

## Steven Higgins, PhD

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### Professional Preparation

University of Massachusetts	Amherst, MA	Biology	B.S. ( <i>Cum Laude</i> )	2008
University of South Dakota	Vermillion, SD	Biology	M.S.	2011
University of Tennessee	Knoxville, TN	Microbiology	Ph.D.	2011- 2017
		Minor in Computational Science		2017

### Appointments

Postdoctoral researcher	Cornell University	July 2017 - Present
Graduate Research Assistantship	Univ. of Tennessee	Feb 2016 – June 2017
DOE SCGSR Fellowship (SCGSR)	Oak Ridge National Laboratory	Feb 2015 – 2016
Graduate Research Assistantship	Univ. of Tennessee	July 2013 – Jan 2015
SCALE-IT NSF IGERT Fellowship	Univ. of Tennessee	June 2011 – June 2013
Graduate Teaching Assistantship	Univ. of South Dakota	January 2009 – May 2011
Field Technician	Univ. of South Dakota	May – August, 2008 - 2010
Field Technician	Univ. of South Dakota	May – August 2007
Research Assistant	Univ. of Massachusetts	Sept. 2007 – May 2008

### First Author Publications

**Higgins, S.A.**, Schadt, C.W., Matheny, P.B., and Frank E. Löffler. 2018. Phylogenomics reveal the dynamic evolution of fungal nitric oxide reductases and their relationship to secondary metabolism. *Genom. Biol. Evol.*, 10 (9), 2474-2489. <https://doi.org/10.1093/gbe/evy187>

**Higgins, S.A.** 2017. Detection, diversity, and evolution of fungal nitric oxide reductases (P450nor) (Doctoral dissertation). University of Tennessee, Knoxville, TN, USA. Available from [https://trace.tennessee.edu/utk\\_graddiss/4693/](https://trace.tennessee.edu/utk_graddiss/4693/)

**Higgins, S.A.**, Welsh, A., Orellana, L.H., Konstantinidis, K. T., Chee-Sanford, J. C., Sanford, R. A., Schadt, C.W., and Frank E. Löffler. 2016. Detection and diversity of fungal nitric oxide reductase genes (*p450nor*) in agricultural soils. *Appl. Env. Micro.*, 82 (10), 2919-2928. <http://dx.doi.org/10.1128/AEM.00243-16>

### Manuscripts in Preparation

**Higgins, S.A.**, Panke-Buisse, K., and Daniel H. Buckley. *In prep.* An *rpoB* gene primer set for high throughput sequencing of *Streptomyces* populations and its application to New Zealand soils. Submission expected summer 2020.

**Higgins, S.A.** and Daniel H. Buckley. *In prep.* Biogeography, functional diversity, and community assembly of the genus *Streptomyces* across the conterminous USA and Mexico. Submission expected summer 2020.

**Higgins, S.A.** Debenport, S.J., and Daniel H. Buckley. *In prep.* Soil microbial community response to <sup>13</sup>C-labeled oak litter additions. Submission expected summer 2020.

**Higgins, S.A.**, Debenport, S.J., and Daniel H. Buckley. *In prep.* The effect of N deposition on microbial communities and carbon dynamics in northeastern US forest soils. Submission expected summer 2020.

### **Other Publications**

Drott, M.T., Debenport, T., **Higgins, S.A.**, Buckley, D.H., and Michael G. Milgroom. 2019. Fitness cost of aflatoxin production in *Aspergillus flavus* when competing with soil microbes could maintain balancing selection. *mBio*. 10 (1), e02782-18.

Kleindienst, S., Chourey, K., Chen, G., Murdoch, R.W., **Higgins, S.A.**, Iyer, R., Campagna, S.R., Mack, E. E., Seger, E.S., Hettich, R.L., Löffler, F.E. 2019. Proteogenomics reveals novel reductive dehalogenases and methyltransferases expressed during anaerobic dichloromethane metabolism. *Appl. Env. Micro.*, 85 (6), e02768-18.

**Higgins, S.A.**, Padilla-Crespo, E, and Frank E. Löffler. 2018. Draft genome sequences of the 1,2-dichloropropane-respiring *Dehalococcoides mccartyi* strains RC and KS. *Micro. Resour. Announc.*, 7 (10), e01081-18.

Shwab, E.K., Saraf, P., Zhu, X., Zhou, D., McFerrin, B.M., Daniel Ajzenberg, Gereon Schares, Kenneth Hammond-Aryee, Paul van Helden, **Higgins, S.A.**, Richard W. Gerhold, Benjamin M. Rosenthal, Xiaopeng Zhao, Jitender P. Dubey, and Chunlei Su. 2018. Human impact on the diversity and virulence of the ubiquitous zoonotic parasite *Toxoplasma gondii*. *PNAS*. 115 (29), E6956-E6963.

Yang, Y., **Higgins, S.A.**, Yan, J., Şimşir, B., Chourey, K., Hettich, R.L., Baldwin, B., Ogles, D.M., and Frank E. Löffler. 2017. Grape pomace compost harbors strictly organohalide-respiring *Dehalogenimonas* species with novel reductive dehalogenase genes. *ISME J.*, 11, 2767–2780.

Kleindienst, S., **Higgins, S.A.**, Tsementzi, D., Chen, G., Konstantinidis, K.T., Mack, E.E., and Frank E. Löffler. 2017. '*Candidatus* Dichloromethanomonas yunquensis' gen. nov., sp. nov., a dichloromethane-degrading anaerobe of the *Peptococcaceae* family. *Sys. Appl. Microbiol.* 40 (3), 150-159.

Kleindienst, S., **Higgins, S.A.**, Tsementzi, D., Kostantinidis, K.T., Mack, E.E., and Frank E. Löffler. 2016. Draft genome sequence of a strictly anaerobic dichloromethane-degrading bacterium. *Genome Announc.*, 4 (2), e00037-16. <http://dx.doi.org/10.1128/genomeA.00037-16>.

Tang, S., Wang, P., **Higgins, S.A.**, Löffler, F.E., and Elizabeth A. Edwards. 2016. Sister *Dehalobacter* genomes reveal specialization in organohalide respiration and recent strain differentiation likely driven by chlorinated substrates. *Front. Microbiol.* <http://dx.doi.org/10.3389/fmicb.2016.00100>

Orellana, L. H., Rodriguez-R, L. M., **Higgins, S.**, Chee-Sanford, J. C., Sanford, R. A., Ritalahti, K. M., Konstantinidis, K. T. (2014). Detecting nitrous oxide reductase (NosZ) genes in soil metagenomes: method development and implications for the nitrogen cycle. *mBio*, 5 (3), e01193–14. <http://dx.doi.org/10.1128/mBio.01193-14>.

Justicia-Leon, S. D., **Higgins, S.**, Mack, E. E., Griffiths, D. R., Tang, S., Edwards, E. A., and Frank E. Löffler. 2014. Bioaugmentation with distinct *Dehalobacter* strains achieves chloroform detoxification in microcosms. *Eviron Sci Tech*, 48 (3), 1851-1858. <http://dx.doi.org/10.1021/es403582f>

**Higgins, S.A.**, and D. L. Swanson. 2013. Urea is not a universal cryoprotectant among hibernating anurans: Evidence from the freeze-tolerant boreal chorus frog (*Pseudacris maculata*). *Comp. Biochem. Phys. A.*, 164 (2), 344-350. <http://dx.doi.org/10.1016/j.cbpa.2012.11.002>

### **Selected Posters and Oral Presentations**

- Microbiology @ Cornell Symposium** 2018  
*Oral presentation*  
 The dynamic evolution of fungal nitric oxide reductases and their relationship to secondary metabolism
- USDA NIFA Project Directors Annual Meeting** 2018  
*Poster presentation*  
 Impacts of nitrogen and sulfur deposition on microbial community dynamics in forest soils
- Middle Atlantic States Mycology Conference (MASMC)** 2017  
*Oral Presentation*  
 More than just passing gas: phylogenomic analyses indicate widespread gene transfer of fungal nitric oxide reductases (*p450nor*) and support an undiscovered role for *p450nor* in secondary metabolism
- Genomics of Energy and the Environment Meeting** 2016  
*Poster Presentation*  
 Comparative genomics of N<sub>2</sub>O-producing fungi reveals extensive denitrification gene modularity and cryptic nitrate utilization genotypes
- International Society for Microbial Ecology Meeting** 2016  
*Poster Presentation*  
 Combined internal transcribed spacer (ITS2) and *p450nor* amplicon sequencing reveals the spatiotemporal dynamics of soil fungal denitrifier communities
- 3rd Annual Southeastern Biogeochemistry Society Meeting** 2016  
*Poster Presentation*  
 The fungal contribution to nitrous oxide formation: Are substrate induced respiration inhibition (SIRIN) studies misleading?
- Middle Atlantic States Mycology Conference (MASMC)** 2015  
*Oral Presentation*  
 Growth and denitrification potential of a *Guehomyces pullulans* soil isolate
- 2rd Annual Southeastern Biogeochemistry Society Meeting** 2015  
*Oral Presentation*  
*p450nor* amplicon sequencing reveals the spatiotemporal dynamics of soil fungal denitrifier communities

### Synergistic Activities

- Undergraduate Research Mentor** Sept. 2018 – Present  
 Assisting Mr. Ethan Katcher with cultivation of a diversity of *Streptomyces* species from US soils using a variety of media. Characterization of the *Streptomyces* isolates will be performed by amplicon and whole genome sequencing with the goal of correlating soil edaphic characters with *Streptomyces* genetic variation.
- School of Integrative Plant Science (SIPS) BioBlitz** Sept. 2017  
 Assisted with soil sampling, DNA extractions, PCR amplifications, and analysis of 16S rRNA gene amplicons collected from a diversity of environments around Tompkins County, NY. Manned the 'Team Microbe' BioBlitz booth during the event.
- Environmental Microbiology KidsU Course** June 2013, 2014, 2015

Co-designed and -taught a week long laboratory-based course entitled, “The Unseen World: Microbes and the Environment”. The course catered to 9-12 grade students interested in environmental microbiology. Students are allowed to sample sediment and soil near Second Creek on the University of Tennessee campus and construct Winogradsky columns, perform DNA extractions, PCR, and learn about the microbiology of this human impacted system.

**Post-Baccalaureate Research Mentor**

April – Sept. 2016

Assisted Ms. Mary Price with cultivation efforts of bacteria and fungi capable of growing on lignin and inorganic nitrogen isolated from soils derived from Puerto Rico. Guided Ms. Price’s microbial cultivation and isolation technique, including medium preparation, microscopy, staining, and finding resources for identification of bacteria and fungi by both morphological and taxonomic methods.

**NSF Research Experience for Undergraduates (REU) Mentor**

June – August 2013

Directed the research experience of Mr. Francisco Lopez, an undergraduate from the Rochester Institute of Technology. Francisco’s research culminated in the creation of a 16S rRNA gene clone library that complemented short sequence read metagenomic DNA libraries from a dichloromethane degrading consortium. Mr. Lopez was also instructed on best practices in preparation and maintenance of anoxic microcosms and use of analytical instrumentation (gas chromatography equipped with a flame ionization detector) for monitoring dichloromethane.

**Contribution of *p450nor* gene alignments to the public Fungene database**

August 2016

Provided *p450nor* alignments and profile hidden markov models derived from alignments to automate *p450nor* searches and allow the public access to an easily accessible repository for these diverse sequences.