

Nathan Michael Springer

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D.O.B. 04/20/1976

RANK:

Presidential McKnight Endowed Professor in Plant Biology

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” at the University of Wisconsin-Madison (Advisor – Shawn Kaeppler)
- 7/2000 - 9/2002: Post-doctoral research associate on N.S.F. Grant “Functional genomics of chromatin global control of plant gene expression” at the University of Wisconsin-Madison (Advisor – Shawn Kaeppler)
- 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:

- 2020 American Association for the Advancement of Science (AAAS) Fellow
- 2019 Charles Albert Schull Award – American Society of Plant Biologists

2016 Emerging Leaders in Plant Sciences Award - University of Minnesota
 2016 Presidential McKnight Endowed Professor in Plant Biology
 2007 Southeast Missouri State University Young Alumni Merit Award
 2002 National Science Foundation Plant Genome Young Investigator
 1997 U.S.D.A. National Needs Fellowship, University of Minnesota
 1996 Phi Kappa Phi
 1994 National Merit Scholarship

TEACHING EXPERIENCE:

Biol4003 Genetics (U of Minnesota): 2006-present, spring semesters (~100 students/semester)
 Biol3020 Molecular Biology and Society (U of Minnesota), co-taught 2018, 2020
 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:

08/19 – 07/23 (\$4,109,406) National Science Foundation “Research-PGR: Uncovering the role of transposons in maize variation”
 06/18 – 05/20 (\$299,967) National Science Foundation “EAGER: Development of tools for probing the role of DNA methylation in maize.”
 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.” (CoPI)
 07/16 - 06/20 (\$2,677,672) National Science Foundation “Discovery and evaluation of inbred-specific and hybrid-specific regulatory modules” (CoPI)
 12/15 – 11/18 (\$408,000) USDA – NIFA “Understanding the role of transposable elements in maize abiotic stress response”
 03/15 - 03/19 (\$5,569,161) National Science Foundation “Enabling Cold Tolerant Maize Using Genomic and Machine Vision Phenomic Approaches” (CoPI)
 10/12 – 09/16 (\$3,424,556) National Science Foundation “Causes and consequences of epigenetic variation 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)
 04/11 – 03/14 (\$499,538) USDA – NIFA “Environmentally Induced Epigenetic Changes in Maize”
 2/10 – 03/13 (\$1,678,620) National Science Foundation “GEPR Maize epigenomic variation.”
 07/07-06/09 (\$126,444) Institute of the environment – IREE Discovery Grant. “Survey of genetic variation for response to density stress.”

- 5/06-4/07. (\$14,300) Minnesota Agriculture Experiment Station. "Dynamics of DNA replication in endosperm."
- 9/04-8/08. (\$597,163) National Science Foundation. "Maize functional genomics of chromatin." (Co-PI)
- 9/04-8/05. (\$30,301) U of Minnesota Grant-in-aid. "Identification of cis-acting elements controlling imprinting."
- 9/02-9/05. (\$450,000) National Science Foundation. "Assessment of the utility of oligonucleotide arrays."

PUBLICATIONS:

143. Zhou P, Enders TA, Myers ZA, Magnusson E, Crisp PA, Noshay JM, Gomez-Cano F, Liang Z, Grotewold E, Greenham K, **Springer NM**. 2022. Prediction of conserved and variable heat and cold stress response in maize using cis-regulatory information. *Plant Cell* 34(1):514-534. doi: 10.1093/plcell/koab267.
142. Noshay JM, Liang Z, Zhou P, Crisp PA, Marand AP, Hirsch CN, Schmitz RJ, **Springer NM**. 2021. Stability of DNA methylation and chromatin accessibility in structurally diverse maize genomes. *G3 (Bethesda)*.11(8):jkab190. doi: 10.1093/g3journal/jkab190.
141. Stitzer MC, Anderson SN, **Springer NM**, Ross-Ibarra J. 2021. The genomic ecosystem of transposable elements in maize. *PLoS Genet*.17(10):e1009768. doi: 10.1371/journal.pgen.1009768.
140. Qiu Y, O'Connor CH, Della Coletta R, Renk JS, Monnahan PJ, Noshay JM, Liang Z, Gilbert A, Anderson SN, McGaugh SE, **Springer NM**, Hirsch CN. 2021. Whole-genome variation of transposable element insertions in a maize diversity panel. *G3 (Bethesda)*.11(10):jkab238. doi: 10.1093/g3journal/jkab238.
139. Birdseye D, de Boer LA, Bai H, Zhou P, Shen Z, Schmelz EA, **Springer NM**, Briggs SP. 2021. Plant height heterosis is quantitatively associated with expression levels of plastid ribosomal proteins. *Proc Natl Acad Sci U S A*.118(47):e2109332118. doi: 10.1073/pnas.2109332118.
138. Lin G, He C, Zheng J, Koo DH, Le H, Zheng H, Tamang TM, Lin J, Liu Y, Zhao M, Hao Y, McFrand F, Wang B, Qin Y, Tang H, McCarty DR, Wei H, Cho MJ, Park S, Kaeppler H, Kaeppler SM, Liu Y, **Springer N**, Schnable PS, Wang G, White FF, Liu S. 2021. Chromosome-level genome assembly of a regenerable maize inbred line A188. *Genome Biol*. 22(1):175. doi: 10.1186/s13059-021-02396-x.
137. Li M, Noshay JM, Dong X, **Springer NM**, Li Q. 2021. A capture-based assay for detection and characterization of transposon polymorphisms in maize. *G3 (Bethesda)*. jkab138. doi: 10.1093/g3journal/jkab138
136. Rogers AR, Dunne JC, Romay C, Bohn M, Buckler ES, Ciampitti IA, Edwards J, Ertl D, Flint-Garcia S, Gore MA, Graham C, Hirsch CN, Hood E, Hooker DC, Knoll J, Lee EC, Lorenz A, Lynch JP, McKay J, Moose SP, Murray SC, Nelson R, Rocheford T, Schnable JC, Schnable PS, Sekhon R, Singh M, Smith M, **Springer N**, Thelen K, Thomison P, Thompson A, Tuinstra M, Wallace J, Wisser RJ, Xu W, Gilmour AR, Kaeppler SM, De Leon N, Holland JB. (2021) The importance of dominance and genotype-by-environment interactions on grain yield variation in a large-scale

- public cooperative maize experiment. *G3 (Bethesda)*. 11(2):jkaa050. doi: 10.1093/g3journal/jkaa050.135.
135. Jarquin D, de Leon N, Romay C, Bohn M, Buckler ES, Ciampitti I, Edwards J, Ertl D, Flint-Garcia S, Gore MA, Graham C, Hirsch CN, Holland JB, Hooker D, Kaeppler SM, Knoll J, Lee EC, Lawrence-Dill CJ, Lynch JP, Moose SP, Murray SC, Nelson R, Rocheford T, Schnable JC, Schnable PS, Smith M, **Springer N**, Thomison P, Tuinstra M, Wisser RJ, Xu W, Yu J, Lorenz A. (2021) Utility of Climatic Information via Combining Ability Models to Improve Genomic Prediction for Yield Within the Genomes to Fields Maize Project. *Front Genet*. 11:592769. doi: 10.3389/fgene.2020.592769.
 134. Anderson SN, Zhou P, Higgins K, Brandvain Y, **Springer NM**. (2021) Widespread imprinting of transposable elements and variable genes in the maize endosperm. *PLoS Genet*. 17(4):e1009491. doi: 10.1371/journal.pgen.1009491.
 133. Long J, Liu J, Xia A, Springer NM, He Y. (2021) Maize Decrease in DNA methylation 1 targets RNA-directed DNA methylation on active chromatin. *Plant Cell*. 33(7):2183-2196. doi: 10.1093/plcell/koab098.
 132. Liang Z, Anderson SN, Noshay JM, Crisp PA, Enders TA, **Springer NM** (2021) Genetic and epigenetic contributions to variation in transposable element expression responses to abiotic stress in maize. *Plant Physiol*. 186(1):420-33. doi: 10.1093/plphys/kiab073.
 131. Noshay JM, **Springer NM** (2021) Stories that can't be told by SNPs; epigenetic variation in plant populations. *Curr Opin Plant Biol*. 61:101989. doi: 10.1016/j.pbi.2020.101989
 130. Tirado SB, St Dennis S, Enders TA, **Springer NM** (2021) Utilizing spatial variability from hyperspectral imaging to assess variation in maize seedlings. *The Plant Phenome Journal* 4 (1), e20013. <https://doi.org/10.1002/ppj2.20013>
 129. Tirado, Sara B., Candice N. Hirsch, and **Nathan M. Springer**. (2021) Utilizing Temporal Measurements from UAVs to Assess Root Lodging in Maize and Its Impact on Productivity. *Field Crops Research*, 262, 108014. <https://doi.org/10.1016/j.fcr.2020.108014>.
 128. Noshay JM, Marand AP, Anderson SN, Zhou P, Mejia Guerra MK, Lu Z, O'Connor CH, Crisp PA, Hirsch CN, Schmitz RJ, **Springer NM**. (2021) Assessing the regulatory potential of transposable elements using chromatin accessibility profiles of maize transposons. *Genetics* 217(1):1-13. doi: 10.1093/genetics/iyaa003.
 127. Li Z, Zhou P, Della Coletta R, Zhang T, Brohammer AB, Vaillancourt B, Lipzen A, Daum C, Barry K, de Leon N, Hirsch CD, Buell CR, Kaeppler SM, **Springer NM**, Hirsch CN (2021) Single-parent expression drives dynamic gene expression complementation in maize hybrids. *Plant J*. 105(1):93-107. doi: 10.1111/tpj.15042.
 126. Zhang M, Ma X, Wang C, Li Q, Meyers BC, Springer NM, Walbot V. (2021) CHH DNA methylation increases at 24-*PHAS* loci depend on 24-nt phasiRNAs in maize meiotic anthers. *New Phytol*. 229(5):2984-2997. doi: 10.1111/nph.17060.
 125. Xu G, Lyu J, Li Q, Liu H, Wang D, Zhang M, **Springer NM**, Ross-Ibarra J, Yang J. (2020) Adaptive Evolution of DNA Methylation Reshaped Gene Regulation in Maize. *Nat Commun*. 11(1):5539. doi: 10.1038/s41467-020-19333-4.

124. Crisp PA, Marand AP, Noshay JM, Zhou P, Lu Z, Schmitz RJ, **Springer NM** (2020) Stable unmethylated DNA demarcates expressed genes and their cis-regulatory space in plant genomes. *Proc Natl Acad Sci U S A.* 117(38):23991-24000. doi: 10.1073/pnas.2010250117.
123. Weiss T, Wang C, Kang X, Zhao H, Elena Gamo M, Starker CG, Crisp PA, Zhou P, **Springer NM**, Voytas DF, Zhang F. (2020) Optimization of multiplexed CRISPR/Cas9 system for highly efficient genome editing in *Setaria viridis*. *Plant J.*104(3):828-838. doi: 10.1111/tpj.14949
122. Tirado SB, Hirsch CN, **Springer NM** (2020) UAV Based Imaging Platform for Monitoring Maize Growth Throughout Development *Plant Direct.* 4(6):e00230. doi: 10.1002/pld3.230.
121. Li Z, Tirado SB, Kadam DC, Coffey L, Miller ND, Spalding EP, Lorenz AJ, de Leon N, Kaeppler SM, Schnable PS, **Springer NM**, Hirsch CN (2020) Characterizing allele-by-environment interactions using maize introgression lines. *Theor Appl Genet.* 133 (10): 2761-2773. doi: 10.1007/s00122-020-03630-z
120. McFarland BA, AlKhalifah N, Bohn M, Bubert J, Buckler ES, Ciampitti I, Edwards J, Ertl D, Gage JL, Falcon CM, Flint-Garcia S, Gore MA, Graham C, Hirsch CN, Holland JB, Hood E, Hooker D, Jarquin D, Kaeppler SM, Knoll J, Kruger G, Lauter N, Lee EC, Lima DC, Lorenz A, Lynch JP, McKay J, Miller ND, Moose SP, Murray SC, Nelson R, Poudyal C, Rocheford T, Rodriguez O, Romay MC, Schnable JC, Schnable PS, Scully B, Sekhon R, Silverstein K, Singh M, Smith M, Spalding EP, **Springer N**, Thelen K, Thomison P, Tuinstra M, Wallace J, Walls R, Wills D, Wisser RJ, Xu W, Yeh CT, de Leon N. (2020) Maize genomes to fields (G2F): 2014-2017 field seasons: genotype, phenotype, climatic, soil, and inbred ear image datasets. *BMC Res Notes.* 13(1):71. doi: 10.1186/s13104-020-4922-8.
119. Zhou P, Li Z, Magnusson E, Gomez Cano F, Crisp PA, Noshay JM, Grotewold E, Hirsch CN, Briggs SP, **Springer NM**. (2020) Meta Gene Regulatory Networks in Maize Highlight Functionally Relevant Regulatory Interactions. *Plant Cell* 32(5):1377-1396. doi: 10.1105/tpc.20.00080.
118. Monnahan PJ, Michno J-M, O'Connor CH, Brohammer AB, **Springer NM**, McGaugh SE, Hirsch CN (2020) Using multiple reference genomes to identify and resolve annotation inconsistencies. *BMC Genomics.* 21(1):281. doi: 10.1186/s12864-020-6696-8.
117. Crisp PA, Hammond R, Zhou P, Vaillancourt B, Lipzen A, Daum C, Barry K, de Leon N, Robin Buell C, Kaeppler SM, Meyers BC, Hirsch CN, **Springer NM** (2020) Variation and inheritance of small RNAs in maize inbreds and F1 hybrids. *Plant Physiol.* 182(1): 318-331. doi: 10.1104/pp.19.00817.
116. Ricci WA, Lu Z, Ji L, Marand AP, Ethridge CL, Murphy NG, Noshay JM, Galli M, Mejía-Guerra MK, Colomé-Tatché M, Johannes F, Rowley MJ, Corces VG, Zhai J, Scanlon MJ, Buckler ES, Gallavotti A, **Springer NM**, Schmitz RJ, Zhang X. (2019) Widespread long-range cis-regulatory elements in the maize genome. *Nat Plants* 5(12): 1237-1249. doi: 10.1038/s41477-019-0547-0
115. Xu J, Chen G, Hermanson PJ, Xu Q, Sun C, Chen W, Kan Q, Li M, Crisp PA, Yan J, Li L, **Springer NM**, Li Q. (2019) Population-level analysis reveals the widespread

- occurrence and phenotypic consequence of DNA methylation variation not tagged by genetic variation in maize. *Genome Biol.* 20(1):243. doi: 10.1186/s13059-019-1859-0.
114. Sartor RC, Noshay J, **Springer NM**, Briggs SP. (2019) Identification of the expressome by machine learning on omics data. *Proc Natl Acad Sci U S A.* 116(36):18119-18125. doi: 10.1073/pnas.1813645116
 113. Anderson SN, Stitzer MC, Zhou P, Ross-Ibarra J, Hirsch CD, **Springer NM** (2019) Dynamic patterns of transcript abundance of transposable element families in maize. *G3 (Bethesda).* 9(11):3673-3682. doi: 10.1534/g3.119.400431.
 112. Anderson SN, Stitzer MC, Brohammer AB, Zhou P, Noshay JM, O'Connor CH, Hirsch CD, Ross-Ibarra J, Hirsch CN, **Springer NM**. (2019) Transposable elements contribute to dynamic genome content in maize. *Plant J.* 100(5):1052-1065. doi: 10.1111/tpj.14489.
 111. **Springer NM**, De Leon N, Grotewold E (2019) Challenges of Translating Regulatory Information Into Agronomic Improvements. *Trends in Plant Sci.* 24(12): 1075-1082. doi: 10.1016/j.tplants.2019.07.004
 110. Noshay JN, Anderson SA, Zhou P, Ji L, Ricci B, Lu Z, Stitzer MC, Crisp PA, Hirsch CN, Zhang X, Schmitz RJ, **Springer NM** (2019) Monitoring the interplay between transposable element families and DNA methylation in maize. *PLoS Genet.* 15(9):e1008291. doi: 10.1371/journal.pgen.1008291.
 109. Xue W, Anderson SN, Wang X, Yang L, Crisp PA, Li Q, Noshay J, Albert PS, Birchler JA, Bilinski P, Stitzer MC, Ross-Ibarra J, Flint-Garcia S, Chen X, **Springer NM**, Doebley JF (2019) Hybrid decay: a transgenerational epigenetic decline in vigor and viability triggered in backcross populations of teosinte with maize. *Genetics* 213(1):143-160. doi: 10.1534/genetics.119.302378.
 108. Tran TM, McCubbin TJ, Bihmidine S, Julius BT, Baker RF, Schauflinger M, Weil C, **Springer N**, Chomet P, Wagner R, Woessner J, Grote K, Peevers J, Slewinski TL, Braun DM. (2019) Maize Carbohydrate Partitioning Defective33 Encodes an MCTP Protein and Functions in Sucrose Export from Leaves. *Mol Plant.* 12(9):1278-1293. doi: 10.1016/j.molp.2019.05.001
 107. Lawrence-Dill CJ, Schnable PS, **Springer NM**. (2019) Idea Factory: the Maize Genomes to Fields Initiative. *Crop Sci.* 59: 1406–1410.
 106. Crisp PA, Noshay JM, Anderson SN, **Springer NM**. (2019) Opportunities to Use DNA Methylation to Distil Functional Elements in Large Crop Genomes. *Mol Plant.* 12(3):282-284. doi: 10.1016/j.molp.2019.02.006.
 105. Wang J, Li X, Do Kim K, Scanlon MJ, Jackson SA, **Springer NM**, Yu J. (2019) Genome-wide nucleotide patterns and potential mechanisms of genome divergence following domestication in maize and soybean. *Genome Biol.* 20(1):74. doi: 10.1186/s13059-019-1683-6.
 104. Enders T, St Dennis S, Oakland J, Callen S, Gehan M, Miller N, Spalding E, **Springer NM**, Hirsch C. (2019) Classifying cold stress responses of inbred maize seedlings using RGB imaging. *Plant Direct.* 3 (1): e00104. doi.org/10.1002/pld3.104

103. Zhou P, Hirsch CN, Briggs SP, **Springer NM**. (2019) Dynamic patterns of gene expression additivity and regulatory variation throughout maize development. *Mol Plant*. 12(3):410-425. doi: 10.1016/j.molp.2018.12.015
102. AlKhalifah N, Campbell DA, Falcon CM, Gardiner JM, Miller ND, Romay MC, Walls R, Walton R, Yeh CT, Bohn M, Bubert J, Buckler ES, Ciampitti I, Flint-Garcia S, Gore MA, Graham C, Hirsch C, Holland JB, Hooker D, Kaeppler S, Knoll J, Lauter N, Lee EC, Lorenz A, Lynch JP, Moose SP, Murray SC, Nelson R, Rocheford T, Rodriguez O, Schnable JC, Scully B, Smith M, **Springer N**, Thomison P, Tuinstra M, Wisser RJ, Xu W, Ertl D, Schnable PS, De Leon N, Spalding EP, Edwards J, Lawrence-Dill CJ. (2018) Maize Genomes to Fields: 2014 and 2015 field season genotype, phenotype, environment, and inbred ear image datasets. *BMC Res Notes*. 2018 Jul 9;11(1):452. doi: 10.1186/s13104-018-3508-1.
101. Liu S, Schnable JC, Ott A, Eddy Yeh CT, **Springer NM**, Yu J, Muehlbauer G, Timmermans MCP, Scanlon MJ, Schnable PS. (2018) Intragenic Meiotic Crossovers Generate Novel Alleles with Transgressive Expression Levels. *Mol Biol Evol*. 35(11):2762-2772. doi: 10.1093/molbev/msy174.
100. **Springer NM**, Anderson SN, Andorf CM, Ahern KR, Bai F, Barad O, Barbazuk WB, Bass HW, Baruch K, Ben-Zvi G, Buckler ES, Bukowski R, Campbell MS, Cannon EKS, Chomet P, Dawe RK, Davenport R, Dooner HK, Du LH, Du C, Easterling KA, Gault C, Guan JC, Hunter CT, Jander G, Jiao Y, Koch KE, Kol G, Kollner T, Kudo T, Li Q, Lu F, Mayfield-Jones D, Mei W, McCarty DR, Noshay J, Portwood II J, Ronen G, Settles AM, Shem-Tov D, Shi J, Soifer I, Stein JC, Suzuki M, Vera DL, Vollbrecht E, Vrebalov JT, Ware D, Wei S, Wimalanathan K, Woodhouse MR, Xiong W, Brutnell TP (2018) The W22 genome: a foundation for maize functional genomics and transposon biology. *Nature Genetics* 50(9):1282-1288. doi: 10.1038/s41588-018-0158-0.
99. Anderson SN, **Springer NM**. (2018) Potential roles for transposable elements in creating imprinted expression. *Curr Opin Genet Dev*. 49:8-14. doi: 10.1016/j.gde.2018.01.008.
98. Hirsch CN, **Springer NM**. (2018) Weeding out bad alleles. *Nat Plants*. 4(4):193-194. doi: 10.1038/s41477-018-0133-x
97. Han Z, Crisp PA, Stelpflug SA, Kaeppler SM, Li Q, **Springer NM**. (2018) Heritable epigenomic changes to the maize methylome resulting from tissue culture. *Genetics*, 209(4):983-995.
96. Anderson SN, Zynda G, Song J, Han Z, Vaughn M, Li Q, **Springer NM**. (2017) Subtle perturbations of the maize methylome reveal genes and transposons silenced by DNA methylation. *G3 (Bethesda)* 8(6):1921-1932.
95. Li Z, Coffey L, Garfin J, Miller ND, White MR, Spalding EP, de Leon N, Kaeppler SM, Schnable PS, **Springer NM**, Hirsch CN. (2018) Genotype-by-environment interactions affecting heterosis in maize. *PLoS One*. 13(1):e0191321
94. Li Q, Hermanson PJ, **Springer NM**. (2018) Detection of DNA Methylation by Whole-Genome Bisulfite Sequencing. *Methods Mol Biol*. 1676:185-196. doi: 10.1007/978-1-4939-7315-6_11.

93. Brohammer A, Kono T, **Springer NM**, McGaugh S, Hirsch CN. (2018). Limited role of differential fractionation in genome content variation and function in maize (*Zea mays L.*) inbred lines. *The Plant Journal*. 93(1):131-141. doi: 10.1111/tpj.13765.
92. Gage JL, Jarquin D, Romay C, Lorenz A, Buckler ES, Kaeppler S, Alkhalifah N, Bohn M, Campbell DA, Edwards J, Ertl D, Flint-Garcia S, Gardiner J, Good B, Hirsch CN, Holland J, Hooker DC, Knoll J, Kolkman J, Kruger G, Lauter N, Lawrence-Dill CJ, Lee E, Lynch J, Murray SC, Nelson R, Petzoldt J, Rocheford T, Schnable J, Schnable PS, Scully B, Smith M, **Springer NM**, Srinivasan S, Walton R, Weldekidan T, Wisser RJ, Xu W, Yu J, de Leon N. (2017) The effect of artificial selection on phenotypic plasticity in maize. *Nat Commun*. 8(1):1348. doi: 10.1038/s41467-017-01450-2.
91. Wicker T, Schulman AH, Tanskanen J, Spannagl M, Twardziok S, Mascher M, **Springer NM**, Li Q, Waugh R, Li C, Zhang G, Stein N, Mayer KFX, Gundlach H. (2017) The repetitive landscape of the 5100 Mbp barley genome. *Mob DNA*. 8:22. doi: 10.1186/s13100-017-0102-3.
90. 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*. 114(46):12231-12236. doi: 10.1073/pnas.1713225114.
89. 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* 546(7659):524-527. doi: 10.1038/nature22971.
88. **Springer NM**, Schmitz RJ. (2017) Exploiting induced and natural epigenetic variation for crop improvement. *Nat Rev Genet*. 18(9):563-575. doi: 10.1038/nrg.2017.45.
87. Köhler C, **Springer N**. (2017) Plant epigenomics-deciphering the mechanisms of epigenetic inheritance and plasticity in plants. *Genome Biol*. 18(1):132. doi: 10.1186/s13059-017-1260-9.
86. Oka R, Zicola J, Weber B, Anderson SN, Hodgman C, Gent JI, 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*. 18(1):137. doi: 10.1186/s13059-017-1273-4.
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*. 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*. 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, Fligel 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, Jeddalo J, Richmond T, Rosenbaum H, Burgess D, **Springer NM**, Grealley 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, Jeddloh JA, **Springer NM**. 2014. Genetic perturbation of the maize methylome. *Plant Cell* 26:4602-4616.
 65. Belova T, Grønvoold 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, Vaughn MW, **Springer NM** 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.
31. **Springer NM**, Jackson SA. 2010. Realizing the potential of genomics for crop improvement. *Brief Func Genomic Proteomic* 9(2) 93-94.

30. Douglas RN, Wiley D, Sarkar A, **Springer NM**, Timmermans MCP, Scanlon MJ. 2010. *ragged seedling2* encodes an ARGONAUTE7-like protein required for mediolateral expansion, but not dorsiventrality, of maize leaves. *Plant Cell* 22(5):1441-5.
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, Jeddeloh J, Schnable PS. 2010. Repeat subtraction-mediated sequence capture from a complex genome. *Plant Journal* 62(5):898-909.
28. Liu S, Chen HD, Makarevitch I, Shirmer R, Emrich SJ, Dietrich CR, Barbazuk WB, **Springer NM**, Schnable PS. 2010. High-Throughput Genetic Mapping of Mutants via Quantitative SNP-typing. *Genetics* 184:19-26.
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 Jeddeloh, 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.
26. **Springer NM**, Ying K, Fu Y, Ji T, Yeh C-T, Jia Y, Wu W, Richmond T, Kitzman J, Rosenbaum H, Iniguez AL, Barbazuk WB, Jeddeloh JA, Nettleton D, Schnable PS. 2009. Maize Inbreds Exhibit High Levels of CNV and Presence/Absence Differences in Genome Content. *PLoS Genetics* 5(11): e1000734.
25. **Springer NM**, Eichten S, Smith A, Papa CM, Steinway S, Kaeppeler SM. 2009. Characterization of a novel maize retrotransposon family SPRITE that shows high levels of variability among maize inbred lines. *Maydica* 54: 417-428.
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.
19. Chaudhary B, Flagel L, Stupar RM, Udall JA, Verma N, **Springer NM**, Wendel J. 2009. Reciprocal silencing, transcriptional bias and functional divergence of homoeologs in polyploid cotton (*Gossypium*). *Genetics* 182:503-517.
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
17. Stupar RM, Gardiner JG, Oldre AG, Haun WJ, Chandler VL, **Springer NM**. 2008. Gene expression analyses in maize inbreds and hybrids with varying levels of heterosis. *BMC Plant Biology* 8:33.
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 effects on gene expression in maize. *Plant Cell* 19: 2391-2402.
13. Makarevitch I, Stupar RM, Iniguez AL, Haun WJ, Barbazuk WB, Kaeppler SM, **Springer NM**. 2007. Natural variation for alleles under epigenetic control by the maize chromomethylase *Zmet2*. *Genetics* 177:749-60.
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, Laoueille-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.

8. **Springer NM**, Kaeppeler SM. 2005. Evolutionary divergence of monocot and dicot methyl-CpG-binding domain proteins. *Plant Physiol.* 138(1):92-104.
7. McGinnis K, Chandler V, Cone K, Kaeppeler H, Kaeppeler S, Kerschen A, Pikaard C, Richards E, Sidorenko L, Smith T, **Springer N**, Wulan T. 2005. Transgene-induced RNA interference as a Tool for Plant Functional Genomics. In *RNA Interference Methods in Enzymology* eds. John Rossi and David Engelke. *Methods Enzymol* 392:1-24.
6. Till BJ, Reynolds SH, Weil C, **Springer NM**, Burtner C, Young K, Bowers E, Codomo CA, Enns LC, Odden AR, Greene EA, Comai L, Henikoff S. 2004. Discovery of induced point mutations in maize genes by TILLING. *BMC Plant Biol.* 4(1):12.
5. **Springer NM**, Xu X, Barbazuk WB. 2004. Utility of different gene-enrichment approaches towards identifying and sequencing the maize gene space. *Plant Physiol.* 136(2):3023-33.
4. **Springer NM**, Napoli CA, Selinger DA, Pandey R, Cone KC, Chandler VL, Kaeppeler HF, Kaeppeler 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
3. **Springer NM**, Danilevskaya O, Hermon P, Helentjaris T, Phillips RL, Kaeppeler HF, Kaeppeler SM. 2002. Sequence Relationships, Conserved Domains, and Expression Patterns for *Zea mays* Homologs of the *Drosophila* Polycomb Group Genes *E(z)*, *esc*, and *E(Pc)*. *Plant Phys.* 128: 1332-1345
2. Papa CM, **Springer NM**, Muszynski MG, Meeley R, Kaeppeler SM. 2001. Maize chromomethylase *Zea methyltransferase2* is required for CpNpG methylation. *Plant Cell* 13: 1919-1928.
1. Cao X, **Springer NM**, Muszynski MG, Phillips RL, Kaeppeler SM, Jacobsen SE. 2000. Conserved plant genes with similarity to mammalian de novo DNA methyltransferases. *Proc. Natl. Acad. Sci.* 9:4979-4984.

BOOK CHAPTERS:

7. Noshay JN, Crisp PA, **Springer NM**. (2018) The maize methylome. In *The Maize Genome* (Eds. Bennetzen J, Flint-Garcia S, Hirsch CN, Tuberosa R) Springer-Verlag. New York.
6. **Springer NM**, Kaeppeler 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, Grealley 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 PRESENTATIONS AT PROFESSIONAL MEETINGS, CONFERENCES, ETC.

<u>Dates</u>	<u>Title/Location</u>
April 11, 2001	“Epigenetic inheritance in plants: Exceptions to Mendel's Laws” Southeast Missouri State University
April 1 st 2003	“Functional genomics of maize chromatin: The journey from sequence towards function” Purdue University
November 4 th , 2003	“Evolution of chromatin gene families in plants” Donald Danforth Plant Sciences Center
February 9 th , 2004	“Searching for the molecular mechanisms that control imprinted gene expression.” University of Minnesota – Plant Biology Seminar series
February 16 th , 2004	“How does mother know best? Mechanisms of plant imprinting” University of Missouri Columbia – Plant Genetics seminar series
March 31 st , 2004	“Applications of oligonucleotide microarrays for polymorphism detection in maize” Texas A&M University – “Development and use of genotyping technology for gene discovery and crop improvement” Symposium
October 20 th , 2004	“Applications of oligonucleotide microarrays for polymorphism detection in maize” University of Minnesota – Cargill Seminar Series
June 30 th , 2005	“Epigenetics and gene expression” University of Minnesota – Bioinformatics summer institute; Minneapolis MN
October 24, 2005	“Are mom and dad interchangeable and how did I get so big: Studying the genome wide gene expression in a heterotic hybrid.” University of Minnesota – Applied Plant Sciences seminar series; Saint Paul MN
November 4 th , 2005	“How does mother know best? Understanding the regulation of imprinting in maize.” Iowa State University – Genetics seminar series; Ames IA
September 21 st , 2006	“Are mom and dad interchangeable and how did I get so big?: Lessons from inbred and hybrid gene expression studies.” Ohio State University – Plant Cellular and Molecular biology seminar series; Columbia OH
February 8 th , 2007	“Genetic and epigenetic variation for gene expression in maize” University of Wisconsin – Plant Breeding and Plant Genetics seminar series; Madison WI

- February 23rd, 2007 “Genetic and epigenetic variation for gene expression in maize: Implications for heterosis.” Minnesota State University, Mankato – Biology department seminar series; Mankato MN
- March 24th, 2007 “Epigenetic variation for gene expression levels in B73 and Mo17” Maize Genetics Conference; Saint Charles IL
- September 19th, 2007 “Genetic and epigenetic allelic variation in maize” Donald Danforth plant Sciences Center – seminar series; Saint Louis MO
- October 12th, 2007 “Epigenetic variation: Is there heritable phenotypic variation beyond Mendel?” Hamline University – Biology Department seminar series; Saint Paul MN
- November 11th 2007 “Epigenetic variation among maize inbreds affects gene expression levels” ASSA-CSSA-SSA: Invited speaker for C7 epigenetic symposia; New Orleans LA
- January 15th, 2008 “Epigenetic variation among maize inbreds affects gene expression levels” Dow AgroSciences invited speaker; Indianapolis IN
- February 28, 2008 “Genomics as a tool to further understand heterosis” Maize genetics Conference: Invited speaker for Translational genomics session; Washington DC
- March 2nd, 2008 “A genomic perspective of heterosis: Using microarray and allele-specific expression profiling to study the hybrid transcriptome.” Illinois Corn Breeders School invited speaker; Champagne IL
- April 1st, 2008 “Dissecting the causes of gene expression variation among maize inbreds” Monsanto Breeding and Statistical Genomics symposia speaker; Saint Louis MO
- September 28, 2008 “Epigenetic natural variation among maize inbred lines” Blackheath Australia International plant epigenome initiative meeting speaker; Blue Mountains Australia
- January 12, 2009 “Epigenetic natural variation among maize inbred lines” PAG – Epigenomics workshop invited speaker; San Diego CA
- January 13, 2009 “Application of Roche NimbleGen Sequence Capture for Complex Plant Genomes” PAG – Roche NimbleGen workshop invited speaker; San Diego CA
- January 28th, 2009 “Genetic and epigenetic variation for gene expression in maize inbreds” University of Guelph, Dept. of Plant Agriculture; Guelph Canada
- February 28, 2009 “Technologies for studying DNA methylation” Developmental Origins of Cancer Symposium, University of Minnesota; Minneapolis MN
- September 9th, 2009 “Potential implications for genome and transcriptome content variation on heterosis in maize” International Conference on heterosis, Stuttgart Germany

- September 22, 2009 "Epigenetics and natural variation among maize inbred lines"
Cold Spring Harbor Laboratory Banbury conference on
Epigenetics; Cold Spring Harbor NY
- October 3rd, 2009 "Epigenetics and natural variation among maize inbred lines"
Plant Epigenetics Symposium at University of Massachusetts –
Amherst; Amherst MA
- October 29th, 2009 "Epigenetics and natural variation among maize inbred lines"
International Plant Molecular Biology Conference, Epigenetics
Symposium; Saint Louis MO
- February 22nd, 2010 "Does a Detailed View of Genomic and Transcriptomic Variation
Contribute to an Understanding of the Mechanisms of
Heterosis?" Applied Plant Sciences seminar series, University of
Minnesota
- February 15th, 2010 "Pervasive variation in genome structure, epigenetic patterns
and transcript levels among maize lines and potential
consequences for heterosis" University of Georgia Genetics
department seminar series; Athens GA
- March 19th, 2010 "Combined analysis of genomic structural variation and gene
expression variation between maize and teosinte populations"
Maize Genetics Conference; Riva del Garda Italy
- January 18, 2011 "Genomic and Epigenomic variation among maize inbreds" PAG
– Roche NimbleGen workshop invited speaker, San Diego CA
- March 16, 2011 "Combined analysis of genomic, transcriptomic and epigenomic
variation among maize inbreds" NCCC167 meeting keynote
presentation, Saint Charles IL
- August 31, 2011 "Genomic and transcriptomic variation among maize inbreds"
Microbial and Plant Genomics Institute 2nd annual symposium,
Saint Paul MN
- September 13, 2011 "Genomic and epigenomic variation among maize inbreds"
University of Arizona department of Plant Sciences seminar;
Tucson AZ
- October 17, 2011 "DNA methylation: What is the value for phenotypic prediction?"
Cold Spring Harbor Banbury conference: Genotype to Phenotype;
Cold Spring Harbor NY
- December 15, 2011 "Genomic and epigenomic variation among maize inbreds" BASF
invited presentation, Durham NC
- January 14, 2012 "Epigenomic variation among maize inbreds" PAG: Maize
workshop invited presentation, San Diego CA
- April 11, 2012 "Epigenomic variation among maize inbreds" Donald Danforth
Plant Sciences Center presentation; Saint Louis MO
- April 20, 2012 "Genomic and epigenomic variation among maize inbreds" Plant
Breeding symposium at University of California Davis
- June 4, 2012 "How does all the molecular variation sum to the phenotype?"
Guelph University invited speaker; Guelph Canada

- June 13, 2012 “Epigenetics and plant breeding: Lessons from studying maize variation” Monsanto Research Fellows symposia; Saint Louis MO
- June 23, 2012 “Applications and issues of large scale transcriptome profiling experiments” Purdue Symposium on Statistics, West Lafayette IN
- September 6, 2012 “Genetic and epigenetic influences on DNA methylation variation in maize” NSF Plant genome Program Awardee meeting Washington DC
- September 18, 2012 “Genomic and epigenomic variation among maize inbreds” Italian Society of Agricultural Genetics, Perugia Italy
- November 14, 2012 “Genomic variation within species: Structural changes and epigenetic variation in maize.” Brigham Young University, Provo UT
- January 13, 2013 “Heterochromatin conservation and divergence among sub-genomes and species” PAG – Comparative Genomics Workshop, San Diego CA
- February 22, 2013 “Genomic variation within species: Structural changes and epigenetic variation in maize” Michigan State University, Science at the Edge, East Lansing MI
- May 8, 2013 “Epigenetic natural variation in maize affecting gene expression” University of Georgia, UGA Plant Center Spring Symposium, Athens GA
- June 10th, 2013 “Systems biology of gene expression in maize” University of Guelph, Sustainable agriculture meeting, Guelph Canada
- July 8th, 2013 “Genetic and epigenetic influences on natural variation for gene expression in maize” Society for Molecular Biology and Evolution meeting; Chicago IL
- August 13th, 2013 “Heterosis and epigenetic variation in maize” Syngenta Epigenetics and non-coding RNA annual meeting; RTP NC
- September 11th, 2013 “Variation in crop genomes and heterosis” Switchgrass II conference, Madison WI
- September 13th, 2013 “Epigenomic variation in maize” University of Wisconsin Plant Breeding Symposium, Madison WI
- November 19th, 2013 “Exploring the sources and consequences of variation for DNA methylation in maize” China Agricultural University, Beijing China
- November 21st, 2013 “Exploring the sources and consequences of variation for DNA methylation in maize” Huazhong Agricultural University, Wuhan China
- December 2nd, 2013 “Exploring the sources and consequences of variation for DNA methylation in maize” University of California Davis, Davis CA
- January 8th, 2014 “A complex interplay between genes and transposons within the maize genome” PAG - Evolution of Genome Size Workshop; San Diego CA

January 10 th , 2014	“Heritable alteration of the maize methylome following tissue culture” PAG – Genomics of tissue regeneration workshop; San Diego CA
January 10 th , 2014	“Application of sequence capture bisulphite sequencing for targeted analysis of DNA methylation patterns in complex plant genomes” PAG – Roche NimbleGen workshop; San Diego CA
February 11 th , 2014	“Sources of methylome variation in maize” Cereal Translational Genomics meeting; Vienna Austria
February 13 th , 2014	“Sources of methylome variation in maize” Gregor Mendel Institute, Vienna Austria
February 24 th , 2014	“Genetics vs Epigenetics; A complex interplay of DNA methylation and transposons in the maize genome” University of Florida; Gainesville FL
April 25 th , 2014	“Epigenetic natural variation in maize” Dupont Pioneer; Johnsonville IA
June 20 th , 2014	“Transposable elements shape plant methylomes and contribute to gene expression regulation” Ohio State University; Columbus OH
September 12 th , 2014	“Variability in the maize methylome” Plant Genomics Congress; Saint Louis MO
September 25 th , 2014	“Through the maize methylome” Syngenta, Research Triangle Park NC
September 29 th , 2014	“Epigenetics: Definitions and Debates” Monsanto, Saint Louis MO
November 10 th , 2014	“Through the maize methylome” Banbury Conference - Epigenetics and Agriculture, Cold Spring Harbor NY
December 8 th , 2014	“Transposable elements shape plant methylomes and contribute to gene expression regulation” North Carolina Biotechnology Consortium; Research Triangle Park NC
January 10 th , 2015	“Maize is not Arabidopsis” PAG – Maize workshop; San Diego CA
February 2015	“Epigenetics and heritable variation in maize” CSIRO – Canberra Australia
February 2015	“Epigenetics and heritable variation in maize” Australian National University; Canberra Australia
February 2015	“Epigenetics and heritable variation in maize” University of Perth; Perth Australia
May 4 th , 2015	“Diverse roles for transposons in shaping plant genomes” Danforth; Saint Louis MO
May 5 th , 2015	“Diverse roles for transposons in shaping plant genomes” Interdisciplinary Plant Group, University of Missouri; Columbia MO
July 27 th , 2015	“Probing the sources of variation for the maize methylome” ASPB Symposium “Epigenetic variation in plants”; Minneapolis MN

- October 13th, 2015 “Learning about the evolution of gene expression from allelic diversity” Division of Biological Sciences seminar series, University of Missouri – Columbia MO
- November 4th, 2015 “Diverse roles for transposons in shaping plant genomes” University of Houston, Houston TX
- January 10th, 2016 “Translating Our Understanding of the Genome to Predictions of Performance in the Field” PAG National Plant Genome Initiative workshop. San Diego, CA
- February 17th, 2016 “Variations on a theme: Methylome patterning in a complex genome” Keystone Plant Epigenetics Conference, Taos NM
- May 25th, 2016 “Genomics and genetics of heterosis” IPG Stadler symposium on Heterosis, Columbia MO
- September 19th, 2016 “Diverse roles for transposons in shaping plant genomes” UCLA
- December 16th, 2016 “Regulatory variation affecting plant traits” VL40 seminar; Boston MA
- January 11th, 2017 “Roles for transposons in shaping plant gene expression” USDA Workshop, San Diego CA
- February 13th, 2017 “Searching for the Mechanisms that Drive Novel Gene Expression Responses to Abiotic Stress in Maize” Phenome 2017, Tucson AZ
- March 9th, 2017 “Shedding light on the dark spaces of the maize genome” Maize Genetics Conference, Saint Louis MO
- March 31, 2017 “Shedding light on the dark spaces of the maize genome” Plant Biology Seminar, Cornell University, Ithaca NY
- May 12, 2017 “Transposable elements as a source of novel regulatory information” NYU Global Research Initiative – Plant Genome evolution workshop, New York University, NY
- June 7, 2017 “Monitoring allelic diversity in maize: transcriptomes to fields” CROPS, Huntsville AL
- June 12, 2017 “Shedding light on the dark spaces of the maize genome” Dow, Indianapolis IN
- August 1, 2017 “Life on the edge: Gene-TE interactions in complex genomes” Epigenetics Gordon Research Conference, Holderness NH
- September 5, 2017 “Hidden variation in plant genomes - epigenetic natural variation” Genomics of Plant Genetic Resources conference, Giessen Germany
- September 14, 2017 “Transposons as sources of genetic and epigenetic variation in crop genomes” Agronomy department seminar, Iowa State University Ames IA
- January 14, 2018 “TE contributions to dynamics of the maize genome and transcriptome: PAG TE Workshop, San Diego CA
- September 12, 2018 “Dynamic crop genomes: Variation in transposons, chromatin and gene expression in maize” University of Illinois Urbana-Champaign departmental seminar

- September 28, 2018 “Current functional genomics for maize” Maize Functional Genomics Workshop, Madison WI
- October 31, 2018 “TE contributions to variation: Variation in transposons, chromatin and gene expression in maize” Plant epi/genetics Conference, Angers France
- June 4, 2019 “Dissecting the role of transposons in genomic, epigenomic and expression variation in maize” International Forum on Crop Genomics, Wuhan China
- July 13, 2019 “The Dynamic Maize Genome” Plant Biology San Jose CA
- December 5, 2019 “Dynamic crop genomes - monitoring the influences of transposons and epigenetics in creating variation” Colorado State University
- January 13, 2020 “Tissue culture influences on genome and epigenome stability in maize” Genomics of Tissue Regeneration workshop at Plant and Animal Genome Conference, San Diego CA
- January 14, 2020 “Dynamic crop genomes - monitoring the influences of transposons in creating variation” University of California-San Diego winter symposium, San Diego CA
- February 3, 2020 “Understanding the sources of variation in dynamic crop genomes” Applied Plant Sciences seminar series, University of Minnesota
- February 11, 2020 “Environmental regulation of gene function in maize” National Academy of Sciences, Engineering and Medicine workshop on functional genomics. Washington DC
- May 6, 2020 “Assessing the relative utility of filtering genomes using chromatin accessibility and DNA methylation” Bayer Crop Sciences, Virtual seminar
- October 2, 2020 “Lighting up dark matter – monitoring expression of transposable elements in the maize genome” Uppsala Transposable Element Conference, Uppsala Sweden (virtual)
- December 4, 2020 “Diverse roles of transposons in shaping plant genomes and gene expression” University of Zurich, Switzerland (virtual)
- February 9, 2021 “Attempts to identify and understand the sources of regulatory variation in crop genomes” Institute for Genome Biology, University of Illinois (virtual)
- February 20, 2021 “Identifying the sources of regulatory variation in crop genomes” Corn Breeding Research conference (virtual)
- June 2, 2021 “Identifying the sources of regulatory variation in crop genomes” HudsonAlpha Institute seminar (virtual)
- December 13, 2021 “Dynamic crop genomes: Understanding how transposons create variation” Academician Hsien-Wen Li Lectureship, Academia Sinica, Taiwan

MENTORING AND TRAINING:

CURRENT POSTDOCTORAL ASSOCIATES

Zhikai Liang 2019 – present
 Zachary Myers 2020-present
 Andy Read 2020 – present
 Manisha Munasinghe 2021-present
 Brett Ferguson 2021-present

CURRENT GRADUATE STUDENTS:

Erika Magnusson 2017-present
 Clair Wootan 2021-present

PAST GRADUATE STUDENTS:

William Haun; Program –PBS; Degree - Ph.D. (05/15/08); Thesis title: Epigenetic and Genetic Control of Imprinting at the Mez1 Locus in Maize. Current employment: University of Minnesota; Tech transfer
 Summer St. Pierre; Program – APS; Degree - M.S. (12/20/09); Thesis title: Surveying genetic and phenotypic variation for response to density stress in maize, wheat and barley. Current employment: Research Scientist; Corteva
 Moumita Chakravartty; Program – PBS; Degree - M.S. (09/14/10) Thesis title: Characterization of maize genes that exhibit present-absent expression in different genotypes. Current employment: Unknown.
 Steven Eichten; Program –PBS; Degree - Ph.D. (05/31/13) Thesis title: Identification and characterization of DNA methylation variation in maize. Current employment: Staff scientist, Inari
 Amanda Waters; Program –PBS; Degree - Ph.D. (04/27/16) Thesis title: Characterizing allelic regulatory variation in maize. Current employment: Scientist, PepsiCo
 Sara Tirado Program - APS Degree – Ph.D. (08/31/2020) Thesis title: Characterizing the genetic and environmental impacts on maize utilizing phenomic approaches. Current employment: Research Scientist - Corteva
 Jaclyn Noshay Program: PMB Degree – PhD (03/31/2021) Thesis title: Connecting genome structure variation and chromatin composition in Zea mays. Current employment: Post-doc: ORNL Jacobsen group.

PAST POSTDOCTORAL ADVISEES:

Robert Stupar; Mar05 - Dec07; Associate Prof UMN Agronomy and Plant Genetics (stup0004@umn.edu)
 Irina Makarevitch; Jun06 – Aug07; Prof Hamline (imakarevitch01@hamline.edu)
 Ruth Swanson-Wagner; Sep09 – Dec10; Monsanto - Genome Informatics Lead
 Qing Li; Jan13-July16; Assistant Professor; Huazhong Ag University
 Cory Hirsch; Sept13-Jan16; Assistant Professor; UMN Plant Pathology
 Tara Enders June 2016- Aug 2019; Assistant Professor, Hofstra University
 Sarah Anderson August 2016 – December 2019; Assistant Professor, Iowa State University Genetics Cell Biology Department

Peter Crisp March 2017 – Jan 2020; Assistant Professor, University of Queensland
 Peng Zhou 2016-2021; Assistant Professor, CAAS Beijing

CURRENT AND PAST VISITING SCHOLARS:

Mei Zhang (Visiting Scientist) Jun14-Dec14 Professor at China Agricultural University
 Zhaoxue Han (Visiting Scientist) Sept15-Sep16 Professor Northeastern Ag University
 Simen Sandve (Visiting scientist) Jan13-July13 Norwegian University of life sciences

CURRENT GRADUATE STUDENT COMMITTEES:

Paul Atkins (MCDB&G)
 Michael Maher (PBS)
 Jaclyn Noshay (PBS)
 Sara Tirado (APS)
 Claire Milsted (PBS)
 Erika Magnusson (PBS)
 Ryan Merry (APS)
 Zion Lee (ChemEng)
 Matthew Zinselmeier (MCDB&G)

PAST GRADUATE STUDENT COMMITTEES:

<u>Name</u>	<u>Date</u>	<u>Type</u>	<u>Program</u>
Lorien Radmer	03/30/2007	MS	Applied Plant Sciences
Anna Selmecki	05/30/2007	PhD	MCDB&G
Matt Walch	06/29/2007	MS	Applied Plant Sciences
Dan Griffin	06/25/2007	PhD	PBS
Brent Hulke	08/31/2007	PhD	Applied Plant Sciences
William Haun	05/15/2008	PhD	PBS
Carol Powers	05/29/2008	PhD	Applied Plant Sciences
Candida Cabral	07/31 2009	PhD	Applied Plant Sciences
Adrianna Telias	03/11/2009	PhD	PBS
Summer Ste. Pierre	12/20/2009	MS	Applied Plant Sciences
Alexander Kahler	05/20/2010	PhD	Applied Plant Sciences
Veronica Justen	07/07/2010	PhD	Applied Plant Sciences
Moumita Chakravarty	09/14/2010	MS	PBS
Christopher Schaefer	04/17/2012	MS	Applied Plant Sciences
Ye Sun	06/08/2012	PhD	PBS
Carrie Eberle	06/18/2012	PhD	PBS
Chris Schaefer	02/11/2013	PhD	Applied Plant Sciences
Steve Eichten	05/31/2013	PhD	PBS
Roman Briskine	11/27/2013	PhD	Computer Science
Addie Thompson	06/05/2014	PhD	Applied Plant Science
Nandita Vishanathan	06/18/2014	PhD	Chemical Engineering
Elizabeth Duffy	08/23/2015	MS	Biostatistics

Rob Schaefer	11/10/2015	PhD	BiCB
Amanda Waters	04/27/2016	PhD	PBS
Eli Krumholz	01/20/17	PhD	PBS
Alex Brohammer	10/31/2018	PhD	APS
Allison Haaning	12/10/2018	PhD	PBS

UNDERGRADUATE STUDENTS (CURRENT AND PAST)

<u>Name</u>	<u>Nature of Experience</u>	<u>Dates</u>
Melissa Royzman	Undergraduate research assistant	Sept03-May04
Nicole Saur	Directed research	Sept04-Dec04
Jena Trask	Directed research / laboratory assistant	May04-May07
Adrienne Escher	Laboratory assistant	Jan04-Aug06
Anne Bergmark	Directed research / laboratory assistant	Jan04-May07
Anna Bredsten	Directed research / laboratory assistant	Aug05-May07
Aaron Oldre	Directed research / laboratory assistant	May06-May07
Rebecca Shirmer	Directed research	Aug06-Dec08
Rebecca Coobs	Directed research	Aug06-Dec06
Chris Thompson	Directed research	Aug06-May07
Kevin Pietel	Directed research	Jan06 - May06
Whittney Egle	Directed Research	Sep08-May09
Amanda Waters	Student worker	04/2010 – 08/2011
Andrew Bergemann	Directed research	May13-Dec13
Patrick West	Directed research	May12-May14
Jaclyn Noshay	Directed research	Sept13-May16
Rachel Nelson	Directed Research	Jan14-May14
Amanda Basham	UROP	Jun14-Aug14
Sarah Houle	Directed Research	Aug14-Dec14
Gerardo Arroyo-Martinez	UROP	Jun16-Aug16
Graham Giesting	UROP	Jun16-Aug16
Phillip Prince	UROP	Jun16-Aug16
Jonathan Giesler	Laboratory Assistant	Nov16-May18
Livia Twohig	Laboratory Assistant	Oct16-May17
Veronica Swanson	Laboratory Assistant	Oct16-Aug17
Emily Stock	Laboratory Assistant	Dec16-May17
Meg Gerold	Laboratory Assistant	May17-May18
Colin Emerson	Laboratory Assistant	May17-Aug17
Justin Oakland	Laboratory Assistant	May17-Aug18
Paradis Vandeputte	Laboratory Assistant	Sept17-May18
Danielle Sorenson	Directed research	Jan18-May19
Shale Demuth	Laboratory Assistant	Jan 18 – May19
Kjell Sandstrom	Laboratory Assistant	Jan 18 – Aug19
Hayden Christensen	Laboratory Assistant	May 18-present

MEMBERSHIPS AND COMMITTEES:

American Society of Plant Biologists (2005-present)
 Genetics Society of America (2009-present)
 American Association for the Advancement of Science (2015-present)
 Maize Genetics Executive committee (2011-2016; Chair – 2015-2016)
 NCCC167 (USDA Corn Breeding research group) UMN representative (2009-2018)
 Maize Genetics Conference steering committee (2011-2013)
 Corn Breeding Executive Committee (2013-2018)
 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)
 PAG Co-organizer of Comparative Genomics Workshop (2013-present)
 Phenome 2019, Tucson AZ Feb 2019 (Chair)

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
May-November 2017	PMB Plant biologist search committee chair

September 2018-present UMN CBS College Documentation, promotion, tenure committee

JOURNALS AND PROPOSAL REVIEWS:

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

Editorial board for Genetics (2016-present)

Editorial board member for Genome Biology (2017-present)

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

Served as peer reviewer for >270 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 (4), NSF Eukaryotic Genetics grant and USDA Physiology of Crop plants grant panels

CONSULTING AND SCIENTIFIC ADVISORY BOARDS:

Syngenta (2013-2016)

EpiCrop (2015-2016)

Malaysian Palm Oil Board (2017-2019)

Inari Ag (2017-present)

HudsonAlpha SAB (2020-present)