

# Steven Higgins

Doctoral Candidate

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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

## Appointments

Graduate Research Assistantship	Univ. of Tennessee	Feb 2016 – Present
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

## Relevant Publications

**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>.

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>.

## Manuscripts in Preparation

**Higgins, S.A.**, Schadt, C.W., Matheny, P.B., and Frank E. Löffler. *In prep.* Phylogenomics of Fungi enable detection of extensive horizontal gene transfer events among *p450nor* and reveal new implications for its function in soils. Submission expected 2016.

**Higgins, S.A.**, Schadt, C.W., Chee-Sanford, J. C., Sanford, R. A., and Frank E. Löffler. *In prep.* High throughput sequencing analysis of fungal *p450nor* and ITS2 gene regions reveals a shift in functional, but not overall, community structure due to pH and moisture and implications for fungal denitrification. Submission expected early 2017.

**Higgins, S.A.**, Schadt, C.W., Chee-Sanford, J. C., Sanford, R. A., and Frank E. Löffler. *In prep.* Evaluation of the substrate induced respiration inhibition (SIRIN) technique applied to fungal denitrification reveals substantial bias and limitations for assessing the contribution of fungi to nitrous oxide production in soils. Submission expected 2017.

### Other Publications

Yang, Y., **Higgins, S.A.**, Yan, J., Şimşir, B., Chourey, K., Hettich, R.L., Baldwin, B., Ogles, D.M., and Frank E. Löffler. *In review*. Grape pomace compost harbors strictly organohalide-respiring *Dehalogenimonas* species with novel reductive dehalogenase genes. *ISME J.* Expected Dec. 2016.

Kleindienst, S., **Higgins, S.A.**, Tsementzi, D., Chen, G., Konstantinidis, K.T., Mack, E.E., and Frank E. Löffler. *In review*. 'Candidatus Dichloromethanomonas yunquensis' gen. nov., sp. nov., a dichloromethane-degrading anaerobe of the *Peptococcaceae* family. *Sys. Appl. Microbiol.* Expected Dec. 2016.

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>

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>

### Synergistic Activities

#### **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.