Dean Sanders

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Education:

University of Wisconsin-Madison	Madison, WI
Ph.D. Genetics	Fall 2013 - Fall 2018
University of Wisconsin-Madison	Madison, WI
M.S. Bacteriology	Fall 2011 - Spring 2013
University of Wisconsin-Oshkosh	Oshkosh, WI
B.S. Microbiology	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