

Nathan Michael Springer

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RANK:

Professor

PROFESSIONAL INTERESTS:

Genetic analysis in maize and other crop plants; emphasis on mechanisms and role of epigenetic inheritance, molecular basis of gene expression variation, heterosis, imprinted gene expression, transposable elements and structural genomic variation

PROFESSIONAL EXPERIENCE:

05/2013 - present: Professor, Department of Plant Biology, University of Minnesota
05/2009 - 05/2013: Associate Professor, Department of Plant Biology, University of Minnesota
08/2009 – 07/2014: Director, Microbial and Plant Genomics Institute, University of Minnesota
8/2003 - 05/2009: Assistant Professor, Department of Plant Biology, University of Minnesota
9/2002 - 8/2003: Post-doctoral research associate on N.S.F. grant "Assessment of the utility of microarrays for SNP detection in maize genomic DNA."
7/2000 - 9/2002: Post-doctoral research associate on N.S.F. Grant "Functional genomics of chromatin global control of plant gene expression."
7/1997 - 7/2000: U.S.D.A. National Needs Fellow, University of Minnesota

EDUCATION:

A.A. with highest honors (1994): Bethany Lutheran College
B.S. with highest honors (1997): Biology Major, Southeast Missouri State University
Ph.D. (2000): Plant Biology, University of Minnesota (Advisor: Ronald L Phillips)

AWARDS AND ACADEMIC HONORS:

1994 National Merit Scholarship
1996 Phi Kappa Phi
1997 U.S.D.A. National Needs Fellowship, University of Minnesota
2002 National Science Foundation Plant Genome Young Investigator
2007 Southeast Missouri State University Young Alumni Merit Award

2016 Presidential McKnight Endowed Professor in Plant Biology
 2016 Emerging Leaders in Plant Sciences Award - University of Minnesota

TEACHING EXPERIENCE:

Biol4003 Genetics (U of Minnesota): Every spring semester (~100 students/semester)
 PBio1212 Plant Biotechnology and Society (U of Minnesota): 2012-2013
 Biol5950 Special topics: Epigenetics (U of Minnesota): 2014
 PBIO5960-2 Microbial and Plant Genomics symposium (U of Minnesota): 2010-2011
 Agro8231 Chromosome Biology (U of Minnesota): 2004-2010 every other fall
 PBS8081 Integrative Plant Biology (U of Minnesota): 2006
 Spring 2005 – present. Directed research courses for 24 students.

FUNDED GRANTS:

9/02-9/05. (\$450,000) National Science Foundation. "Assessment of the utility of oligonucleotide arrays."
 9/04-8/05. (\$30,301) U of Minnesota Grant-in-aid. "Identification of cis-acting elements controlling imprinting."
 9/04-8/08. (\$597,163) National Science Foundation. "Maize functional genomics of chromatin." (Co-PI)
 5/06-4/07. (\$14,300) Minnesota Agriculture Experiment Station. "Dynamics of DNA replication in endosperm."
 07/07-06/09 (\$126,444) Institute of the environment – IREE Discovery Grant. "Survey of genetic variation for response to density stress."
 2/10 – 03/13 (\$1,678,620) National Science Foundation "GEPR Maize epigenomic variation."
 04/11 – 03/14 (\$499,538) USDA – NIFA "Environmentally Induced Epigenetic Changes in Maize"
 09/11 – 08/14 (\$970,000) National Science Foundation "Using Natural Variation to Probe the Evolution, Mechanisms and Function of Imprinting in Plants" (Co-PI)
 10/12 – 09/16 (\$3,424,556) National Science Foundation "Causes and consequences of epigenetic variation in maize"
 03/15 - 03/19 (\$5,569,161) National Science Foundation "Enabling Cold Tolerant Maize Using Genomic and Machine Vision Phenomic Approaches" (CoPI)
 12/15 – 11/18 (\$408,000) USDA – NIFA "Understanding the role of transposable elements in maize abiotic stress response"
 07/16 - 06/20 (\$2,677,672) National Science Foundation "Discovery and evaluation of inbred-specific and hybrid-specific regulatory modules" (CoPI)
 02/18-01/22 (\$4,884,272 - \$627,831 to MN) National Science Foundation "RESEARCH-PGR: Elucidating Maize Gene Regulatory Networks to Accelerate Translational Genomics."

PUBLICATIONS:

93. He Y, Wang M, Dukowic-Schulze S, Zhou A, Tiang, C-L, Shilo S, Sidhu GK, Eichten S, Bradbury PJ, Springer NM, Buckler ES, Levy AA, Sun Q, Pillardy J, Kianian PMA,

- Kianian SF, Chen C, Pawlowski WP. (2017) Genomic features shaping the landscape of meiotic double-strand break hotspots in maize. PNAS. In press.
92. Brohammer A, Kono T, Springer NM, McGaugh S, Hirsch CN. (2017). Limited role of differential fractionation in genome content variation and function in maize (*Zea mays* L.) inbred lines. The Plant Journal. In press.
 91. Jiao Y, Peluso P, Shi J, Liang T, Stitzer MC, Wang B, Campbell MS, Stein JC, Wei X, Chin CS, Guill K, Regulski M, Kumari S, Olson A, Gent J, Schneider KL, Wolfgruber TK, May MR, **Springer NM**, Antoniou E, McCombie WR, Presting GG, McMullen M, Ross-Ibarra J, Dawe RK, Hastie A, Rank DR, Ware D. (2017) Improved maize reference genome with single-molecule technologies. Nature. 2017 Jun 22;546(7659):524-527. doi: 10.1038/nature22971.
 90. **Springer NM**, Schmitz RJ. (2017) Exploiting induced and natural epigenetic variation for crop improvement. Nat Rev Genet. 2017 Sep;18(9):563-575. doi: 10.1038/nrg.2017.45.
 88. Köhler C, **Springer N**. (2017) Plant epigenomics-deciphering the mechanisms of epigenetic inheritance and plasticity in plants. Genome Biol. 2017 Jul 6;18(1):132. doi: 10.1186/s13059-017-1260-9.
 87. Oka R, Zicola J, Weber B, Anderson SN, Hodgman C, Gent JJ, Wesselink JJ, **Springer NM**, Hoefsloot HCJ, Turck F, Stam M (2017) Genome-wide mapping of transcriptional enhancer candidates using DNA and chromatin features in maize. Genome Biol. 2017 Jul 21;18(1):137. doi: 10.1186/s13059-017-1273-4.
 86. Li Q, Hermanson PJ, **Springer NM**. (2017) Detection of DNA Methylation by Whole-Genome Bisulfite Sequencing. Methods Mol Biol. 2018;1676:185-196. doi: 10.1007/978-1-4939-7315-6_11.
 85. Mei W, Liu S, Schnable JC, Yeh CT, **Springer NM**, Schnable PS, Barbazuk WB. (2017) A Comprehensive Analysis of Alternative Splicing in Paleopolyploid Maize. Front Plant Sci. 2017 May 10;8:694. doi: 10.3389/fpls.2017.00694. eCollection 2017.
 84. Vishwanathan N, Bandyopadhyay A, Fu HY, Johnson KC, **Springer NM**, Hu WS. (2017) A comparative genomic hybridization approach to study gene copy number variations among chinese hamster cell lines. Biotechnol Bioeng. 2017 Apr 14. doi: 10.1002/bit.26311.
 83. Grotewold E, **Springer NM** (2017) News from the plant world: Listening to transcription. Biochim Biophys Acta. 1860(1):1-2.
 82. Waters AJ, Makarevitch I, Noshay J, Burghardt LT, Hirsch CN, Hirsch CD, **Springer NM**. (2017) Natural variation for gene expression responses to abiotic stress in maize. Plant J. 89(4):706-717
 81. Li L, Briskine R, Schaefer R, Schnable PS, Myers CL, Flagel LE, **Springer NM**, Muehlbauer GJ. (2016) Co-expression network analysis of duplicate genes in maize (*Zea mays* L.) reveals no subgenome bias. BMC Genomics. 17(1):875.
 80. Hirsch CN, Hirsch CD, Brohammer AB, Bowman MJ, Soifer I, Barad O, Shem-Tov D, Baruch K, Lu F, Hernandez AG, Fields CJ, Wright CL, Koehler K, **Springer NM**, Buckler E, Buell CR, de Leon N, Kaeppler SM, Childs KL, Mikel MA. (2016) Draft Assembly of Elite Inbred Line PH207 Provides Insights into Genomic and Transcriptome Diversity in Maize. Plant Cell. 28(11):2700-2714.

79. Niederhuth CE, Bewick AJ, Ji L, Alabady MS, Kim KD, Li Q, Rohr NA, Rambani A, Burke JM, Udall JA, Egesi C, Schmutz J, Grimwood J, Jackson SA, **Springer NM**, Schmitz RJ. (2016) Widespread natural variation of DNA methylation within angiosperms. *Genome Biol.* 17(1):194.
78. Altpeter F, **Springer NM**, Bartley LE, Blechl A, Brutnell TP, Citovsky V, Conrad L, Gelvin SB, Jackson D, Kausch AP, Lemaux PG, Medford JI, Orozco-Cardenas M, Tricoli D, VanEck J, Voytas DF, Walbot V, Wang K, Zhang ZJ, Stewart CN Jr. (2016) Advancing Crop Transformation in the Era of Genome Editing. *Plant Cell* 28(7):1510-1520
77. Hirsch CD, **Springer NM** (2016) Transposable element influences on gene expression in plants. *Biochim Biophys Acta* 1860: 157-165.
76. **Springer NM**, Lisch D, Li Q (2016) Creating Order from Chaos: Epigenome Dynamics in Plants with Complex Genomes. *Plant Cell* 28:314-325.
75. Li Q, Gent JI, Zynda G, Song J, Makarevitch I, Hirsch CD, Hirsch CN, Dawe RK, Madzima TF, McGinnis KM, Lisch D, Schmitz RJ, Vaughn MW, **Springer NM**. (2015) RNA-directed DNA methylation enforces boundaries between heterochromatin and euchromatin in the maize genome. *Proc Natl Acad Sci USA.* 112(47):14728-33.
74. Hirsch C, **Springer NM**, Hirsch CN. 2015. Genomic limitations to RNAseq expression profiling. *Plant Journal* 84: 491–503.
73. **Springer NM**, McGinnis KM. 2015. Paramutation in evolution, population genetics and breeding. *Semin Cell Dev Biol.* 44:33-38.
72. Brady S, Burow M, Busch W, Carlborg O, Denby K, Glazebrook J, Hamilton E, Maloof J, **Springer N**, Kliebenstein D. 2015. Reassess the t-test: interact with all your data via ANOVA. *Plant Cell* 27(8):2088-94.
71. Eichten SR, **Springer NM** 2015. Minimal evidence for consistent changes in maize DNA methylation patterns following environmental stress. *Frontiers in Plant genetics and Genomics* 6:308.
70. Li Q, Song J, West PT, Zynda G, Eichten SR, Vaughn MW, **Springer NM**. 2015. Examining the causes and consequences of context-specific differential DNA methylation in maize. *Plant Physiology* 168(4):1262-1274.
69. Li Q, Suzuki M, Wendt J, Patterson N, Eichten SR, Hermanson PJ, Green D, Jeddeloh J, Richmond T, Rosenbaum H, Burgess D, **Springer NM**, Greally JM. 2015. Post-conversion targeted capture of modified cytosines in mammalian and plant genomes. *Nucleic Acids Research* 43(12):e81.
68. Springer NM. 2015. Transposable elements: Microbiomes in the genomes. *Nature Plants* 1:15004.
67. Makarevitch I, Waters AJ, West PT, Stitzer M, Ross-Ibarra J, **Springer NM**. 2015. Transposable elements contribute to activation of maize genes in response to abiotic stress. *PLoS Genetics* 11:e1004915.
66. Li Q, Eichten SR, Hermanson PJ, Zaunbrecher V, Song J, Wendt J, Rosenbaum H, Madzima TF, Sloan AE, Huang J, Burgess D, Richman TA, Kaeppler SM, McGinnis KM, Meeley RB, Danilevskaya ON, Vaughn MW, Jeddeloh JA,

- Springer NM.** 2014. Genetic perturbation of the maize methylome. *Plant Cell* 26:4602-4616.
65. Belova T, Grønvold L, Kumar A, Kianian S, He X, Lillemo M, **Springer NM**, Lien S, Olsen O, Sandve S. 2014. Utilization of deletion bins to anchor and order sequences along the wheat 7B chromosome. *Theor Appl Genet.* 127(9):2029-2040.
 64. West PT, Li Q, Ji L, Eichten SR, Song J, Vaughn MW, Schmitz RJ, **Springer NM.** 2014. Genomic distribution of H3K9me2 and DNA methylation in a maize genome. *PLoS One* 9(8):e105267.
 63. Hirsch CN, Flint-Garcia SA, Beissinger TM, Eichten SR, Deshpande S, Barry K, McMullen MD, Holland JB, Buckler ES, **Springer NM**, Buell CR, de Leon N, Kaeppler SM. 2014 Insights into the effects of long-term artificial selection on seed size in maize. *Genetics* 198(1):409-21
 62. Stelpflug SC, Eichten SR, Hermanson PJ, **Springer NM**, Kaeppler SM. 2014. Consistent and heritable alterations of DNA methylation are induced by tissue culture in maize. *Genetics* 198(1):209-18.
 61. Penning BW, Sykes RW, Babcock NC, Dugard CK, Held MA, Klimek JF, Shreve JT, Fowler M, Ziebell A, Davis MF, Decker SR, Turner GB, Mosier NS, **Springer NM**, Thimmapuram J, Weil CF, McCann MC, Carpita NC. 2014. Genetic determinants for enzymatic digestion of lignocellulosic biomass are independent of those for lignin abundance in a maize recombinant inbred population. *Plant Physiology* 165(4):1475-1487.
 60. Shaefer RJ, Briskine R, **Springer NM**, Myers CL. 2014. Discovering Functional Modules Across Diverse Maize Transcriptional Datasets Using COB, The Co-expression Browser. *PLoS One* 9(6):e99193.
 59. Eichten SR, Schmitz, RS, Springer NM. 2014. Epigenetics, more than chromatin modifications and complex regulatory systems. *Plant Physiology* 165: 933-947.
 58. Li Q, Eichten SR, Hermanson PJ, **Springer NM.** 2014. Inheritance patterns and stability of DNA methylation variation in maize near-isogenic lines. *Genetics* 196(3):667-676.
 57. Thompson AM, Crants JE, Schnable PS, Yu J, Timmermans MC, **Springer NM**, Scanlon MJ, Muehlbauer GJ. 2014. Genetic Control of Maize Shoot Apical Meristem Architecture. *G3* 4: 1327-1337.
 56. Lin L, Eichten SR, Shimizu R, Petsch K, Yeh C-T, Wu W, Scanlon MJ, Yu J, Schnable PS, Timmermans MCP, **Springer NM**, Muehlbauer GJ. 2014. Genome-wide discovery and characterization of maize long non-coding RNAs (lncRNAs). *Genome Biology.* 15(2):R40.
 55. Waters AJ, Bilinski P, Eichten SR, Vaughn MW, Ross-Ibarra J, Gehring M, **Springer NM.** 2013. Comprehensive analysis of imprinted genes in maize reveals allelic variation for imprinting and limited conservation with other species. *Proc Natl Acad Sci USA* 110(48):19639-44.
 54. Eichten SR, Briskine R, Song J, Li Q, Swanson-Wagner R, Hermanson PJ, Waters AJ, Starr E, West PT, Tiffin P, Myers CL, Vaughn MW, **Springer NM.** 2013.

- Epigenetic and genetic influences on DNA methylation variation in maize populations. *Plant Cell* 25:2783-2797.
53. Sekhon RS, Briskine R, Hirsch CN, Myers CL, **Springer NM**, Buell CR, de Leon N, Kaeppler SM. 2013. Maize Gene Atlas Developed by RNA Sequencing and Comparative Evaluation of Transcriptomes Based on RNA Sequencing and Microarrays. *PLoS One* 8(4):e61005.
 52. Muñoz-Amatriaín M, Eichten SR, Wicker T, Richmond TA, Mascher M, Steuernagel B, Scholz U, Ariyadasa R, Spannagl M, Nussbaumer T, Mayer KF, Taudien S, Platzer M, Jeddelloh JA, **Springer NM**, Muehlbauer GJ, Stein N. 2013. Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. *Genome Biol.* 14(6):R65.
 51. Makarevitch I, Eichten SR, Briskine R, Danilevskaya ON, Meeley RB, Myers C, Vaughn MW, **Springer NM**. 2013. Genomic distribution of maize facultative heterochromatin marked by trimethylation of H3K27. *Plant Cell.* 25(3): 780-793.
 50. Schnable PS, **Springer NM**. 2013. Progress Toward Understanding Heterosis in Crop Plants. *Annu Rev Plant Biol.* 64:71-88.
 49. Li L, Petsch K, Shimizu R, Liu S, Xu W, Ying K, Schnable PS, Yu J, Timmermans MCP, Scanlon MJ, **Springer NM**, Muehlbauer GJ. 2013. Mendelian and non-Mendelian regulation of gene expression in maize. *PLoS Genetics* 9(1): e1003202
 48. Springer NM. 2013. Epigenetics and crop improvement. *Trends in Genetics* 29(4):241-247.
 47. Eichten SR, Vaughn MW, Hermanson PJ, **Springer NM**. 2013. Variation in DNA methylation patterns is more common among maize inbreds than among tissues. *The Plant Genome* doi: 10.3835/plantgenome2012.06.0009
 46. Swanson-Wagner RA, Briskine R, Schaefer R, Hufford MB, Ross-Ibarra J, Myers CL, Tiffin P, **Springer NM**. 2012. Reshaping of the maize transcriptome by domestication. *Proc Natl Acad Sci USA*, 109(29):11878-11883.
 45. Eichten SR, Ellis NA, Makarevitch I, Yeh C-T, Gent JI, Guo L, McGinnis KM, Zhang X, Schnable PS, Vaughn MW, Dawe RK, **Springer NM**. 2012. Spreading of heterochromatin is limited to specific families of maize retrotransposons. *PLoS Genet* 8(12): e1003127.
 44. Liu S, Ying K, Yeh C-T, Yang J, Swanson-Wagner RA, Wu W, Richmond T, Gerhardt DJ, Albert TJ, Lai J, **Springer NM**, Nettleton D, Jeddelloh JA, Schnable PS. 2012. Changes in genome content generated via segregation of non-allelic homologs. *The Plant Journal* 72:390-399.
 43. Hufford MB, Xu X, van Heerwaarden J, Pyhajarvi T, Chia J-M, Cartwright RA, Elshire RJ, Glaubitz JC, Guill KE, Kaeppler SM, Lai J, Morrell PL, Shannon LM, Song C, **Springer NM**, Swanson-Wagner RA, Tiffin P, Wang J, Zhang G, Doebley J, McMullen MD, Ware D, Buckler ES, Yang S, Ross-Ibarra J. 2012. Comparative population genomics of maize domestication and improvement. *Nature Genetics* 44(7):808-811.

42. Makarevitch I, Thompson A, Muehlbauer GJ, **Springer NM**. 2012. Brd1 gene in maize encodes a brassinosteroid C-6 oxidase. *PLoS One* 7: e30798.
41. Waters A, Makarevitch I, Eichten SR, Swanson-Wagner RA, Gehring M, Hermanson PJ, Yeh C-T, Schnable PS, Vaughn MW, **Springer NM**. 2011. Parent-of-origin effects on gene expression and DNA methylation in the maize endosperm. *Plant Cell* 23: 4221-4233.
40. Eichten SR, Swanson-Wagner RA, Schnable JC, Waters AJ, Hermanson PJ, Liu S, Yeh C-T, Jia Y, Freeling M, Schnable PS, **Springer NM**, Vaughn MW 2011. Heritable epigenetic variation among maize inbreds. *PLoS Genetics* 7: e1002372.
39. Eichten SR, Foerster J, de Leon, N, Kai, Y, Yeh C-T, Liu S, Jeddelloh J, Schnable PS, Kaeppler SM, **Springer NM** 2011. B73-Mo17 near isogenic lines (NILs) demonstrate dispersed structural variation in maize. *Plant Physiology* 156(4): 1679-1690.
38. Schnable J, **Springer NM**, Freeling M. 2011. Differentiation of the maize subgenomes by genome dominance and both ancient and ongoing gene loss. *Proc Natl Acad Sci USA* 108:4069-4074.
37. St Pierre S, **Springer NM**, Muehlbauer GJ. 2011. Density stress has minimal impacts on the barley or maize seedling transcriptome. *The Plant Genome* 4:47-54
36. Haun WJ, Hyten DL, Xu WW, Gerhardt DJ, Albert TJ, Richmond T, Jeddelloh JA, Jia G, **Springer NM**, Vance CP, Stupar RM. 2011. The composition and origins of intravarietal genomic heterogeneity in soybean. *Plant Physiology* 155: 645-655.
35. Fu Y, **Springer NM**, Ying K, Yeh C-T, Iniguez, AL, Richmond T, Wu W, Barbazuk WB, Nettleton D, Jeddelloh J, Schnable PS. 2010. High-resolution genotyping via whole genome hybridizations to microarrays containing long oligonucleotide probes. *PLoS One* 5(12):e14178.
34. Lai J, Li R, Xu X, Jin W, Xu M, Zhao H, Xiang Z, Song W, Ying K, Zhang M, Jiao Y, Ni P, Zhang J, Li D, Guo X, Ye K, Jian M, Wang B, Zheng H, Liang H, Zhang X, Wang S, Chen S, Li J, Fu Y, **Springer NM**, Yang H, Wang J, Dai J, Schnable PS, Wang J 2010. Genome-wide genetic variation among elite maize inbreds: implications for crop improvement. *Nature Genetics* 42(11):1027-1030.
33. Swanson-Wagner RA, Eichten SR, Kumari S, Tiffin P, Stein JC, Ware D, **Springer NM**. 2010. Pervasive gene content variation and copy number variation in both maize and its undomesticated progenitor. *Genome Research* 20(12):1689-99.
32. **Springer NM**. 2010. Shaping a better rice plant. *Nat Genet* 42(6); 475-476.
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29. Fu Y, **Springer NM**, Gerhardt D, Ying K, Yeh C-T, Wei W, Swanson-Wagner R, D'Ascenzo M, Millard T, Freeberg L, Aoyama N, Kitzman J, Burgess D, Richmond T, Albert T, Barbazuk WB, Jeddelloh J, Schnable PS. 2010. Repeat

- subtraction-mediated sequence capture from a complex genome. *Plant Journal* 62(5):898-909.
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 27. Schnable PS, D Ware, RS Fulton, JC Stein, F Wei, S Pasternak, C Liang, J Zhang, L Fulton, TA Graves, P Minx, AD Reily, L Courtney, SS Kruchowski, C Tomlinson, C Strong, K Delehaunty, C Fronick, W Courtney, SM Rock, E Belter, F Du, K Kim, RM Abbott, M Cotton, A Levy, P Marchetto, K Ochoa, SM Jackson, B Gillam, W Chen, L Yan, J Higginbotham, M Cardenas, J Waligorski, E Applebaum, L Phelps, J Falcone, K Kanchi, T Thane, A Scimone, N Thane, J Henke, T Wang, J Ruppert, N Shah, K Rotter, J Hodges, E Ingenthron, M Cordes, S Kohlberg, J Sgro, B Delgado, K Mead, A Chinwalla, S Leonard, K Crouse, K Collura, D Kudrna, J Currie, R He, A Angelova, S Rajasekar, T Mueller, R Lomeli, G Scara, A Ko, K Delaney, M Wissotski, G Lopez, D Campos, M Braidotti, E Ashley, W Golser, H Kim, S Lee, J Lin, Z Dujmic, W Kim, J Talag, A Zuccolo, C Fan, A Sebastian, M Kramer, L Spiegel, L Nascimento, T Zutavern, B Miller, C Ambroise, S Muller, W Spooner, A Narechania, L Ren, S Wei, S Kumari, B Faga, M Levy, L McMahan, PV Buren, MW Vaughn, K Ying, CT Yeh, SJ Emrich, Y Jia, A Kalyanaraman, AP Hsia, WB Barbazuk, RS Baucom, TP Brutnell, NC Carpita, C Chaparro, J Chia, J Deragon, JC Estill, Y Fu, JA Jeddelloh, Y Han, H Lee, P Li, DR Lisch, S Liu, Z Liu, DH Nagel, MC McCann, P SanMiguel, AM Myers, DS Nettleton, J Nguyen, BW Penning, L Ponnala, KL Schneider, DC Schwartz, A Sharma, C Soderlund, **NM Springer**, Q Sun, H Wang, M Waterman, R Westerman, TK Wolfgruber, L Yang, Y Yu, L Zhang, S Zhou, Q Zhu, JL Bennetzen, RK Dawe, J Jiang, N Jiang, GG Presting, SR Wessler, S Aluru, RA Martienssen, SW Clifton, WR McCombie, RA Wing, RK Wilson. 2009. The B73 maize genome: complexity, diversity and dynamics. *Science*, 326(5956): 1112-1115.
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 24. Flint-Garcia SA, Buckler ES, Tiffin P, Ersoz E, **Springer NM**. 2009. Heterosis is prevalent for multiple traits in diverse maize germplasm. *PLoS One* 4:e7433.
 23. **Springer NM**. 2009. Small RNAs: how seeds remember to obey their mother. *Curr Biol.* 19:R649-51.
 22. Johnson KJ, **Springer NM**, Bielinsky AK, Largaespada DA, Ross JA. 2009. Developmental origins of cancer. *Cancer Res.* 69:6375-6377.
 21. Gray J, Bevan M, Brutnell T, Buell CR, Cone K, Hake S, Jackson D, Kellogg E, Lawrence C, McCouch S, Mockler T, Moose S, Paterson A, Peterson T, Rokhsar D, Souza GM, **Springer N**, Stein N, Timmermans M, Wang GL, Grotewold E. 2009. A

- recommendation for naming transcription factor proteins in the grasses. *Plant Physiol.* 149:4-6.
20. Haun WJ, Danilevskaya O, Meeley RM, **Springer NM**. 2009. Disruption of Imprinting by *Mu* Transposon Insertions in the 5' Proximal Regions of the *Zea mays Mez1* Locus. *Genetics* 181:1229-1237.
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 18. Haun WJ, **Springer NM**. 2008. Maternal and paternal alleles exhibit differential histone methylation and acetylation at the maize imprinted genes. *The Plant Journal* 56: 903-912
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 16. Makarevitch I, Phillips RL, **Springer NM**. 2008. Profiling expression changes caused by a segmental aneuploid in maize. *BMC Genomics* 9:7. 15. Stupar RM, Hermanson PJ, **Springer NM**. 2007. Nonadditive expression and parent-of-origin effects identified by microarray and allele-specific expression profiling of maize endosperm. *Plant Physiology* 145: 411-425.
 14. **Springer NM**, Stupar RM. 2007. Allele-specific expression analysis reveals prevalent cis-acting variation and parent-of-origin affects on gene expression in maize. *Plant Cell* 19: 2391-2402.
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 12. McGinnis K, Murphy N, Carlson AR, Akula A, Akula C, Basinger H, Carlson M, Hermanson PJ, Kovacevic N, McGill MA, Seshadri V, Yoyokie J, Cone KC, Kaeppler HF, Kaeppler SM, **Springer NM**. 2007. Assessing the efficiency of RNA interference for maize functional genomics. *Plant Physiology* 143:1441-51.
 11. **Springer NM**, Stupar RM. 2007. Allelic variation and heterosis in maize: How do two halves make more than a whole? *Gen. Res.* 17:264-75.
 10. Haun WJ, Laouelle-Duprat S, O'Connell MJ, Spillane C, Grossniklaus U, Phillips AR, Kaeppler SM, **Springer NM**. 2007. Genomic imprinting, methylation and molecular evolution of maize *Enhancer of zeste (Mez)* homologs. *The Plant Journal* 49: 325-337.
 9. Stupar RM, **Springer NM**. 2006. Cis-transcriptional variation in maize inbred lines B73 and Mo17 leads to additive expression patterns in the F1 hybrid. *Genetics* 173:2199-2210.
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 4. **Springer NM**, Napoli CA, Selinger DA, Pandey R, Cone KC, Chandler VL, Kaeppler HF, Kaeppler SM. 2003. Comparative Analysis of SET Domain Proteins in Maize and Arabidopsis Reveals Multiple Duplications Preceding the Divergence of Monocots and Dicots. Plant Physiol. 132:907-925
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BOOK CHAPTERS:

6. **Springer NM**, Kaeppler SM. 2008. Epigenetics: The Second Genetic Code. In *Advances in Agronomy: Volume 100* (Ed. Donald Sparks) Academic Press. San Diego, CA.
5. Hollick J, **Springer NM**. 2008. Paramutation, imprinting and epigenomics in maize. In *Epigenomics* (Eds. Martienssen R, Greally J, Anne Ferguson-Smith A) Springer-Verlag. New York
4. **Springer NM**, Gutierrez-Marcos JF. 2008. Imprinting in maize. In *The Maize handbook*. (Eds. Hake S, Bennetzen J) Springer-Verlag. New York.
3. Grotewold E, **Springer NM**. 2008. Decoding the transcriptional hardwiring of the plant genome. In *The Annual Plant Biology Review – Systems Biology* (Eds. Coruzzi G, Gutierrez R). Blackwell, Oxford UK.
2. **Springer NM**. 2007. Isolation of DNA from plants. In *Genetic Variation: A Laboratory Manual* (ed. Michael Weiner) Cold Spring Harbor Press, Cold Spring Harbor New York.
1. Kaeppler SM, **Springer NM**. 2002. Silence of the genes: Epigenetic gene silencing as a tool in genetic research and cultivar development. Proceedings of the 56th Annual Corn and Sorghum Research Conference.

INVITED TALKS:

- 2017 (7) Phenome 2017; Maize Genetics Conference Plenary speaker; Cornell University; Malaysian Palm Oil conference; NYU Plant Genome Evolution workshop; CROPS, Dow
- 2016 (4) Keystone Conference on Plant Epigenetics; IPG Stadler symposium on Heterosis; FFAR Phenomics Convening Event; Inari Agriculture
- 2015 (8) Plant and Animal Genome Conference – Maize workshop; CSIRO – Black Mountain; Australian National University; University of Perth; Donald Danforth Plant Sciences Center; University of Missouri-Columbia; ASPB “Epigenetic Variation” Workshop invited speaker; University of Houston
- 2014 (11) Plant and Animal Genome: Genomics of tissue culture workshop; Plant and Animal Genome: Evolution of Genome size workshop; Translational Genomics of Cereals (Vienna); Gregor Mendel Institute (Vienna); University of Florida; Dupont-Pioneer; Ohio State University Functional Genomics Workshop; Plant Genomics Congress (Saint Louis); Syngenta (RTP North Carolina); Monsanto (Saint Louis); Cold Spring Harbor Banbury Epigenetics meeting; North Carolina Plant Molecular Biology Consortium
- 2013 (13) Plant and Animal Genome Conference, Michigan State University, Maize Corn Breeding Conference (NCCC-167), University of Georgia, Dupont Pioneer, University of Guelph (Canada), Society of Molecular Biology and Evolution, Syngenta, Switchgrass II conference; University of Wisconsin Plant Breeding Symposium, China Agriculture University, Beijing, Huazhong Agricultural University (Wuhan), UC-Davis
- 2012 (10) Plant and Animal Genome Conference, Monsanto Research Fellows symposia, Guelph University, Donald Danforth Plant Sciences Center, Plant Breeding symposium at UC-Davis, Purdue Symposium on Statistics, Italian Society of Agricultural Genetics, University of Minnesota, Brigham Young University, NSF Plant Genome Awardee meeting
- 2011 (5) Plant and Animal Genome Conference, NCCC-167 Corn breeding conference, Cold Spring Harbor Banbury conference, University of Arizona, BASF
- 2010 (3) University of Georgia; Maize Genetics Conference; University of Minnesota Phillips symposium
- 2009 (5) University of Guelph, PAG, IPMB Conference, Amherst Epigenetic Symposia, Developmental origins of cancer symposia, Stuttgart International heterosis conference
- 2008 (5) Dow Agrosiences; Maize Genetics Conference; Illinois Corn Breeders School; Monsanto; International Plant Epigenome Initiative
- 2007 (3) University of Wisconsin Plant Breeding and Genetics program; Minnesota State University at Mankato Biology Program; Hamline
- 2006 (1) Ohio State University Plant Molecular Biology Program
- 2005 (2) Iowa State University Genetics program; University of Minnesota Applied Plant Sciences program

- 2004 (4) Texas A&M University genotyping symposium; University of Missouri-Columbia Plant Genetics program; University of Minnesota Plant Biology program; University of Minnesota Cargill seminar series
- 2003 (2) Purdue University; Donald Danforth Plant Sciences center
- 2001 (1) Southeast Missouri State University

MEMBERSHIPS AND COMMITTEES:

American Society of Plant Biologists

Genetics Society of America

American Association for the Advancement of Science

Maize Genetics Executive committee (2011-2016; Chair – 2015-2016)

NCCC167 (USDA Corn Breeding research group) representative

Maize Genetics Conference steering committee (2011-2013)

Corn Breeding Executive Committee (2013-present)

American Society of Plant Biology Science Policy Committee (2013-2016; Chair: 2016-present)

Genomes 2 Fields Executive Committee member (2013-present)

CONFERENCES ORGANIZED:

Transformation-enabled genomic research in crop plants. Tampa Bay FL; Nov 16-17, 2015 (co-organizer)

Keystone Symposia “Plant Epigenetics: From Genotype to Phenotype” Taos NM; Feb 15-18, 2016 (co-organizer)

UNIVERSITY SERVICE:

Sept 2003-Jan 2004	Plant Biology Strategic Planning committee
Sept 2004-May 2006	Plant Biology colloquium committee (chair)
November 2004-Sept. 2005	Developmental Biology Symposium Steering committee
Sept 2005-Oct 2009	Biosciences facilities committee
November 2005-Oct 2009	Scientific Data Management Lab (SDML) steering committee
August 2006 – 2008	Plant Sciences Cluster steering committee
September 2006 – 2008	Plant Biological Sciences graduate program steering committee
March 2008-August 2009	MPGI steering committee
September 2008-May 2009	PBIO Evolutionary Biology Search Committee
September 2008-May 2009	PBIO Computation Biology Search Committee
December 2008-Oct 2012	University Committee on Committees
August 2009-August 2014	Director, Microbial and Plant Genomics Institute
September 2010-present	RISS informatics analysis search committee
October 2010-Sept 2012	PBS admissions committee
October 2010-Sept 2012	CBS Core Curriculum committee
March 2011- May 2011	PBIO-CFANS relationship committee
February 2013 – 2015	RISS Oversight Committee chair
June 2012-May 2013	Chair of Genome Variation cluster hire search committee
October 2012-May 2013	Agronomy Dept; Maize translational genetics search committee
Sept 2013-present	Documentation, promotion, tenure committee

August 2015-present	PBS Steering Committee
August 2015-present	Plant Biology Departmental awards committee
August 2016-present	PBS Graduate program awards committee

JOURNALS AND PROPOSAL REVIEWS:

Associate editor for PLoS Genetics (08/11-present)

Editorial Board for Genetics (2016-present)

Monitoring editor for Plant Physiology (06/08 – 12/13)

Served as peer reviewer for >200 manuscripts at BMC Genomics, Crop Science, FEBS, Genetics, Genome Research, Journal of Biological Chemistry, Journal of Heredity, Nature Genetics, Nature Reviews Genetics, Nucleic Acids Research, Plant Cell, Plant Cell and Physiology, Plant Molecular Biology, Plant Physiology, Planta, Plant Genome, PLoS Biology, PLoS Genetics, PNAS, The Plant Journal, Nature, Nature Plants, Nature Biotechnology, Science, and Trends in Plant Science

Served as peer reviewer for BARD-ISIS (3), NSF (>20), USDA (>20), ERA-NET Plant Genomics (1), CDRF (1)

Member of USDA Plant Genetic Mechanisms (3), NSF Plant Genome (3), NSF Eukaryotic Genetics grant and USDA Physiology of Crop plants grant panels

TRAINING:

Graduate students: Jaclyn Noshay (current), Sara Tirado (current) Amanda Waters (2016), Steve Eichten (PhD 2013), Moumita Chakravarty (MS 2010), William Haun (PhD 2008); Summer St. Pierre (MS 2009)

Post-doctoral research scientists: Soma Narsimhulu (2004), Robert Stupar (2005-2008), Irina Makarevitch (2006-2007), Ruth Swanson-Wagner (2009-2010); Qing Li (2013-2016), Cory Hirsch (2013-2015). Tara Enders (current), Peng Zhou (current), Sarah Anderson (current), Peter Crisp (current)

Graduate student committees: Lorien Radmer (APS), Matt Walch (APS), Brent Hulke (APS), Veronica Justen (APS), Adrianna Telias (APS), Candida Cabral (APS), Anna Selmecki (MDCB&G), Carrie Eberle (PBS), Alexander Kahler (APS), Carol Powers (APS), Daniel Griffin (PBS), Stephanie Westcot (MCDB&G), Nelson Garcia (PBS), Ye Sun (PBS), Alexander Kahler (APS), Veronica Justen (APS), Nandita Vishwanathan (CE), Rob Schaefer (BICB), Addie Thompson (APS), Darren Abbey (MCDB&G), Roman Briskine (CS), Chris Schaefer (APS), Yuan Xu (PBS), Alison Haaning (PBS), Eli Krumholz (PBS)