

Sarah N Anderson

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PROFESSIONAL INTERESTS

A major theme of the Anderson Genomics Lab is to better understand the regulatory landscape of large crop genomes, particularly with respect to the role that Transposable Elements (TEs) play in distributing regulatory regions across the genome. TEs contribute substantially to the genetic diversity in maize, however little is known about how these variable TEs influence chromatin and gene expression dynamics genome-wide.

The Anderson Genomics Lab utilizes a two-step approach to understand the role of TEs in creating expression variation in maize. First, bioinformatic analysis integrating information from genomic, epigenomic, and transcriptomic datasets are used to identify features of TEs associated with particular gene expression patterns and to predict putative regulatory regions within TEs that vary among maize genomes. Then, predictions are tested experimentally in controlled and field conditions using either diverse inbred lines or CRISPR-generated modifications to regulatory sequences. These approaches are currently being applied to study transcriptional networks in response to abiotic stress and to understanding the role of imprinted gene expression in maize endosperm development.

PROFESSIONAL EXPERIENCE

2020 – current Assistant professor in the Department of Genetics, Development, and Cell Biology at Iowa State University.

2016 – 2019 Postdoctoral associate at the University of Minnesota, Twin Cities.
Advisor: Nathan Springer, Department of Plant and Microbial Biology.

2012 – 2016 Graduate student researcher at the University of California, Davis. Advisor: Venkatesan Sundaresan, Department of Plant Biology. Dissertation: Maternal to Zygotic Transition in *Oryza sativa*.

2009 – 2011 Undergraduate research assistant at Iowa State University. Advisor: Yanhai Yin, Department of Genetics, Development and Cell Biology.

EDUCATION

2016 Ph.D. Integrative Genetics and Genomics. University of California, Davis.

2011 B.S. Genetics, Magna Cum Laude with Honors. Iowa State University.

MEMBERSHIPS

American Society of Plant Biologists (ASPB)
Maize Genetics Cooperation
Genetics Society of America (GSA)
Predictive Plant Phenotyping Faculty in Plant Biology and Data Science
Crop Bioengineering Center
Bioinformatics & Computational Biology Graduate Group Faculty
Interdepartmental Genetics & Genomics Graduate Group Faculty

PUBLICATIONS

- Asterisks denote corresponding author; underlined names denote advised graduate students

- 2021 JM Noshay, AP Marand, **SN Anderson**, P Zhou, MK Mejia Guerra, Z Lu, C O'Connor, PA Crisp, CN Hirsch, RJ Schmitz, NM Springer. Assessing the regulatory potential of transposable elements using chromatin accessibility profiles of maize transposons. *Genetics*.
- 2021 Y Qiu, C O'Connor, R Della Coletta, JS Renk, P Monnahan, JM Noshay, Z Lang, A Gilbert, **SN Anderson**, SE McGaugh, NM Springer, C Hirsch. Whole genome variation of transposable element insertions in a maize diversity panel. *G3*.
- 2021 MC Stitzer, **SN Anderson**, NM Springer, J Ross-Ibarra. The genomic ecosystem of transposable elements in maize. *PLOS Genetics*.
- 2021 **SN Anderson***, P Zhou, K Higgins, Y Brandvain, NM Springer. Widespread imprinting of transposable elements and young genes in the maize endosperm. *PLoS genetics* 17 (4), e1009491.
- 2021 Z Liang, **SN Anderson**, JM Noshay, PA Crisp, TA Enders, NM Springer. Genetic and epigenetic variation in transposable element expression responses to abiotic stress in maize. *Plant Physiology*.
- 2020 JM Noshay, AP Marand, **SN Anderson**, P Zhou, MKM Guerra, Z Lu, C O'Connor, PA Crisp, CN Hirsch, RJ Schmitz, NM Springer. Assessing the regulatory potential of transposable elements using chromatin accessibility profiles of maize transposons. *Genetics*, 2020.
- 2019 **SN Anderson**, MC Stitzer, P Zhou, J Ross-Ibarra, CD Hirsch, NM Springer. Dynamic patterns of transcript abundance of transposable element families in maize. *G3: Genes, Genomes, Genetics*. <https://doi.org/10.1534/g3.119.400431>.
- 2019 JM Noshay, **SN Anderson**, P Zhou, L Ji, W Ricci, Z Lu, MC Stitzer, PA Crisp, CN Hirsch, X Zhang, RJ Schmitz, NM Springer. Monitoring the interplay between transposable element families and DNA methylation in maize. *PLoS Genetics* 15(9):e1008291. <https://doi.org/10.1371/journal.pgen.1008291>.
- 2019 **SN Anderson**, MC Stitzer, AB Brohammer, P Zhou, JM Noshay, CH O'Connor, CD Hirsch, J Ross-Ibarra, CN Hirsch, NM Springer. Transposable elements contribute to dynamic genome content in maize. *The Plant Journal*. <https://doi.org/10.1111/tpj.14489>.

- 2019 W Xue, **SN Anderson**, X Wang, L Yang, PA Crisp, Q Li, JM Noshay, PS Albert, JA Birchler, P Bilinski, MC Stitzer, J Ross-Ibarra, S Flint-Garcia, X Chen, NM Springer, JF Doebley. Hybrid decay: a transgenerational epigenetic decline in vigor and viability triggered in backcross populations of teosinte with maize. *Genetics*. <https://doi.org/10.1534/genetics.119.302378>.
- 2019 PA Crisp, JM Noshay, **SN Anderson**, NM Springer. Opportunities to use DNA methylation to distil functional elements in large crop genomes. *Molecular Plant*. 12(3): 282-284. <https://doi.org/10.1016/j.molp.2019.02.006>.
- 2018 NM Springer, **SN Anderson**, CM Andorf, KR Ahern, F Bai, O Barad, WB Barbazuk, HW Bass, K Baruch, G Ben-Zvi, ES Buckler, R Bukowski, MS Campbell, EKS Cannon, P Chomet, RK Dawe, R Davenport, HK Dooner, LH Du, C Du, KA Easterling, C Gault, JC Guan, CT Hunter, G Jander, Y Jiao, KE Koch, G Kol, TG Köllner, T Kudo, Q Li, F Lu, D Mayfield-Jones, W Mei, DR McCarty, JM Noshay, JL Portwood, G Ronen, AM Settles, D Shem-Tov, J Shi, I Soifer, JC Stein, MC Stitzer, M Suzuki, DL Vera, E Vollbrecht, JT Vrebalov, D Ware, S Wei, K Wimalanathan, MR Woodhouse, W Xiong, TP Brutnell. The maize W22 genome provides a foundation for functional genomics and transposon biology. *Nature Genetics* 50, 1282-1288.
- 2018 **SN Anderson**, G Zynda, J Song, Z Han, M Vaughn, Q Li, NM Springer. Subtle perturbations of the maize methylome reveal genes and transposons silenced by chromomethylase or RNA-directed DNA methylation pathways. *G3: Genes, Genomes, Genetics* 8(6), 1921-1932.
- 2018 C Johnson, LJ Conrad, R Patel, **SN Anderson**, C Li, A Pereira, V Sundaresan. Reproductive lincRNAs in rice consist of male gamete specific and PRC2- repressed classes. *Plant Physiology* pp.01269.2017.
- 2018 **SN Anderson**, NM Springer. Potential roles for transposable elements in creating imprinted expression. *Current Opinion in Genetics & Development* 49, 8-14.
- 2017 **SN Anderson**, C Johnson, J Chesnut, DS Jones, I Khanday, M Woodhouse, C Li, LJ Conrad, S Russell, V Sundaresan. The zygotic transition is initiated in unicellular plant zygotes with asymmetric activation of parental genomes. *Developmental Cell* 43 (3), 349-358.
- 2017 SD Russell, DS Jones, **SN Anderson**, X Wang, V Sundaresan, X Gou. Isolation of rice sperm cells for transcriptional profiling. *Plant Germline Development*, 211-219.
- 2017 R Oka, J Zicola, B Weber, **SN Anderson**, C Hodgman, JI Gent, J Wesslink, NM Springer, HCJ Hoefsloot, F Turck, M Stam. Genome-wide mapping of transcriptional enhancer candidates using DNA and chromatin features in maize. *Genome Biology* 18(1):137.
- 2013 **SN Anderson**, C Johnson, D Jones, LJ Conrad, X Gou, S Russell, V Sundaresan. Transcriptomes of isolated rice gametes characterized by deep sequencing: Evidence for distinct sex-dependent chromatin and epigenetic states before fertilization. *The Plant Journal* (Cover article) 76(5):729-41.

- 2011 X Yu, L Li, J Zola, M Aluru, H Ye, A Foudree, H Guo, **SN Anderson**, S Aluru, P Liu, S Rodermeil, Y Yin. A Brassinosteroid transcriptional network revealed by genome-wide identification of BES1 target genes in *Arabidopsis thaliana*. *The Plant Journal* 65(4):634-646.

PREPRINT PUBLICATIONS AWAITING PEER-REVIEW

- Asterisks denote corresponding author; underlined names denote advised graduate students

- 2021 Gent JI, Swentowsky KW, Higgins KM, Fu FF, Zeng Y, Kim DW, Dawe RK, Springer NM, **Anderson SN**. The maize gene maternal derepression of r1 (mdr1) encodes a DNA glycosylase with maternal and paternal fertility functions. *bioRxiv*.

GRANTS AWARDED

- 2021 NSF-2114797
Title: DNA demethylation in maize endosperm gene regulation
Agency and Program: NSF MCB Genetic Mechanisms
PI: Jonathan Gent (University of Georgia)
Co-PI: SN Anderson
Funding \$936,153 total; \$433,000 to SN Anderson
Role: Co-PI (15% contribution)
- 2021 DBI-2147083
Title: BIORETS: Biological pathways to adaptability – interactions among the genome, epigenome, and environment
Agency and Program: NSF DBI
PI: Jeanne Serb
Co-PI: Maureen Griffin
Funding \$599,937 total
Role: Senior Personnel

INVITED TALKS

- 2020 “Understanding the contribution of Transposable Elements to maize genome and transcriptome diversity.” Invited talk at the University of Georgia Department of Plant Biology in Athens, GA.
- 2019 “Transposable element contributions to the dynamic genome and transcriptome in maize.” Invited talk at the Danforth Plant Sciences Center in St. Louis, MO.

CONFERENCE PRESENTATIONS

- 2020 “Widespread imprinting of transposable elements and young genes in the maize endosperm.” Cold Spring Harbor Laboratory Transposable Elements Meeting. Virtual.
- 2020 “Transposable Element contributions to dynamic maize genomes and transcriptomes.” Plant and Animal Genomes conference; Transposon Workshop. San Diego, CA.
- 2019 “Variable transposable element insertions contribute to maize genome dynamics.” Mobile Genetic Elements Conference. Woods Hole, MA.

- 2018 “Transposable element contributions to the dynamic maize genome and transcriptome.” 60th Annual Maize Genetics Conference. St. Malo, France.
- 2017 “Analysis of transposon expression provides insights into TE-genome conflicts in maize.” MPGI Fall Symposium: Genomics of Conflict. University of Minnesota. St. Paul, MN.
- 2017 “Dynamic transposable element expression across development in maize.” Plant and Animal Genomes conference; Transposon Workshop. San Diego, CA.
- 2017 “Initiation of zygotic genome activation in the unicellular rice zygote.” Plant and Animal Genomes conference; NuGen Workshop. San Diego, CA.
- 2015 “Transcriptome analysis of the plant zygotic transition reveals differential contributions of parental genomes.” NAIST Biology Workshop. Osaka, Japan.
- 2015 “Transcriptome analysis of the plant zygotic transition reveals differential contributions of parental genomes.” 13th International Symposium on Rice Functional Genomics. Wuhan, China.
- 2015 “Transcriptome analysis of the plant zygotic transition.” Invited talk at Shanxi University in Taiyuan, China.
- 2013 “Expression of epigenetic regulators in rice gametes suggests dynamic changes during plant fertilization.” 11th International Symposium on Rice Functional Genomics. New Delhi, India.

INTERNAL PRESENTATIONS

- 2022 “Regulatory rewiring creates phenotypic diversity in maize.” Crop Bioengineering Center Seminar Series, February 2022.
- 2021 “Transposable element genomics in maize.” Lightning talk for the USDA-AFRI information session in March, 2021 (Virtual).
- 2021 “Uncovering the contributions of transposable elements to maize diversity.” Two seminars presented to graduate students in GEN 691 and BCB 691 in Fall 2021.
- 2020 “Uncovering the contributions of transposable elements to maize diversity.” Department of Genetics, Development, and Cell Biology seminar series. Ames, IA (Virtual).
- 2020 “Uncovering the contributions of transposable elements to maize diversity” Plant Biology Graduate Group seminar series. Ames, IA (Virtual).

PRESENTATIONS CANCELED DUE TO COVID-19

- 2020 “Uncovering the contributions of transposable elements to maize diversity.” Invited talk, Purdue Plant Science Symposium entitled Building Bridges in Plant Science Research and Beyond at Purdue University. August 2020.

- 2020 "Transposable Element contributions to maize genome diversity and transcriptional dynamics in the seed." Invited seminar, Department of Ecology, Evolution, and Organismal Biology at Iowa State University. April 2020.
- 2020 "Widespread imprinting of young genes and transposable elements uncovered with whole genome assemblies." Maize Genetics Conference. March 2020.
- 2020 "Dynamic TE transcripts suggest open chromatin in repetitive regions of the maize genome." Maize EPIC workshop ahead of the Maize Genetics Conference. March 2020.

POSTER PRESENTATIONS

- 2019 "Transposable element contributions to maize genome variation". 61st Annual Maize Genetics Conference. St. Louis, MO.
- 2018 "Transposable element contributions to structural and epigenomic variation among maize genomes". Meeting on Transposable Elements. Cold Spring Harbor, NY.
- 2017 "Dynamic transposable element expression across development and stress in maize." 59th Annual Maize Genetics Conference. St. Louis, MO.
- 2016 "The rice zygote transcriptome reveals early initiation of the maternal to zygotic transition and partial activation of the paternal genome before the first zygotic cell division." 58th Annual Maize Genetics Conference. Jacksonville, FL.
- 2015 "The maternal to zygotic transition in plants occurs before the first zygotic division." Society for Developmental Biology West Coast Meeting. Yosemite, CA.
- 2014 "Investigating the timing and regulation of the maternal to zygotic transition in plants through the study of gamete and zygote transcriptomes of *Oryza sativa*." 12th International Symposium on Rice Functional Genomics. Tucson, AZ.
- 2012 "Genomics of the maternal to zygotic transition in rice." 54th Annual Maize Genetics Conference. Portland, OR.

AWARDS AND HONORS

- 2020 Liberal Arts and Sciences Dean's Faculty Fellowship
- 2019 Center for Precision Plant Genomics travel award
- 2018 University of Minnesota MPGI travel grant
- 2017 University of Minnesota Postdoctoral Associate Career Development Award
- 2016 Integrative Genetics and Genomics Academic Excellence Award
- 2015 UC Davis Graduate Student Travel Award
- 2015 Henry A. Jastro Graduate Research Scholarship Award
- 2014 Outstanding Poster Award, International Symposium on Rice Functional Genomics
- 2014 Elise Stocking Memorial Fellowship

ACADEMIC SERVICE

- 2021 – 2022 Genetics and Genomics Graduate Group Admissions Committee

- 2020 – 2022 Bioinformatics and Computational Biology Graduate Group Supervisory Committee
- 2020 – 2022 Genetics, Development, and Cell Biology Department Seminar Committee
- 2019 Participated in Congressional Agricultural Research Exhibition and Reception in Washington DC
- 2019 University of Minnesota undergraduate research symposium judge
- 2015 – 2016 Integrative genetics and genomics graduate group student chair
- 2016 Integrative genetics and genomics colloquium planning committee student chair
- 2014 – 2015 Integrative genetics and genomics graduate group admissions committee
- 2012 – 2014 Genetics graduate group recruitment committee

Served as reviewer for peer-reviewed journals (since 2020)

BMC Plant Biology, Frontiers in Genetics, G3, Genes, Molecular Ecology Resources, Nature Plants, New Phytologist, Plant Communications, PLOS Genetics, PNAS, The Plant Journal, Trends in Plant Science

Served as grant external reviewer (since 2020)

NSF PGRP

Israel Science Foundation

Served as reviewer (prior to 2020)

Bioinformatics, Current Biology, Gene, International Journal of Molecular Sciences, Nature Communications, Nature Plants, PLOS Genetics, PNAS, Scientific Reports, The Plant Journal

TEACHING EXPERIENCE

- 2021 Co-Instructor: Intro to Genetics, Iowa State University. Fall 2022.
- 2021 Co-Instructor: Analytical Genetics, Iowa State University. Spring 2021.
- 2019 Guest lecturer on molecular markers and gene mapping: Introduction to genetics, University of Minnesota. Instructor: Nathan Springer. April 2019.
- 2017 Guest lecturer on transposable elements: Plant genomics, University of Minnesota. Instructor: Cory Hirsch. September 2017.
- 2017 Guest lecturer on plant reproduction: Introduction to genetics, University of Minnesota. Instructor: Nathan Springer. February 2017.
- 2015 Teaching assistant: Principals of genetics laboratory, University of California, Davis. Instructors: JoAnne Engebrecht and Venkatesan Sundaresan.
- 2014 Guest lecturer on gametophyte genetics: Plant biology graduate group core course series, University of California, Davis. Instructor: Luca Comai.
- 2012 – 2014 Instructor, University of Oklahoma-University of California Davis Summer Internship Program in Plant Molecular Biology.
- 2013 Teaching assistant: Introductory genetics, University of California, Davis. Instructors: Michael Turelli and Chuck Langley.

TRAINING

Postdoctoral Trainees

Stephanie Klein (2021 – current).

Graduate Students

Kaitlin Higgins (2020 – current). Interdepartmental Genetics and Genomics and Predictive Plant Phenomics

Undergraduate researchers since 2020

William Clore IV (2020 – current). Iowa State University.

Karli Fritz (2021). Iowa State University.

Ella Townsend (2022 – current). Iowa State University.

POSC Committees

Shatabdi Sen, BCB, Major professor Carson Andorf

Elena (Qiuhan) Jiang, BCB, Major professor Matt Hufford

Sean McLaughlin, IGG, Major professor Erik Vollbrecht

Jennifer Jaqueth, IGG, Major professor Erik Vollbrecht

Madison Lane, MCDB, Major professor Marna Yandau-Nelson

Undergraduate assistants prior to 2020

Dominick Tucker (2015-2016). University of California, Davis.

Jonathan Giesler (2016-2017). University of Minnesota.

Paradis Vandeputte (2017-2018). University of Minnesota.

TRAINEE PRESENTATIONS

- * denotes advised graduate students, # denotes advised undergraduate students

2021 “Identifying putative LTR retrotransposons in maize insertions using LTR Predictor.” #Clore WH, Davis ME, Peterson TA, Anderson SN. Maize Genetics Conference 2021 (virtual). Poster presentation.

2021 “Exploring genetic and epigenetic contributions to imprinting in maize.” *Higgins K, Zeng Y, Kim DW, Gent J, Anderson SN. Maize Genetics Conference 2021 (virtual). Poster presentation.

2020 “Uncovering imprinting of PAV genes and transposable elements using whole genome assemblies.” *Higgins K, Zhou P, Brandvain Y, Springer N, Anderson SN 2020. Maize Genetics Conference 2020 (**canceled due to COVID-19, then hosted virtually**). Poster presentation. https://andersongenomicslab.github.io/posters/Higgins_maize20/.