geological databases constructed for those individuals and populations. Extensive genomic and phenomic data has already been collected for several mapping populations and accessions derived from natural populations in well established model species like *A. thaliana*, and major crops like maize, rice, soybean, wheat and barley across a variety of environmental conditions. Data for these plant systems is increasing exponentially. In addition, there are several emerging plant systems, such as

Mimulus, Aquilegia, Populus, and Arabidopsis relatives that will be especially useful for studying mechanisms of plant adaptation and evolution.

Genomic and phenotypic data from these emerging ecological models, as well as that from less studied crops, are rapidly accumulating and need to be pipelined. The use of common quality control standards and data structures will facilitate comparisons among species and environments. Parallel experiments across multiple species make it possible to start to develop models about how populations and species evolve and change, and how communities function, and will rapidly move us away from the outmoded concept of model organisms.

Certainly some cyberinfrastructure tools have already been developed that can handle population genomic, phenomic, and environmental data. Others exist to statistically analyze the genetic architecture of complex traits across environments. However, these tools are not yet integrated into publically available archives that make it possible to coordinate and compare the sheer volume and variety of the data anticipated in the near future.

A more fundamental problem to achieving the types of advances required is that most of the existing bioinformatics, computational, and statistical approaches for dealing with data were developed for specific applications for specific species, and therefore have limited use for other, more general situations. In terms of genomics, most analysis tools were developed with Sanger sequencing of a "reference" human genome in mind. We need next generation pipelines to deal with massive amounts of data from new sequencing technologies in plants with species level variation that is 20-50 times higher than in humans. We also need ways of representing genome diversity that are not anchored in the misleading concept of a single reference genome. The current algorithms and approaches need to be remodeled and openly packaged. In terms of phenomics, the plant community can collect data on millions of individuals and robust pipelines must be created to deal with large sample sizes, complex image processing, biochemical and metabolite profiles and other types of data. This processing needs to be integrated with geographic information systems (GIS) and be capable of tracking complex interactions between genotype, phenotype, and the environment over time.

Perhaps some of the most challenging problems lie in the arena of computational and statistical approaches to studying how genetic variation relates to plant adaptation. Traditional QTL mapping and association mapping methods can be improved beyond the analysis of simplified breeding designs to include realistic or empirical species' population genetic structures, as well as interactions among multiple genes and alleles which underlie the genetic basis of complex traits. Implementation of improved models can be evaluated on known true positives across independent populations and experiments. It is becoming clear that within a species different sets of genes contribute to trait variation in different environments or in different genetic backgrounds. It is also becoming clear that many traits relevant to adaptation are themselves heterogeneous and complex, in the sense that a given trait, say yield response of a crop to drought stress, has a different underlying allelic, genetic, and thus physiological basis at different stages in the life of a plant and in different environments. And yet currently our statistical methods are designed to focus on a single genetic model that provides the "best" or maximum likelihood explanation of the data. In the future it would be highly desirable to adjust our statistical methods to look for multiple genetic models in the context of epistasis and environmental conditionality. Finally, given the diversity of species and environments under study in the plant community, model comparison methods are needed.

In addition to data analysis, management tools will be needed to allow for efficient sharing of seeds and samples across laboratories, along with communication tools to facilitate collaboration and outreach. Incorporation of advanced computer science concepts such as context-aware database searches, schema matching, crowd sourcing and automatic data trawling would also enhance the functionality of such an

integrated system. Technologies are available that address individual components of such a system. Currently, there is no off-the-shelf system available that address all of the needs described above.

A general description of data sets currently available or that will be available to the community during the next 6-24 months.

Non crop plants. Full genome sequences are available for *A. thaliana* (Col-0), *Selaginella moellendorffii*, *Populus trichocarpa* and *Physcomitrella patens*. Genome sequences will also shortly be available through the JGI community sequencing project for *Arabidopsis lyrata*, *Capsella rubella*, *Mimulus guttatus*, *Aquilegia caerulea*, *Thellungiella halophila* and *Panicum virgatum* (Switchgrass). There are also extensive genotyped collections of *A. thaliana*, including array-based whole-genome variation scans on 19 accessions (Clark et al., 2007) and scoring of 500 divergent accessions using an Affymetrix genotyping array containing 250,000 SNPs (<http://naturalvariation.org/haplotype>). Such genotyping will soon be extended to approximately 1,300 accessions (<http://walnut.usc.edu/2010/SNPs>). There are also large phenotypic datasets for *A. thaliana* including transcripts (<http://www.weigelworld.org/resources/microarray/AtGenExpress/>), metabolites, proteins (Chevalier et al., 2004), interactome and the ionome which includes the shoot and seed concentration of P, Ca, K, Mg, Cu, Fe, Zn, Mn, Co, Ni, B, Se, S, Mo, Na, As and Cd in over 100 accessions and 4 RIL populations curated in a publically accessible relational database at www.purdue.edu/dp/ionomics (Baxter et al., 2007). RIL populations and accessions have also been analyzed for flowering time, fruit size, dormancy, seed sugar composition and storability, hypocotyl length, phytate content (<http://www.dpw.wau.nl/natural/>), other growth related traits (<http://www.mpiz-koeln.mpg.de/english/research/koornneefGroup/index.html>), glucosinolates (Kliebenstein et al., 2001) drought (Bouchabke et al., 2008), self incompatibility (Nasrallah et al., 2004), seed oil composition (O'Neill et al., 2003), and freezing tolerance (Hannah et al., 2006). Natural variation in methylation has also been surveyed in 96 accessions (Vaughn et al., 2007). For *Arabidopsis lyrata petraea* there are detailed demographic and genetic information from 30+ wild populations ranging from Ireland and Wales to Sweden, Norway and Iceland, plus common gardens set up in four sites. There is also transcriptomics, metabolomics and proteomics information available for these collections. For *Mimulus* species, the community has collected thousands of genotypes from over 500 populations of *M. guttatus* as well as from numerous closely related, interfertile species. These genotypes have been used to develop very large collections of F2s, RILs, NILs and natural accession, which have been genotyped and scored for numerous floral, vegetative, and root morphological and growth related traits, leaf trichome production, floral color patterning, flowering time, male and female fertility, tolerance to Cu and serpentine soils, water use efficiency and other drought related traits like stomatal density. Extensive collections of ESTs, highly polymorphic genetic markers based on genes and SSRs, fingerprinted BAC libraries, and integrated physical and genetic maps, and microarrays are also available for *Mimulus*). For *Aquilegia* reference inbred lines, advanced recombinant lines, and hundreds of population samples are available. Two species BAC libraries are fingerprinted and end sequenced. 87,000 ESTs (revealing 16,000 SNPs) were sequenced to which microarrays have been designed and floral whorl specific genes identified.

Crop plants. A full genome sequence is currently available for rice, an 8x reference sequence for soybean has recently been completed, and the reference sequence for maize will be complete by the end of 2008. In rice, a diverse panel of 20 landrace varieties of *O. sativa* was recently re-sequenced by Perlegen Sciences as part of the *OryzaSNP* project (McNally et al., 2006) and 8 additional lines are currently being sequenced using next-generation sequencing technology to provide the basis for SNP chip development. For association mapping, a panel of 1000 purified lines has been genotyped and phenotyped for 40 traits (flowering time, plant height, tiller number, tiller angle, seed color, seed shape, seed weight, grain quality, developmental traits, etc.) in replicated trials over two years (www.ricediversity.org). Additional phenotyping is underway to evaluate biotic and abiotic stresses, including drought, submergence, salt, heat, cold, acid soils, mineral deficiencies and toxicities, etc. A set of 2,000

recombinant inbred lines derived from 8 different crosses are under development at the International Rice Research Institute (IRRI) and an additional 1,500 lines are being purified for association mapping. All materials will be phenotyped for diverse traits and genotyped using Affymetrix arrays in collaboration with international partners. The entire germplasm collection of ~20,000 soybean accessions (*G. max* and *G. soja*) are being genotyped for 50,000 SNPs by the USDA-ARS, Beltsville (Hyten, personal communication).

In maize, numerous phenotypic and genotypic diversity projects are underway. 5000 diverse recombinant inbred lines (RILs) derived from 25 crosses have been genotyped and the lines were released to the public in the spring of 2008. They have already been evaluated in up to 10 environments for 30 traits by multiple groups (flowering, developmental traits, metabolite compositional, pathogen induced secondary metabolites, plant composition, grain quality, etc.) The phenotypic data will be published over the next years for these traits. Additionally, several groups are using next generation sequencing technologies to sequence key maize lines. With the publication of the maize genome, there will be a couple of projects publishing millions of SNPs across key germplasm, which can then be integrated with the vast RIL resources. Overall, there are hundreds of researchers looking at aspects of maize adaptation, and if given a place to store and share data numerous other datasets would become available and remarkable advances could be made.

Goals and outcomes of the Grand Challenge workshop

The goal of the proposed Grand Challenge workshop is to coalesce a diverse group of people around the concept that an integrated cyberinfrastructure would improve the group's ability to more efficiently determine the fundamental genetic, biochemical and physiological mechanisms underlying plant adaptation, by improving;

1. Cooperation and integration of information across laboratories, field sites and species.
2. Training of future academic and international leaders in the integrative concepts underlying evolutionary genetics and plant adaptation, which cut across ecology, genetics, genomics, plant biology, plant breeding, environmental studies, bioinformatics and modeling.
3. Education of the public, policy makers and elected officials on the significance of understanding the mechanisms of plant adaptation for agriculture and future sustainable utilization of natural resources.

The outcome of the proposed grand challenge workshop will be the establishment of a team to develop a Grand Challenge project for submission to the iPlant Collaborative. This team will have a designated leader to manage and guide development and submission of the proposal. Networks of expertises in various critical discipline areas will also be developed to help the proposal team during development of the Grand Challenge project. Mechanisms will also be established at the workshop to allow feedback on the GC proposal from the broader community to be incorporated into the proposal before submission. Such mechanisms would likely include a community WIKI and BLOG site.

Other biology or interdisciplinary groups working in this or related areas.

The maize, rice and soybean communities are developing tools to utilize natural variation for improvement of particular agronomic traits. These tools include full genome sequences, various mapping populations including RILs, CSSLs and association panels, and curated diversity collections. These research communities also have well developed information resources for natural diversity including <http://www.panzea.org/> and <http://www.gramene.org/> and <http://www.comparative-legumes.org/>. We will also coordinate with the GIS community, including remote sensing, to maintain strong connections to sources of geographic data. Collaboration with environmental historian will further enrich this data set. We will also establish close ties to the broader ecological, evolutionary and phylogenetic communities. Representatives from each of these communities will be asked to attend the grand challenge workshop.

Outline of the proposed grand challenge workshop

- Opening remarks and background, goals and deliverables of the workshop, and overview of the organization of the workshop.
- Presentation of a draft of the proposed cyberinfrastructure functionalities as a starting point for discussion.
- Discussion of each of the proposed components of the cyberinfrastructure including:
 1. Organisms to be represented
 2. Existing data that needs to be incorporated
 3. Phenotypes of interest and formalized data acquisition platforms to support data collection in the laboratory, field and across sites.
 4. Other resources that the cyberinfrastructure should be able to access.
 5. Data analysis and visualization tools that would be helpful.
 6. Modeling tools for hypothesis generation and annotation.
 7. Fundamental computer science questions that need to be address including annotation, provenance and other database issues.
 8. Educational outreach strategies.
- Nomination and election of the 5 member writing team and proposal coordinator.
- Establishment of expertise networks to help the proposal writing team when needed.
- Planning of the workflow for proposal preparation, and development of tools for community input during the process.
- Concluding remarks summarizing the draft cyber infrastructure as envisioned by the workshop.

References

- Clark RM, Schweikert G, Toomajian C, Ossowski S, Zeller G, Shinn P, Warthmann N, Hu TT, Fu G, Hinds DA, Chen H, Frazer KA, Huson DH, Schölkopf B, Nordborg M, Rättsch G, Ecker JR, Weigel D (2007). Common sequence polymorphisms shaping genetic diversity in *Arabidopsis thaliana*. *Science*. 317:338-42.
- Chevalier F, Martin O, Rofidal V, Devauchelle AD, Barteau S, Sommerer N, Rossignol M (2004). Proteomic investigation of natural variation between *Arabidopsis* ecotypes. *Proteomics* 4:1372-81.
- Baxter I, Ouzzani M, Orcun S, Kennedy B, Jandhyala SS, Salt DE (2007) Purdue Ionomics Information Management System (PIIMS): An integrated functional genomics platform. *Plant Physiology* 143: 600-611.
- Kliebenstein DJ, Kroymann J, Brown P, Figuth A, Pedersen D, Gershenzon J, Mitchell-Olds T (2001). Genetic control of natural variation in *Arabidopsis* glucosinolate accumulation. *Plant Physiol* 126:811-25.
- Bouchabke O, Chang F, Simon M, Voisin R, Pelletier G, Durand-Tardif M (2008). Natural variation in *Arabidopsis thaliana* as a tool for highlighting differential drought responses. *PLoS ONE* 3(2):e1705.
- Nasrallah ME, Liu P, Sherman-Broyles S, Boggs NA, Nasrallah JB (2004). Natural variation in expression of self-incompatibility in *Arabidopsis thaliana*: implications for the evolution of selfing. *Proc Natl Acad Sci U S A*. 101(45):16070-4.
- O'Neill CM, Gill S, Hobbs D, Morgan C, Bancroft I (2003). Natural variation for seed oil composition in *Arabidopsis thaliana*. *Phytochemistry* 64:1077-90.
- Hannah MA, Wiese D, Freund S, Fiehn O, Heyer AG, Hincha DK (2006). Natural genetic variation of freezing tolerance in *Arabidopsis*. *Plant Physiol* 142:98-112.
- Vaughn MW, Tanurd Ié M, Lippman Z, Jiang H, Carrasquillo R, Rabinowicz PD, Dedhia N, McCombie WR, Agier N, Bulski A, Colot V, Doerge RW, Martienssen RA (2007). Epigenetic Natural Variation in *Arabidopsis thaliana*. *PLoS Biol*: 5:e174.
- McNally KL, Bruskiewich R, Mackill D, Buell CR, Leach JE, Leung H (2006). Sequencing multiple and diverse rice varieties. Connecting whole-genome variation with phenotypes. *Plant Physiol* 141:26-31.

Suggested Reviewers

Carlos Alonso-Blanco, Centro Nacional de Biotecnología, Spain.

Joy Bergelson, University of Chicago, USA.

Jeff Dangl, University of North Carolina, USA.

Mary Lou Guerinot, Dartmouth College, USA.

Maarten Koornneef, Max Planck Institute for Plant Breeding, Germany.

Magnus Nordborg, University of Southern California, USA.

Doug Schemske, Michigan State University, USA.

Detlef Weigel, Max Planck Institute for Developmental Biology, Germany.

Torbert Rocheford, University of Illinois, USA.

Greg May, National Center for Genome Resources, USA.

Major Goodman, North Carolina State University, USA.

Dave Bubeck, Pioneer, USA.

Antoni Rafalski, DuPont, USA.

Keith Allen, Syngenta, USA.

Sam Eathington, Monsanto, USA.