

# Dean Sanders

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## Education:

### University of Wisconsin-Madison

Ph.D. Genetics

Madison, WI

Fall 2013 - Fall 2018

### University of Wisconsin-Madison

M.S. Bacteriology

Madison, WI

Fall 2011 - Spring 2013

### University of Wisconsin-Oshkosh

B.S. Microbiology

Oshkosh, WI

Fall 2008 - Spring 2011

## Skills:

### Computational experience:

- **Designed** bioinformatic pipelines for:
  - Genotype By Sequencing
  - *de novo* genome assembly
  - Genome Wide Association Studies
  - mRNA, ChIP, Bisulfite Seq
- **Proficiency in Python and R** for program design and **HTML, CSS, Javascript** for interactive report generation:
  - Pandas, Numpy, Scipy, Multiprocessing, and Cython
  - dplyr, ggplot2, Bioconductor packages
  - Jupyter notebook (Python 3 and R)
  - Wrote automated HTML reporting for GBS analysis
- **Develops software using** accepted software reproducibility practices, container based and virtualized environments:
  - git
  - Conda
  - Docker and Singularity
- **Direct experience** using high throughput computing systems:
  - Sun Grid Engine
  - Condor
  - Amazon Web Services
- Eight years experience using Unix Shell

**Analytical techniques:** Personal experience with ESI-MS/MS orbi-trap mass spectrometry and HPLC, sample prep and MS/MS data analysis

**General molecular biology:** Site directed mutagenesis, plasmid Isolation, molecular cloning, PCR, Sanger sequencing

**Microscopy:** Performed Epifluorescence and Confocal Microscopy

## Experience:

### Computational Biologist at the University of Wisconsin Bioinformatics

**Resource Center** with Dr. Derek Pavelec and Dr. Mark Berres, University of Wisconsin, Madison. December 2018 - Present.

- ❖ Genotype by sequencing
- ❖ SNP imputation
- ❖ GWAS and QTL analysis
- ❖ *de novo* genome assembly
- ❖ mRNA and Bisulfite-seq analysis

**Graduate research assistant investigating histone lysine to methionine mutations and loss of DNA methylation during plant development and stress in *Arabidopsis thaliana*** with Dr. Xuehua Zhong, University of Wisconsin, Madison. December 2013 - November 2018.

- ❖ Bioinformatic analysis of mRNA, ChIP, SNP and Bisulfite sequencing data
- ❖ Mass spectrometry sample preparation, injection and customized MS/MS data analysis
- ❖ General molecular cloning, transgenic plant production

**Graduate research assistant examining bacterial biofilm disruption and production of antimicrobial secondary metabolites by the social amoeba *Dictyostelium*** with Dr. Marcin Filutowicz and Dr. Kalin Vetsigian. University of Wisconsin, September 2011- May 2013.

- ❖ Epifluorescence and confocal microscopy
- ❖ C-18 solid phase extraction, HPLC and LC/MS-TOF

### Communication: Mentoring experience:

- Personally mentored two graduate and four undergraduate students (4/6 now pursuing higher education)

### Teaching assistantship:

- 3 semesters TA experience (>20 hours lecture time)

### Python study group leader:

- Member of combee python study group since Fall 2016, leader in Fall 2017

### Scientific meeting presentations:

- 6 conference presentations, 9 public outreach in the Wisconsin Institute for Discovery

### Publications:

**Sanders D \***, Jiang J\*, Wang B, Liu F, Zhong X (2020) CMT2 mutation in a Tibetan A. *thaliana* accession reduces DNA methylation genomewide and increased tolerance to environmental stressors (In preparation)

Jiang J, **Sanders D**, Wang B, Zhong X (2019) Regulation of plant DNA methylation by UV-B (In submission at Mol. Cell)

Mayer K\*, Chen X \*, **Sanders D**, Nyugen P, Moreno G, Zhong X (2019) HOS15 acts with HISTONE DEACETYLASE 9 to modulate transcription and development. Plant Physiology. DOI: <https://doi.org/10.1104/pp.18.0115>

**Sanders D**, Fieweger R, Lu L, Qian S, Dowell J, Denu JM, Zhong X (2017) Histone lysine-to-methionine mutations reduce histone methylation and cause developmental pleiotropy. *Plant Physiology*. 173, 2243-2252.

**Sanders D**, Katarzyna B, Fikrullah K, Rakowski S, Lozano M, Filutowicz M (2017) Multiple dictyostelid species destroy biofilms of *Klebsiella oxytoca* and other Gram negative species. *Protist*. 168, 311-325.

Lu L, Chen X, **Sanders D**, Qian S, Zhong X (2015) High-resolution mapping of H4K16 and H3K23 acetylation reveals conserved and unique distribution patterns in Arabidopsis and rice. *Epigenetics*. 10, 1044-1053.

### Patent:

Marcin Filutowicz, Katarzyna Dorota Borys, **Dean Sanders** (2014). Dictyostelid amoeba and biocontrol uses thereof. US20140056850 A1. Amoebagone, LLC