

**Joseph Guhlin**  
140 Gortner Lab  
1479 Gortner Avenue  
St. Paul, MN, 55108  
469-867-2100  
[guhli007@umn.edu](mailto:guhli007@umn.edu)

## CURRICULUM VITAE

### EDUCATION

#### **Ph.D. Student**

*University of Minnesota, Minneapolis, MN*

2013 – present

Advisor: Dr. Peter Tiffin.

Degree expected December 2017

#### **B.S. Applied Plant Sciences**

2013

*University of Minnesota, Minneapolis, MN*

### EMPLOYMENT

University of Minnesota, Minneapolis, MN

Undergraduate Researcher in Dr. Nevin Young's Lab

2012 – 2013

Minneapolis Community and Technical College, Minneapolis, MN

2009 – 2011

Microbiology and Biotechnology Lab Tech

Engram Nine Inc, Dallas, TX

2006 – 2010

Lead Programmer and Database Administrator

Independent Consulting

2000 – 2006

Programmer and Unix Administrator

### RESEARCH INTERESTS

Genomic architecture underlying complex quantitative traits, Plant breeding and related, Structural variants, QTL Mapping, Protein Interaction Networks, Machine learning applied to biological problems, Large database and dataset integration

## TEACHING INTERESTS

Genetics, Botany, Plant Breeding, Biological Sciences, Genomics, Bioinformatics, Plant-Microbe Interaction

## COMPUTATIONAL SKILLS

- Perl, JavaScript, Clojure, R, UNIX, HTML, Java, Python, BASH Scripting
- Databases, including: MySQL, Neo4j, PostgreSQL
- Short and long read alignment, assembly, analysis, annotation
- SNP Calling, Association Studies, LD Analysis
- Very large datasets, Parallel Programming
- Machine learning (Random Forests, Bayesian Analyses, HMMs)

## TEACHING EXPERIENCE

**Teaching Assistant**, University of Minnesota, Fall 2016

General Biology Lab: Bioinformatics Section

Nominated for 2016 Outstanding Performance Award for Teaching Assistants

**PULSE Workshop**, University of Minnesota, January 2016

Teaching workshop focused on active learning and writing intensive courses

**Preparing Future Faculty**, University of Minnesota, Fall 2014

Instruction for future teachers in a variety of active learning strategies and educational theory.

## PUBLICATIONS

**Guhlin, J.**, Silverstein, K. A.T., Zhou, P., Tiffin, P., Young, N. D. (2017). ODG: Omics database generator – a tool for generating, querying, and analyzing multi-omics comparative databases to facilitate biological understanding. *BMC Bioinformatics*, 18(1), 367.

Burghardt, L.T., **Guhlin, J.**, Chun, C.L., Liu, J., Sadowsky, M.J., Stupar, R.M., Young, N.D., Tiffin, P. (2017). Transcriptomic basis of genome by genome variation in a legume-rhizobia mutualism. *Molecular Ecology*.

Zhou, P., Silverstein, K.A.T., Ramaraj, T., **Guhlin, J.**, Denny, R., Liu, J., Farmer, A.D., Steele, K.P., Stupar, R.M., Miller, J.R., Tiffin, P., Mudge, J., Young, N.D. (2017). Exploring structural variation and gene family architecture with *De Novo* assemblies of 15 *Medicago* genomes. *BMC Genomics*, 18(1), 261.

Curtin, S. J., Tiffin, P., **Guhlin, J.**, Trujillo, D. I., Burghardt, L. T., Atkins, P., Baltes, N. J., Denny, R., Voytas, D. F., Stupar, R. M., & Young, N. D. (2017). Validating Genome-Wide Association candidates through quantitative variation in nodulation. *Plant Physiology*, pp-01923.

Shamseldin, A., Nelson, M. S., Staley, C., **Guhlin, J.**, & Sadowsky, M. J. (2016). Draft genome sequences of four novel thermal-and alkaline-tolerant Egyptian Rhizobium strains nodulating berseem clover. *Genome Announcements*, 4(5), e00988-16.

Zhou, P., Silverstein, K. A., Gao, L., Walton, J. D., Nallu, S., **Guhlin, J.**, & Young, N. D. (2013). Detecting small plant peptides using SPADA (Small Peptide Alignment Discovery Application). *BMC bioinformatics*, 14(1), 335.

*Manuscripts in Review:*

\*Nelson, M. S., \***Guhlin, J.**, Epstein, B., Tiffin, P., Sadowsky, M. "Replicons and Horizontal Gene Transfer."

\* *These authors contributed equally to this work.*

Burghardt, L.T., Epstein, B., **Guhlin, J.**, Nelson, M.S., Taylor, M.R., Young, N.D., Sadowsky, M.J., Tiffin, P. Revealing rhizobial fitness across symbiotic and free-living environments: identifying fitness tradeoffs and genomic variants.

*Manuscripts in Preparation:*

**Joseph Guhlin**, Kevin AT Silverstein, Peng Zhou, Andrew Farmer, Peter Tiffin, Nevin D. Young. Standing Variation in Copy Number of NCRs plays a role in Rhizobial Nodulation. Submission expected Fall 2017.

**SCIENTIFIC PRESENTATIONS**

*Medicago Genetics and Genomics Workshop* 2016  
Structural Variation and its Potential Role in Rhizobial Nodulation. **Joseph Guhlin**, P. Tiffin, N. D. Young

*Plant Biology 2015, Minneapolis, MN* 2015  
Standing Variation in Copy-Number of Nodule Cysteine-Rich Peptides Plays a Role in Rhizobial Nodulation. **Joseph Guhlin**, K. AT Silverstein, P. Zhou, A.Farmer, P. Tiffin, N. D. Young

*Plant Biological Sciences Retreat, Minneapolis, MN* 2015

Genome Wide Association Study Using Copy-Number Variants in *Medicago truncatula*. **Joseph Guhlin**, K. AT Silverstein, P. Zhou, A. Farmer, P. Tiffin, N. D. Young

*Plant and Animal Genome Conference, San Diego, CA* 2015  
Genome Wide Association Study Using Copy-Number Variants in *Medicago truncatula*. **Joseph Guhlin**, K. AT Silverstein, P. Zhou, A. Farmer, P. Tiffin, N. D. Young

*Plant and Animal Genome Conference, San Diego, CA* 2015  
Genome Wide Association Study Using Copy-Number Variants in *Medicago truncatula*. **Joseph Guhlin**, K. AT Silverstein, P. Zhou, A. Farmer, P. Tiffin, N. D. Young

*Plant and Animal Genome Conference, San Diego, CA* 2015  
Multiple *Medicago* assemblies Enable Analysis of Large Gene Families on a Genome Scale. P. Zhou, K. AT Silverstein, J. R. Miller, J. Mudge, R. M. Stupar, P. Tiffin, A. D. Farmer, **J. Guhlin**, R. Denny, N. D. Young

*Plant and Animal Genome Conference, San Diego, CA* 2014  
ODG: A Graph Database Generator for Omics Data. **J Guhlin**, K. AT Silverstein, P. Zhou, S. Curtin, R. Denny, T. Wennblom, N. D. Young

*Plant and Animal Genome Conference, San Diego, CA,* 2014  
A genome engineering toolbox for legume functional genomics Curtin SJ, Denny R, **Guhlin J**, Michno JM, Campbell BW, Donohue RC, Cermak T, Christian M, Atkins P, Baltes N, Starker C, Zhang Y, Yiping Q, Tiffin P, Voytas DF, Stupar RM and Young ND

*Undergraduate Research Opportunities, Minneapolis, MN* 2013  
Prioritizing Genome Wide Association Candidates: An Informatic Approach **J Guhlin**, K. AT Silverstein, N. D. Young

*Student Science, Minneapolis Community and Technical College, Mpls, MN)* 2010  
Nickel Accumulation in *Solanum lycopersicum* in Hydroponic Systems, **J. Guhlin**

## HONORS AND AWARDS

MnDRIVE Fellowship from University of Minnesota Informatics Institute 2016  
Plant Biological Sciences Summer Fellowship 2015

## PROFESSIONAL ACTIVITIES

Plant Biological Sciences Speaker Seminar Series Committee 2016-2017

## RESEARCH EXPERIENCE

*Research Assistant:* Plant Biological Sciences, 2013 – Present  
Medicago HapMap Project: SNP Calling, Genome Wide Association Studies,  
Structural Variant detection and Analysis, Informatics Support, Contact for  
Collaborators, Population Studies on Rhizobial Genomes

Advisor: Dr. Peter Tiffin  
*University of Minnesota, Minneapolis, MN*