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EDUCATION

Cornell University, B.S., Agronomy, 1981
Iowa State University, Ph.D., Plant Breeding and Cytogenetics, 1986

PROFESSIONAL EXPERIENCE

1981-1986 Graduate Research Assistant, Laboratory of Peter Peterson, Iowa State University
1986-1988 NIH Postdoctoral Fellow, Laboratory of Heinz Saedler, Max-Planck-Institut für Züchtungsforschung, Köln, Germany
1988-1994 Assistant Professor, Iowa State University
1994-1998 Associate Professor, Iowa State University
1998-present Professor, Iowa State University
1999-present Founding Member, Center for Bioinformatics and Biological Statistics
1999-2003 Founding Director, Center for Plant Transformation & Gene Expression
1999-present Founding Director, Center for Plant Genomics
2002-2006 Associate Chair and Chair, Interdepartmental Genetics Graduate Program
2005-2010 Associate Director, Plant Sciences Institute
2007-2013 Director, Center for Carbon Capturing Crops
2007-2013 Baker Professor of Agronomy
2013-present Iowa Corn Promotion Board Endowed Chair in Genetics
2013-present C.F. Curtiss Distinguished Professor
2014-present Baker Scholar of Agricultural Entrepreneurship
2014-present Director, Plant Sciences Institute
2009-present ChangJiang Scholar, China Agriculture University
2010-present Co-Founder and Managing Partner, Data2Bio LLC

HONORS

- ISU Department of Agronomy Plant Breeding Research Award, 1985

- Max-Planck-Institute Postdoctoral Fellowship, 1986
- Iowa State Research Excellence Award, 1986
- Gamma Sigma Delta Honor Society, 1986
- National Institutes of Health Postdoctoral Fellowship, 1987-1988
- Raymond and Mary Baker Agronomic Excellence Award, 2000
- College of Agriculture Research Team Award, 2005
- Best Paper Award, IEEE International Parallel and Distributed Processing Symposium, 2006
- Finalist, Computerworld Honors Program, 2007
- ChangJiang Scholar, China Agriculture University, 2009
- Outstanding Achievement in Research Award, College of Agriculture and Life Sciences, Iowa State University, 2010
- Fellow, American Association for the Advancement of Science (AAAS), 2010

REVIEW PANELS, ADVISORY BOARDS and EDITORIAL POSTS

1990	DOE, Energy Biosciences Panel
2001	NSF Technical Review Team of Missouri MaizeDB
2001-2003	Scientific Advisory Board, NSF-funded Potato Genome Project
2003	Committee of Visitors, Training Cluster, NSF-DBI
2003-2004	Grant Review Panel, NSF Small Business Innovation Research, Agricultural Biotechnology
2003-2007	Scientific Advisory Board, NSF-funded Cell Wall Project
2003-2007	Scientific Advisory Board, NSF-funded Wheat SNP Project
2003-2008	Scientific Advisory Board, NSF-funded Maize Genomic Diversity Project
2005-2009	Elected Member-at-Large of the AAAS Section Committee, Agriculture, Food and Renewable Resources Section
2006	Grant Review Panel, NSF SEI-BIO
2006-2011	MaizeGDB Working Group
2007	Invited to testify to National Research Council Committee: "The National Plant Genome Initiative: Achievements and Future Directions"
2007	Invited to testify to National Research Council Committee: "A Study of Technologies to Benefit Farmers in Africa and South Asia"
2008-2011	Associate Editor, The Plant Genome
2008-present	Associate Editor, PLoS Genetics
2009	Grant Review Panel, Agriculture and Agri-Food Canada
2009	Grant Review Panel, NSF Bioinformatics
2009-present	NextGen Sequencing Working Group, NSF iPlant Consortium
2009-2010	Steering Committee, "Functionality and the Corn Genome" workshop (NCGA)
2009-2011	Organizer, Maize Genetics Workshop, Plant and Animal Genome Meeting
2009-2013	External Advisory Board, French wheat chromosome 3B genome sequencing project
2010-2012	International Scientific Advisory Board, 10th International Congress on Plant Molecular Biology 2012, Jeju, Korea

2011	Co-organizer, Banbury Conference (CSHL): “Genotype to Phenotype: Deriving Biological Knowledge from Large Genomic Datasets”, 16-19 October 2011, Cold Spring Harbor, NY
2011	Organizer “Genomics to Agronomics” Session, American Seed Trade Association, Chicago IL 8 December 2011
2011-2012	Organizing Committee, International Conference of Heterosis Utilization in Crops, 21-24 August 2012, Xian, China
2011-present	Scientific Advisory Board, NSF-funded <i>Amborella</i> Genome Project
2013-2018	International Advisory Board, Centre for Biotechnological and Agricultural Research, Olomouc, Czech Republic
2013-present	Scientific Advisory Council, GeneSeek
2013-present	National Plant Science Council
2013-present	Scientific Advisory Board, NSF-funded <i>Aegilops tauschii</i> Genome Sequencing Project
2013-present	Co-lead, Maize Genomes to Fields Initiative

PROFESSIONAL AFFILIATIONS

- American Association for the Advancement of Science
 - “Golden Goose Award” Nominating Committee (ASPB Representative)
- American Society of Plant Biologists
 - Executive Committee, 2012-2016
 - Science Policy Committee, 2008-2016
 - Chair, 2012-2016
 - Pioneer Hi-Bred International Graduate Student Prize Committee, 2009-2013
- Genetics Society of America
 - Public Policy Committee, 2013-Present
- Maize Genetics Cooperative
 - Steering Committee, 1993-1996; 2002-2004
 - Maize Genetics Executive Committee
 - Member, 2000-2004, 2006-2012
 - Chair, 2003-2004, 2007-2009

PUBLICATIONS (refereed; *invited author*):

Schnable has an h-index of 52 (as calculated by Google Scholar, <http://scholar.google.com/citations?user=UW4mNTW0nOkC&hl=en>, on 9/30/13) with a total of 9,051 citations. Reflecting his interest in computational approaches to biology he has an Erdős number of 4.

- **Schnable PS, PA Peterson (1986)** Distribution of genetically active *Cy* elements among diverse maize lines. **Maydica (McClintock issue)** 31:59-81.
- **Schnable PS, PA Peterson (1988)** The *Mutator*-related *Cy* transposable element of *Zea mays* L. behaves as a near-Mendelian factor. **Genetics** 120:587-596.

- **Schnable PS, PA Peterson** (1989) Genetic evidence of a relationship between two maize transposable element systems: *Cy* and *Mutator*. **Mol Gen Genet** 215:317-321.
- **Schnable PS, PA Peterson, H Saedler** (1989) The *bz-rcy* allele of the *Cy* transposable element system of *Zea mays* contains a *Mu*-like element insertion. **Mol Gen Genet** 217:459-463.
- **Menssen A, S Höhmann, W Martin, PS Schnable, PA Peterson, H Saedler, A Gierl** (1990) The En/Spm transposable element of *Zea mays* contains splice sites at the termini generating a novel intron from a dSpm element in the A2 gene. **EMBO J** 9:3051-3057.
- **Stinard PS, DS Robertson, PS Schnable** (1993) Genetic isolation, cloning, and analysis of a *Mutator*-induced, dominant antimorph of the maize *amylose-extender1* locus. **Plant Cell** 5:1555-1566.
- **Schnable PS, RP Wise** (1994) Recovery of heritable, transposon-induced, mutant alleles of the *rf2* nuclear restorer of T-cytoplasm maize. **Genetics** 136:1171-1185.
- **Wen T-J, PS Schnable** (1994) Analyses of mutants of three genes that play a role in root hair development of *Zea mays* (*Gramineae*) suggest that root hairs are dispensable. **Am J Bot** 81:833-842.
- **Civardi L, YJ Xia, K Edwards, PS Schnable, BJ Nikolau** (1994) The relationship between the genetic and physical distances of the cloned *a1-sh2* interval of the *Zea mays* L. genome. **Proc Natl Acad Sci** 91:8268-8272.
- **Wise RP, PS Schnable** (1994) Mapping complementary genes in maize: Positioning the *rf1* and *rf2* nuclear-fertility restorer loci of Texas (T)-cytoplasm relative to RFLP and morphological markers. **Theoretical & Applied Genetics**, 88: 785-795.
- **Schnable PS, PS Stinard, T-J Wen, S Heinen, D Weber, L Zhang, JD Hansen, BJ Nikolau** (1994) The genetics of cuticular wax biosynthesis. **Maydica (Robertson issue)**, 39:279-287.
- **Bensen RJ, GS Johal, VC Crane, JT Tossberg, PS Schnable, RB Meeley, SP Briggs** (1995) *Anther ear 1* of maize encodes a cyclase. **Plant Cell**, 7:75-84.
- **Han C-D, RJ Derby, PS Schnable, RA Martienssen** (1995) Characterization of the plastids affected by class II albino mutations of maize at the morphological and transcript levels. **Maydica (Coe issue)** 40:13-22.
- **Kasemsuwan T, J Jane, PS Schnable, P Stinard, D Robertson** (1995) Characterization of the dominant mutant amylose-extender (*Ael-5180*) maize starch. **Carbohydrates**, 72:457-464.
- **Xu XJ, A-P Hsia, L Zhang, BJ Nikolau, PS Schnable** (1995) Meiotic recombination breakpoints resolve at high rates at the 5' end of a maize coding sequence. **Plant Cell**, 7:2151-2161.
- **Hsia A-P, PS Schnable** (1996) DNA sequence analyses support the role of interrupted gap-repair in the origin of internal deletions of the maize *MuDR* transposon. **Genetics**, 142:603-618.

- Cui XQ, RP Wise, **PS Schnable** (1996) The *rf2* nuclear restorer gene of male-sterile, T-cytoplasm maize. **Science**, 272:1334-1336. (A commentary on this manuscript solicited by journal editors and written by Charles S. Levings III was provided in 272: 1279-1280)
- Wise RP, CL Dill, **PS Schnable** (1996) Interaction of *Mutator*-induced mutations of the *rf1* nuclear fertility restorer and T-*urf13* of T-cytoplasm maize mitochondria. **Genetics**, 143:1383-1394.
- Xia YJ, BJ Nikolau, **PS Schnable** (1996) Cloning and characterization of *CER2*, an *Arabidopsis* gene that affects cuticular wax accumulation. **Plant Cell**, 8: 1291-1304.
- Hansen JD, J Pyee, YJ Xia, T-J Wen, DS Robertson, PE Kolattukudy, BJ Nikolau, **PS Schnable** (1997) The *glossy1* locus of *Zea mays* L. and an epidermis-specific cDNA from *Kleinia odora* define a novel class of plant receptor-like proteins required for the normal accumulation of cuticular waxes. **Plant Physiology**, 113:1091-1100.
- Xu X, C Dietrich, M Delledonne, Y Xia, TJ Wen, DS Robertson, BJ Nikolau, **PS Schnable** (1997) Sequence analysis of the cloned *glossy8* gene of *Zea mays* L. suggests that it may code for a beta-keto acyl reductase required for the biosynthesis of cuticular waxes. **Plant Physiology**, 115:501-510.
- Dill CL, RP Wise, **PS Schnable** (1997) *Rf8* and *rf** mediate unique T-*urf13*-transcript accumulation, revealing a conserved motif associated with RNA processing and restoration of pollen fertility in T-cytoplasm maize. **Genetics**, 147:1367-1379.
- Xia Y, BJ Nikolau, **PS Schnable** (1997) Developmental and hormonal regulation of the *Arabidopsis CER2* gene which codes for a nuclear localized protein required for the normal accumulation of cuticular waxes. **Plant Physiology**, 115:925-937.
- **Schnable PS**, RP Wise (1998) The molecular basis of cytoplasmic male sterility. **Trends in Plant Science**, 3:175-180.
- **Schnable PS**, A-P Hsia, BJ Nikolau (1998) Genetic recombination in plants. **Current Opinion in Plant Biology**, 1:123-129.
- Wise RP, C Bronson, **PS Schnable**, HT Horner (1999) The genetics, pathology, and the molecular biology of T-cytoplasm male sterility in maize. **Adv in Agronomy**, 65:79-130.
- **Rothschild MF**, **PS Schnable** (1999) Animal and Plant Genomics: Driving the Golden Spike. **AgBiotech News**, January:1-2.
- Frame BR, H Zhang, SM Cocciolone, L Sidorenko, CR Dietrich, SE Pegg, S Zhen, **PS Schnable**, K Wang (2000) Production of transgenic maize from bombarded type II callus: effect of gold particle size and callus morphology on transformation efficiency. **In Vitro and Developmental Biology-Plant**, 36:21-29.
- Liu F, X Cui, HT Horner, H Weiner, **PS Schnable** (2001) Mitochondrial aldehyde dehydrogenase activity is required for male fertility in maize (*Zea mays* L.). **Plant Cell**, 13:1063-1078. (Cover image)
- Bennetzen, JL, VL Chandler, **PS Schnable** (2001) National Science Foundation-Sponsored Workshop Report: "Maize Genome Sequencing Project". **Plant Physiology**, 127:1572-1578.

- Dietrich C, F Cui, M Packila, J Li, DA Ashlock, BJ Nikolau, **PS Schnable** (2002) Maize *Mu* transposons are targeted to the 5' UTR of the *gl8a* gene and sequences flanking *Mu* target site duplications exhibit non-random nucleotide composition throughout the genome. **Genetics**, 160: 697-716.
- Xu X, Dietrich CR, Lessire R, Nikolau BJ, **PS Schnable** (2002) The endoplasmic reticulum-associated maize GL8 protein is one of the components of the acyl-CoA elongase complex involved in the production of cuticular waxes. **Plant Physiology**, 128: 924-934.
- Yao H, Q Zhou, J Li, H Smith, M Yandeu, B Nikolau, **PS Schnable** (2002) Molecular characterization of meiotic recombination across the 140-kb multigenic maize *a1-sh2* interval. **Proc Natl Acad Sci**, 99:6157-6162. (*A commentary on this manuscript solicited by journal editors and written by Cliff Weil was provided in 99:5763-5765; selected as a "must read" by the Faculty of 1000 Biology*)
- Skibbe D, F Liu, TJ Wen, MD Yandeu, XQ Cui, J Cao, CR Simmons, **PS Schnable** (2002) Characterization of the aldehyde dehydrogenase gene families of *Zea mays* and *Arabidopsis*. **Plant Molecular Biology**, 48:751-764.
- Liu F, **PS Schnable** (2002) Functional specialization of maize mitochondrial aldehyde dehydrogenases. **Plant Physiology**, 130:1657-1674.
- Cui X, A-P Hsia, F Liu, D Ashlock, RP Wise, **PS Schnable** (2003) Alternative transcription initiation sites and polyadenylation sites are recruited during *Mu* suppression at the *rf2a* locus of maize. **Genetics**, 163:685-698.
- Nakazono M, F Qiu, L Borsuk, **PS Schnable** (2003) Laser capture microdissection, a tool for the global analysis of gene expression in specific plant cell types: Identification of genes differentially expressed in epidermal cells or vascular tissues of maize. **Plant Cell**, 15:583-596. (*Selected as a "must read" by the Faculty of 1000 Biology*)
- Qiu F, L Guo, TJ Wen, DA Ashlock, **PS Schnable** (2003) DNA sequence-based "bar-codes" for tracking the origins of ESTs from a maize cDNA library constructed using multiple mRNA sources. **Plant Physiology**, 133:475-481.
- Hochholdinger F, L Guo, **PS Schnable** (2004) Cytoplasmic regulation of the accumulation of nuclear-encoded proteins in the mitochondrial proteome of maize. **Plant Journal**, 37:199-208.
- **Schnable, PS**, F Hochholdinger, M Nakazono (2004) Global expression profiling applied to plant development. **Current Opinion in Plant Biology**, 7:50-56.
- Emrich SJ, S Aluru, Y Fu, TJ Wen, M Narayanan, L Guo, DA Ashlock, **PS Schnable** (2004) A strategy for assembling the maize (*Zea mays* L.) genome. **Bioinformatics**, 20:140-147.
- da Costa é Silva O, R Lorbiecke, P Garg, L Müller, M Waßmann, P Lauert, M Scanlon, AP Hsia, **PS Schnable**, K Krupinska, U Wienand (2004) The *Etched1* gene of *Zea mays* (L.) encodes a zinc ribbon protein that belongs to the transcriptionally active chromosome (TAC) of plastids and is similar to the transcription factor TFIIS. **Plant Journal**, 37: 199-208.

- Kirch HH, D Bartels, Y Wei, **PS Schnable**, AJ Wood (2004) The ALDH gene superfamily of *Arabidopsis*. **Trends in Plant Science**, 9:371-377.
- Chou HH, AP Hsia, D Mooney, **PS Schnable** (2004) PICKY: an oligo microarray design tool for large genomes. **Bioinformatics**, 20:2893-2902. (Epub 2004 Jun 4)
- Fu Y, AP Hsia, L Guo, **PS Schnable** (2004) Types and frequencies of sequencing errors in methyl-filtered and high C_ot maize genome survey sequences. **Plant Physiology**, 135:2040-2045. (Epub: 2004 Aug 6)
- Hochholdinger F, L Guo, **PS Schnable** (2004) Lateral roots affect the proteome of the primary root of maize (*Zea mays* L.). **Plant Mol Biology**, 56:397-412. *Selected as an Editors' Choice by MaizeGDB, 2/05*.
- Yandea-Nelson MD, Q Zhou, H Yao, X Xu, BJ Nikolau, **PS Schnable** (2005) *MuDR* transposase increases the frequency of meiotic crossovers in the vicinity of a *Mu* insertion in the maize *al* gene. **Genetics**, 169:917-929. (Epub: 2004 Oct 16)
- Hsia A-P, T-J Wen, HD Chen, Z Liu, MD Yandea-Nelson, Y Wei, L Guo, **PS Schnable** (2005) Temperature Gradient Capillary Electrophoresis (TGCE) – A tool for the high throughput discovery and mapping of SNPs and IDPs. **Theoretical Applied Genetics**, 111: 218-225. (Epub: 2005 May 24)
- Yao H, L Guo, Y Fu, LA Borsuk, T-J Wen, DS Skibbe, X Cui, BE Scheffler, J Cao, SJ Emrich, DS. Ashlock, **PS Schnable** (2005) Evaluation of five *ab initio* gene prediction programs for the discovery of maize genes. **Plant Mol Biology**, 57:445-460.
- Ding J, K Viswanathan, D Berleant, L Hughes, E Wurtele, D Ashlock, JA Dickerson, A Fulmer, **PS Schnable** (2005) Using the biological taxonomy to access biological literature with PathBinderH. **Bioinformatics**, 21:2560-2562. (Epub: 2005 Mar 15)
- Dietrich CR, MA Perera, M Yandea-Nelson, RB Meeley, BJ Nikolau, **PS Schnable** (2005) Characterization of two *gl8* paralogs reveals that the 3-ketoacyl reductase component of fatty acid elongase is essential for maize (*Zea mays* L.) development. **Plant Journal**, 42:844-861.
- Wen TJ, F Hochholdinger, M Sauer, W Bruce, **PS Schnable** (2005) The *roothairless1* gene of maize (*Zea mays*) encodes a homolog of *sec3*, which is involved in polar exocytosis. **Plant Physiology**, 138:1637-1643. (Epub: 2005 Jun 24; *Selected as an Editors' Choice by MaizeGDB, 4/07*)
- Fu Y, SJ Emrich, L Guo, T-J Wen, S Aluru, DA Ashlock, **PS Schnable** (2005) Quality assessment of maize assembled genomic islands (MAGIs) and large-scale experimental verification of predicted novel genes. **Proceedings National Academy Science**, 102:12282-12287. (Epub: 2005 Aug 15)
- Woll K, LA Borsuk, H Stransky, D Nettleton, **PS Schnable**, F Hochholdinger (2005) Isolation, characterization and pericycle specific transcriptome analyses of the novel maize (*Zea mays* L.) lateral and seminal root initiation mutant *rum1*. **Plant Physiology**, 139:1255-1267. (Epub: 2005 Oct 7)
- Skibbe DS, **PS Schnable** (2005) Male sterility in maize. **Maydica**, 50:367-376.

- Kresovich S and 35 additional authors including **PS Schnable** (2005) Toward sequencing the sorghum genome: a US National Science Foundation-sponsored workshop report. **Plant Physiology**, 138:1898-1902.
- Yao H, **PS Schnable** (2005) *Cis*-effects on meiotic recombination across distinct *al-sh2* intervals in a common *Zea* genetic background. **Genetics**, 170:1929-1944. (Epub: 2005 Jun 3)
- Hochholdinger F, K Woll, L Guo, **PS Schnable** (2005) The accumulation of abundant soluble proteins changes early in the development of the primary roots of maize (*Zea mays* L.). **Proteomics**, 5:4885-4893. (Cover image)
- Maher PM, H-H Chou, E Hahn, T-J Wen, **PS Schnable** (2006) GRAMA: A genetic mapping tool for the analysis of temperature gradient capillary electrophoresis (TGCE) data. **Theoretical Applied Genetics**, 113:156-162. (Epub: 2006 Apr 20)
- Swanson-Wagner R, Y Jia, R DeCook, LA Borsuk, D Nettleton, **PS Schnable** (2006). All possible modes of gene action are observed in a global comparison of gene expression in a maize F₁ hybrid and its inbred parents. **Proceedings National Academy Science**, 103: 6805-6810. (Epub: 2006 Apr 25; “recommended” by the Faculty of 1000 Biology; identified by Thomson Reuters Scientific's Essential Science Indicators as the most highly cited paper in the research front map “On Applying Genome-Wide Selection”; podcast solicited by ScienceWatch.com: <http://www.in-cites.com/media/podcasts/PatSchnable.mp3>)
- Skibbe DS, X Wang, X Zhao, LA Borsuk, D Nettleton, **PS Schnable** (2006) Scanning cDNA microarrays at multiple intensities increases the number of statistically significant differences detected. **Bioinformatics**, 22:1863-1870. (Epub: 2006 May 26)
- Yandea-Nelson MD, Y Xia, J Li, MG Neuffer **PS Schnable** (2006) Unequal sister chromatid and homolog recombination at a tandem duplication of the *al* locus in maize. **Genetics**, 173:2211-2226. (Epub: 2006 Jun 4)
- Yandea-Nelson MD, BJ Nikolau, **PS Schnable** (2006) Effects of *trans*-acting genetic modifiers on the rates and distribution of meiotic recombination across the *al-sh2* interval of maize. **Genetics**, 174:101-112. (Epub: 2006 Jul 2; “recommended” by the Faculty of 1000 Biology)
- Fu Y, T-J Wen, YI Ronin, HD Chen, L Guo, DI Mester, Y Yang, M Lee, AB Korol, DA Ashlock, **PS Schnable** (2006) Genetic dissection of intermated recombinant inbred lines using a new genetic map of maize. **Genetics**, 174: 1671-1683. (Epub 2006 Sep 1)
- Ohtsu K, H Takahashi, **PS Schnable**, M Nakazono (2007) Cell type-specific gene expression profiling in plants by using a combination of laser microdissection and high-throughput technologies. **Plant & Cell Physiology**, 48:3-7. (Epub: 2006 Dec 5)
- Emrich SJ, WB Barbazuk, L Li, **PS Schnable** (2007) Gene discovery and annotation using LCM-454 transcriptome sequencing. **Genome Research**, 17: 69-73. (Epub: 2006 Nov 9)
- Emrich SJ, L Li, TJ Wen, MD Yandea-Nelson, Y Fu, L Guo, HH Chou, S Aluru, DA Ashlock, **PS Schnable** (2007) Nearly identical paralogs (NIPs) and implications for maize genome evolution. **Genetics**, 175:429-439. (Epub: 2006 Nov 16) (Featured in

Science (315:302) as in Editor's Choice: Highlights of the recent literature; selected as an Editors' Choice by MaizeGDB, 12/06).

- Travers SE, MD Smith, J Bai, SH Hulbert, JE Leach, **PS Schnable**, AK Knapp, GA Milliken, PA Fay, A Saleh, KA Garrett (2007) Ecological genomics: making the leap from model systems in the lab to native populations in the field. **Front Ecol Environ**, 5:19-24.
- Li J, AP Hsia, **PS Schnable** (2007) Recent advances in plant recombination. **Current Opinion in Plant Science**, 10:131-135.
- Buckner B, J Beck, KF Browning, AE Fritz, E Hoxha, LD Grantham, ZN Kamvar, AN Lough, O Nikolova, **PS Schnable**, MJ Scanlon, and D Janick-Buckner (2007) Involving undergraduates in the annotation and analysis of global gene expression studies: creation of a maize shoot apical meristem expression database. **Genetics**, 176:741-747.
- Kalyanaraman A, SJ Emrich, **PS Schnable**, S. Aluru (2007) Assembling genomes on large-scale parallel computers. **Journal of Parallel and Distributed Computing**, Vol. 67:1240-1255. (*Special issue devoted to IPDPS best papers*)
- Zhang X, S Medi, L Borsuk, DS Nettleton, B Buckner, D Janick-Buckner, J Beck, M Timmermans, **PS Schnable**, MJ Scanlon (2007) Laser microdissection of narrow sheath mutant maize uncovers novel gene expression in the shoot apical meristem. **PLoS Genetics**, 3:1040-1052. (*Selected an Editors' Choice by MaizeGDB, 7/07*).
- Li J, LC Harper, I Golubovskaya, CR Wang, DF Weber, RB Meeley, J McElver, B Bowen, WZ Cande, **PS Schnable** (2007) Functional analysis of maize RAD51 in meiosis and DSBs repair. **Genetics**, 176: 1469–1482. (*Selected by journal editors as an "Issue Highlight"; selected as an Editors' Choice by MaizeGDB, 8/07*).
- Barbazuk WB, SJ Emrich, HD Chen, **PS Schnable** (2007) SNP discovery via 454 transcriptome sequencing. **Plant J**, 51: 910-918. (*Cited in Wikipedia: <http://en.wikipedia.org/wiki/RNA-Seq>*)
- Ohtsu K, M Smith, SJ Emrich, LA Borsuk, R Zhou, T Chen, X Zhang, M Timmermans, J Beck, B Buckner, D Janick-Buckner, D Nettleton, MJ Scanlon, **PS Schnable** (2007) Global gene expression analysis of the shoot apical meristem of maize (*Zea mays* L.). **Plant J**, 52(3):391-404. (*"Recommended" by the Faculty of 1000 Biology; selected as an Editors' Choice by MaizeGDB, 10/07*).
- Dembinsky D, K Woll, M Saleem, Y Liu, Y Fu, LA Borsuk, T Lamkemeyer, C Fladerer Claudia, J Madlung, B Barbazuk, A Nordheim, D Nettleton, **PS Schnable**, F Hochholdinger (2007) Pericycle-specific transcriptome and proteome analyses of maize (*Zea mays* L.) primary root. **Plant Physiology**, 145:575-578. (Epub: 2007 Aug 31)
- Li J, T-J Wen, **PS Schnable** (2008) The role of RAD51 in the repair of *MuDR*-induced DSBs in *Zea mays* L. **Genetics**, 178:57-66. (*Selected as an Editors' Choice by MaizeGDB, 2/08*).
- Hochholdinger F, T-J Wen, R. Zimmermann, P Lauert, O da Costa e Silva, W Bruce, KR Lamkey, U Wienand, **PS Schnable** (2008) The maize (*Zea mays* L.) *roothairless3* gene encodes a putative GPI-anchored, monocot-specific COBRA-like protein required for

normal root hair development and grain yield. **Plant Journal**, 54:888-898. (*Selected as an Editors' Choice by MaizeGDB, 6/08*).

- Buckner B, KA Swaggart, CC Wong, HA Smith, KM Aurand, MJ Scanlon, **PS Schnable**, D Janick-Buckner (2008) Expression and nucleotide diversity of the maize *RIK* gene. **J Heredity**, 99(4):407-16. Epub 2008 Feb 28.
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- Jung KH, C Dardick, LE Bartley, P Cao, J Phetsom, P Canlas, YS Seo, M Shultz, S Ouyang, Q Yuan, BC Frank, E Ly, L Zheng, Y Jia, AP Hsia, K An, HH Chou, D Rocke, GC Lee, **PS Schnable**, G An, CR Buell, PC Ronald (2008) Refinement of light-responsive transcript lists using rice oligonucleotide arrays: evaluation of gene-redundancy. **PLoS ONE**. Oct 6;3(10):e3337.
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