

# Jaclyn M. Noshay

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## EDUCATION

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### **Doctor of Philosophy in Biological Sciences – University of Minnesota**

Plant Biological Sciences – February 2021

- **Thesis:** Connecting Variation in Genome Structure and Chromatin Composition in *Zea Mays*
- **Advisor:** Nathan Springer

### **Bachelor of Science in Genetics, Cell Biology and Development – University of Minnesota**

College of Biological Sciences - May 2016

**Techniques:** ML, RNA-seq, ATAC-seq, ChIP-seq, HiC, WGBS, DNA/RNA isolation, plant field trials

**Computer Programming:** R, Perl, Python

**Soft Skills:** Critical thinking, Communication, Collaboration, Presentation, Organization

## PROFESSIONAL POSITIONS

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### **Postdoctoral Research Scientist, Computational Systems Biology – Oak Ridge National Lab**

March 2021 – Present

- *Generation of a machine learning predictive model for sgRNA cut site efficiency in non-eukaryotic organisms utilizing iterative random forest processing*
- *SEED-SFA grant proposal lead [A genome editing toolkit for CRISPR-Cas9 sgRNA library generation within the KBase platform]*
- *Group expert in epigenetics*
- *Comparative analysis of epigenetic regulation (ATAC-seq, ChIP-seq, Hi-C, exomSNP) in human brain tissue (multi-tissue, multi-stress)*
- *Structural variation across a poplar population and TE identification*

### **Graduate Research Assistant, Springer Lab – University of Minnesota**

2016 – 2021

- *Field trials, DNA/RNA isolation, and genotyping*
- *Analysis of epigenetic regulation in maize (histone variation and DNA methylation)*
- *Transposable element and DNA methylation association*
- *Large scale computational analysis on genomic datasets (RNA-seq, WGBS, ATAC-seq, ChIP-seq)*

### **Graduate Teaching Assistant, Botany & Bioinformatics – University of Minnesota**

2018

- *Botany: conduct lab sessions, generate weekly lab quizzes, grade lab material and course exams*
- *Bioinformatics: assist in coding lab and hold weekly office hours to help student problem solve coding questions for lab projects*

### **Undergraduate Research Assistant, Springer Lab – University of Minnesota**

2013 – 2016

- *Lab bench, field, computational analysis and interpretation*
- *Characterization of mutant maize phenotypes*
- *Fine-mapping and RNAseq analysis*

## ACTIVITIES

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### Mill City Running – Minneapolis, MN

- **Race Team Member**  
2016 – Present
  - Leading and participating in weekly group runs
  - Boston qualifier 2020, Ultramarathon competitor
- **Employee**  
2019 – 2021
  - Shoe-fit specialist and customer relations on the floor
  - Merchandising and re-stocking

### Graduate Student Committees – Plant and Microbial Biology, University of Minnesota

- **Phytograds President**  
2018– 2019
  - Graduate club group working to organize events to assist in creating a community within the program for support across hierarchical positions as well as to involve students within the university and surrounding regions.
- **Graduate Outreach Committee**  
2017– 2019
  - Organized outreach opportunities for graduate students throughout the Twin Cities community
- **PBS Seminar Committee – University of Minnesota**  
2017– present
  - Assist in invitation and organization of all departmental seminar speakers

### Science Fair Mentor, Murray Middle School – Minneapolis, MN

2016 – 2017

- *Presented to 6<sup>th</sup> and 7<sup>th</sup> grade classrooms regarding how to approach a science fair project*
- *Mentored students on the scientific process for their science fair project*

### Market Science – Minneapolis/St. Paul, MN

2016 – 2018

- *Bringing science to Farmer's Markets around the twin cities area*
- *Outreach to provide and encourage science knowledge in the community*
- *Graduate Student Working Board Member*

### Teaching Abroad, International Volunteer HQ – Cusco, Peru

2015

- *Taught basic English and enhanced social and educational skills in a pre-school classroom*
- *Facilitated introduction of cultural variation within a classroom setting*

## PUBLICATIONS

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Zhikai Liang, Sarah N Anderson, **Jaclyn M Noshay**, Peter A Crisp, Tara A Enders, Nathan M Springer. (2021). Genetic and Epigenetic contributions to variation in transposable element expression responses to abiotic stress in maize. *Plant Physiology*. 186 (1): 420-433.

**Jaclyn M Noshay**, Zhikai Liang, Peng Zhou, Peter A Crisp, Alexandre P Marand, Candice N Hirsch, Robert J Schmitz, Nathan M Springer. Stability of DNA methylation and chromatin accessibility in structurally diverse maize genomes. (2021). *G3 Genes|Genomics|Genetics*. 10.1093/g3journal/jkab190

**Jaclyn M Noshay**, Nathan M Springer. (2021). Stories that can't be told by SNPs; DNA methylation variation in plant populations. *Current Opinion in Plant Biology*. 10.1016/j.pbi.2020.101989

M Li, **J.M Noshay**, X. Dong, N.M Springer, Q. Li. (2021). A capture-based assay for detection and characterization of transposon polymorphisms in maize. *G3 Genes|Genomes|Genetics*. 10.1093/g3journal/jkab138

**Jaclyn M Noshay**, Alexandre P Marand, Sarah N Anderson, Peng Zhou, Maria Katherine Mejia-Guerra, Zefu Lu, Christine O'Connor, Peter A Crisp, Candice N Hirsch, Robert J Schmitz, Nathan M Springer. (2021). Assessing the regulatory potential of transposable elements using chromatin accessibility profiles of maize transposons. *Genetics*. 10.1093/genetics/iyaa003.

Yinjie Qiu, C O'Connor, R Della Coletta, J.S Renk, P Monnahan, **J.M Noshay**, Z Liang, A Gilbert, S.N Anderson, S.E McGaugh, N.M Springer, C.N Hirsch. Whole Genome Variation of Transposable Element Insertions in a Maize Diversity Panel. (2021). *bioRxiv*. 10.1101/2020.09.25.314401

Peng Zhou, T.A Enders, Z.A Myers, E Magnusson, P.A Crisp, **J.M Noshay**, F Gomez-Cano, Z Liang, E Grotewold, K Greenham, N.M Springer. Applying cis-regulatory codes to predict conserved and variable heat and cold stress response in maize. (2021). *bioRxiv*. 10.1101/2021.01.15.426829

**Jaclyn M Noshay**, Alexandre P Marand, Sarah N Anderson, Peng Zhou, Maria Katherine Mejia Guerra, Zefu Lu, Christine O'Connor, Peter A Crisp, Candice N Hirsch, Robert J Schmitz, Nathan M Springer. Assessing the regulatory potential of transposable elements using chromatin accessibility profiles of maize transposons. (2020). *GENETICS*.

Peter A Crisp, Alexandre P Marand, **Jaclyn M Noshay**, Peng Zohu, Zefu Lu, Robert J Schmitz, Nathan M Springer. (2020). Stable Unmethylated DNA Demarcates Expressed Genes and their Cis-regulatory Space in Plant Genomes. *Proceedings of the National Academy of Sciences of the United States of America*, September. 10.1073/pnas.2010250117.

Peng Zhou, Zhi Li, Erika Magnusson, Fabio Gomez Cano, Peter A Crisp, **Jaclyn M Noshay**, Erich Grotewold, Candice N Hirsch, Steven P Briggs, Nathan M Springer. (2020). Meta Gene Regulatory Networks in Maize Highlight Functionally Relevant Regulatory Interactions. *The Plant Cell*. 32 (5): 1377-96.

William A Ricci, Zefu Lu, Lexiang Ji, Alexandre P Marand, Christina L Ethridge, Nathalie G Murphy, **Jaclyn M Noshay**, Mary Galli, Maria Katherine Mejia-Guerra, Maria Colome-Tatche, Frank Johannes, M Jordan Rowley, Victor G Corces, Jixian Zhai, Michael J Scanlon, Edward S Buckler, Andre Gallavotti, Nathan M Springer, Robert J Schmitz, Xiaoyu Zhang. (2019). Widespread long-range cis-regulatory elements in the maize genome. *Nature Plants*. 10.1038/s41477-019-0547-0

Sarah N Anderson, M.C Stitzer, A.B Brohammer, P. Zhou, **J.M Noshay**, C.D Hirsch, J. Ross-Ibarra, C.N Hirsch, N.M Springer. 2019. Transposable elements contribute to dynamic genome content in maize. *The Plant Journal*. 10.1111/tpj.14489

**Jaclyn M Noshay**, Sarah N Anderson, Peng Zhou, Lexiang Ji, William Ricci, Zefu Lu, Michelle Stitzer, Peter A Crisp, Candice N Hirsch, Xiaoyu Zhang, Robert J Schmitz, Nathan M Springer. (2019). Monitoring the interplay between transposable element families and DNA methylation in maize. *PLOS Genetic*. 10.1371/journal.pgen.1008291

Xue W, Sarah Anderson, Xufeng Wang, Liyan Yang, Peter Crisp, Qing Li, **Jaclyn M Noshay**, Patrice Albert, James Birchler, Paul Bilinski Michelle Stitzer, Jeffrey Ross-Ibarra, Sherry Flint-Garcia, Xuemei Chen, Nathan Springer, John

Doebley. (2019). Hybrid decay: a transgenerational epigenetic decline in vigor and viability triggered in backcross population of teosinte with maize. *Genetics*. 10.1534/genetics.119.302378

Sartor C Ryan, **Jaclyn Noshay**, Nathan M Springer, Steven P Briggs. (2019). Identification of the expressome by machine learning on omics data. *PNAS*. 10.1073/pnas.1813645116.

Crisp A Peter, **Jaclyn M Noshay**, Sarah N Anderson, Nathan M Springer. (2019). Opportunities to Use DNA Methylation to Distil Functional Elements in Large Crop Genomes. *Molecular Plant*. <https://doi.org/10.1016/j.molp.2019.02.006>

**Jaclyn M Noshay**, Peter Crisp, Nathan Springer (2018). The Maize Methyloome. *The Zea Mays Genome*.

Springer N.M, S.N. Anderson, C.M. Andorf, K. Ahern, F. Bai, O. Barad, B.W. Barbazuk, H.W. Bass, K. Baruch, G. Ben-Zvi, E.S. Buckler, R. Bukowski, M. S. Campbell, E.K.S. Cannon, P.l Chomet, K.R. Dawe, R. Davenport, H.K. Dooner, L.H. Du, C. Du, K.A. Easterling, C. Gault, J.C. Guan, G. Jander, C.T. Hunter, Y. Jiao, K.E. Koch, G. Kol, T. Kudo, Q. Li, F. Lu, D. Mayfield-Jones, W. Mei, D.R. McCarty, **J.M. Noshay**, J.L. Portwood II, G. Ronen, M.A. Settles, D. Shem-Tov, J. Shi, I. Soifer, J.C. Stein, M. Suzuki, D. L. Vera, E. Vollbrecht, J.T. Vrebalov, D. Ware, X. Wei, K. Wimalanathan, M.R. Woodhouse, W. Xiong, and T.P. Brutnell. (2018). The W22 genome: a foundation for maize functional genomics and transposon biology. *Nature Genetics*. 10.1038/s41588-018-0158-0.

Waters J Amanda, Irina Makarevitch, **Jaclyn M Noshay**, Liana Burghardt, Candice Hirsch, Cory Hirsch, Nathan Springer. (2016). Natural variation for gene expression responses to abiotic stress in maize. *The Plant Journal*. 89. 10.1111/tpj.13414.

## CONFERENCE ABSTRACTS

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**Jaclyn Noshay**. (2020). *The genetic and epigenetic contribution of TEs in shaping the maize genome*. 62<sup>nd</sup> Maize Genomics Meeting. Virtual. (oral presentation)

Peter Crisp, Alexandre Marand, **Jaclyn Noshay**, Lexiang Ji, Zefu Lu, Peng Zhou, Robert Schmitz, Nathan Springer. (2020). *DNA methylomes as a tool fo functional annotation of genes and their regulatory regions*. 62<sup>nd</sup> Maize Genomics Meeting. Virtual

**Jaclyn Noshay**, Sarah Anderson, Zefu Lu, Lexiang Ji, Xiaoyu Zhang, Robert Schmitz, Nathan Springer. (2019). *TE DNA methylation dynamic in maize and the influence on maize regulatory regions*. Gordon Research Conference on Epigenetics. Holderness, NH. Presenting author.

**Jaclyn Noshay**. (2019). *Analysis of Polymorphic TE Insertions in Maize Reveals Family Specific Influences on Insertion Site Preferences and Spreading of DNA methylation*. Plant and Animal Genome Conference XXVII. San Diego, CA. (oral presentation)

Nathan Springer, Sarah Anderson, **Jaclyn Noshay**, Michelle Stitzer. (2018). *Transposable Element Contributions to Dynamics of the Maize Genome and Transcriptome*. Plant and Animal Genome Conference XXVI. San Diego, CA.

**Jaclyn Noshay**, Sarah Anderson, Peng Zhou, Michelle Stitzer, Lexiang Ji, Robert Schmitz, Nathan Springer. (2018). *Documenting the role of transposable elements in DNA methylation variation in maize*. 60<sup>th</sup> Annual Maize Genetics Conference. St. Louis, MO. Presenting author.

Alex Brohammer, Sarah Anderson, **Jaclyn Noshay**, Peng Zhou, Michelle Stitzer, Jeffrey Ross-Ibarra, Nathan Springer, Candice Hirsch. (2018). *Characterization of polymorphic transposable element content between maize inbred lines*. 60<sup>th</sup> Annual Maize Genetics Conference. St. Louis, MO.

**Jaclyn Noshay**, Zefu Lu, Candice Hirsch, Robert Schmitz, Nathan Springer. (2017). *Application of ATAC-seq to monitor variation in open chromatin among maize tissues and genotypes*. 59<sup>th</sup> Annual Maize Genetics Conference. St. Louis, MO. Presenting author.

Steven Briggs, Ryan Sartor, **Jaclyn Noshay**, Nathan Springer. (2017). *W592 DNA Methylation Can be Used to Predict Whether Genes Express Transcripts, Proteins, or Both*. Plant and Animal Genome Conference. San Diego, CA.

**Jaclyn Noshay**, Amanda Waters, Cory Hirsch, Nathan Springer. (2016). *Phylogenetic and transcriptome analysis of CBF and ICE gene families in maize*. 58<sup>th</sup> Annual Maize Genetics Conference. Jackson, FL. Presenting author

**Jaclyn Noshay**, Amanda Waters, Peter Hermanson, Irina Makarevitch, Nathan Springer. (2015). *Characterization of QTL Influencing Seedling Cold Tolerance*. 57<sup>th</sup> Annual Maize Genetics Conference. St. Charles, IL. Presenting author.

## AWARDS

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*Doctoral Dissertation Fellowship (2020)*

*Phinney Fellowship (2020)*

*Center for Precision Plant Genomics Travel Award (2019)*

*ASPB Convivon Scholar (2018-2019)*

*Plant and Microbial Biology Travel Award (2018)*

*CBS Excellence Fellowship (2016-2017)*

*MPGI graduate student recruitment award (2016)*

*MPGI travel award (2017)*

*Bentson Foundation Scholarship (2012-2016)*

*John T Stout Memorial Scholarship (2014-2015)*

*Deans List Fall 2012, Spring 2013, Fall 2013, Spring 2015*