Brandon Monier

Curriculum Vitae
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Professional Experience

2018 - present **Postdoctoral Researcher** in Dr. Ed Buckler's laboratory
School of Integrated Plant Sciences, Cornell University

Education

2018 **Ph.D.** **Department of Biology and Microbiology**
South Dakota State University
Supervisors: Drs. Heike Bücking and Jose Gonzalez-Hernandez

2013 **M.S.** **Department of Agronomy, Horticulture and Plant Science**
South Dakota State University
Supervisor: Dr. Jose Gonzalez-Hernandez

2008 **B.S.** **Microbiology**
South Dakota State Univeristy

Programming Languages

R, Python, Perl, bash/shell, C/C++, markup languages including LaTeX, R Markdown, HTML, CSS, and some superficial knowledge of JavaScript, and Java.

Publications

Master's Thesis

1. Monier, B (2013). "The Analysis of Cytotypic Variation and Construction of a BAC Library of Midwestern Prairie Cordgrass (*Spartina pectinata* Link) Genotypes". MS Thesis. South Dakota State University.

PhD Thesis

1. Monier, B (2018). "Microbial Communities and Their Impact on Bioenergy Crops in Dynamic Environments". PhD thesis. South Dakota State University.

Book Chapters

1. Monier, B, V Peta, J Mensah, and H Bücking (2017). "Inter- and Intraspecific Fungal Diversity in the Arbuscular Mycorrhizal Symbiosis". In: *Mycorrhiza - Function, Diversity, State of the Art*. Ed. by A Varma, R Prasad, and N Tuteja. Cham: Springer International Publishing, pp. 253–274. https://doi.org/10.1007/978-3-319-53064-2_12.

Research Papers (in preparation)

1. Monier, B, M Burch, A DeMell, LA Cat, J Gonzalez-Hernandez, and H Bücking (forthcoming). Impact of the arbuscular mycorrhizal symbiosis on the biomass potential of the bioenergy crop, prairie cordgrass.
2. Monier, B, J Gonzalez-Hernandez, and H Bücking (forthcoming). Transcriptome analysis of a model grass species reveals differential gene expression under mycorrhizal symbiosis.
3. Ma, A, J Xie, B Monier, S Cao, C Zhang, and Q Ma (forthcoming). BRIC: A shiny package for gene regulation inference and cell type prediction based on single-cell RNA-Seq data.

Research Papers

1. McDermaid, A, B Monier, J Zhao, B Liu, and Q Ma (2018). Interpretation of differential gene expression results of RNA-seq data: review and integration. *Briefings in Bioinformatics*, bby067. eprint: /oup/backfile/content_public/journal/bib/pap/10.1093_bib_bby067/2/bby067.pdf.
2. McDermaid, A, B Monier, J Zhao, and Q Ma (2018). ViDGER: An R package for integrative interpretation of differential gene expression results of RNA-seq data. *bioRxiv*. eprint: https://www.biorxiv.org/content/early/2018/02/21/268896.full.pdf.

3. Monier, B, A McDermaid, J Zhao, A Fennell, and Q Ma (2018). IRIS-EDA: An integrated RNA-Seq interpretation system for gene expression data analysis. *bioRxiv*. eprint: https://www.biorxiv.org/content/early/2018/06/24/283341.full.pdf.
4. Monier, B, M Burch, A DeMell, LA Cat, J Gonzalez-Hernandez, and H Bücking (forthcoming). Impact of the arbuscular mycorrhizal symbiosis on the biomass potential of the bioenergy crop, prairie cordgrass.
5. Monier, B, J Gonzalez-Hernandez, and H Bücking (forthcoming). Transcriptome analysis of a model grass species reveals differential gene expression under mycorrhizal symbiosis.
6. Ma, A, J Xie, B Monier, S Cao, C Zhang, and Q Ma (forthcoming). BRIC: A shiny package for gene regulation inference and cell type prediction based on single-cell RNA-Seq data.

Teaching and Mentoring Experience

2018 **Teaching Assistant**
BOT-327L, Plant Physiology
South Dakota State University

2016 **Teaching Assistant**
BIOL-153L, General Biology II
South Dakota State University