

# John Miraszek

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**Location:** Columbia, MO

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Ph.D. student researching Evolutionary biology, comparative genomics and population genetics using bioinformatic pipelines

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## Education

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<b>University of Missouri, Ph.D. student</b>	2021-Present
Genetics Area Program Supervisor: Dr. Jared Decker	
<b>Temple University, Masters of Science in Biology</b>	2019-2021
Department of Biology Supervisor: Dr. David Liberles	
<b>Penn State Behrend, Bachelors of Science in Biology</b>	2014-2018
College of Science	

## Research Experience

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<b>Decker Lab</b>	2021-Present
Modeling evolutionary history using Population genetics, quantitative genetics, and comparative genomics. Projects currently include detecting signals of selection and admixture in cattle and their wild relatives using whole genome level data at large sample sizes over 5000 individual animals representing over 250 unique breeds, utilizing archeological dating as a variable to detect selection in modern and ancient humans worldwide, modeling population dynamics in an endangered minnow species undergoing government conservation efforts.	
<b>Liberles Research Group</b>	2019-2021
Constructed bioinformatic pipelines for comparative genomic research. Projects included analyzing spider genomics, studying molecular evolutionary pathways in salmon, and modeling whole genome duplication of monocots.	

## **Research assistant Penn State Behrend Genetics Lab**

2018

Performed PCR amplification phylogenetic analysis of the highly conserved barcoding gene CO1 from insect DNA samples collected from Behrend campus as part Gruwell Lab's project to catalog the diversity of arthropods on campus

- Scholarship And Research Integrity (SARI) training requirements completed
- Penn State Environmental Health and Safety (EHS) training completed

## **Publications**

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Miraszek, John Louis. *Construction of a Spider Comparative Genomic Database for Analyzing the Araneae Tree of Life*. Temple University, 2021.

Henry, C. Nicholas, Kathryn Piper, Amanda E. Wilson, John L. Miraszek, Claire S. Probst, Yuying Rong, and David A. Liberles. "WGDTree: a phylogenetic software tool to examine conditional probabilities of retention following whole genome duplication events." *BMC bioinformatics* 23, no. 1 (2022): 1-15.

## **Conference Attendance, Oral and Poster Presentations**

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### **The Allied Genome Conference (TAGC24) 2024**

Poster first author "Whole genome sequence data elucidates signatures of cattle domestication and global bovid migration patterns"

### **Plant and Animal Genome Conference (PAG 31) Domestication Session 2024**

Oral presentation "Whole genome sequence data elucidates signatures of cattle domestication and global bovid migration patterns"

### **Plant and Animal Genome Conference (PAG 31) Populations and Conservation Genomics I Session 2024**

Oral presentation "Whole genome sequence data identifies admixture and selection in wild members of the Bos genus"

### **Plant and Animal Genome Conference (PAG 31) 2024**

Poster first author "Whole genome sequence data elucidates signatures of cattle domestication and global bovid migration patterns"

### **The Gordon Research Conference (GRC) on Quantitative Genetics and Genomics 2023**

Poster first author "Cattle Demography and Evolution"

### **Tel Aviv, Toronto, Temple (T3) Molecular Evolution Symposium 2021**

Attendee

## **Great lakes Annual Meeting of Evolutionary Genomics (GLAM-evogen) 2020**

Attendee

## **Evolution in Philadelphia Conference (EPIC) 2019**

Poster middle author "Whole genome duplication events drive diversification of myostatin in Salmonidae"

## **Teaching Experience**

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### **TA AnSci 4323 Applied Livestock Genetics**

January-May 2023

Led lectures presenting new units on historical genetics theories and practical quantitative approaches for over 100 upperclassmen in animal science. met with students to provide feedback, answer questions and concerns, assist with missed classes and explain homework problems. Responsible for reviewing and grading honor section students assigned R programming problems, and providing lessons in syntax, better programming practices, and debugging procedures in the effort to familiarize with and encourage students to pursue future works in animal science computational research.

### **Grader AnSci 4323 Applied Livestock Genetics**

May 2022

Graded and provided feedback on over 50 student end of term project papers where they had to design a breeding program for a species of their choosing and use the lesson material from the course to justify their approaches.

## **Memberships**

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Genetics Society of America 2023

Society for the Study of Evolution 2024

American Genetic Association 2024

## **Administrative Experience**

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### **Liberles Lab Systems Administrator**

August 2019 - July 2021

Responsible for upkeep over 20 dedicated computing machines, ensured regular data backup, proper compilation of programs essential for each of the lab's research projects, performed data recoveries, reconstructions of computer hardware, operating system reinstallations, maintained remote connectivity to

laboratory computers using a secure shell client for each member of the research group.

## Public Outreach

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### **Dogwood Elementary School Field Day DNA Demonstration and Activity** May 23<sup>rd</sup> 2023

Instructed school children from Kindergarten to 5th grade with a hands-on activity where each student or a pair of students extracted DNA from strawberries. Gave age appropriate information and fun facts about biology, DNA and cells. Provided demonstration of the extraction experiment with easy to follow explanations for what each step is for. Brought supplies and led parent volunteers in distributing and supervising each student's experiment. Encouraged students to consider studying or careers related to science, and to think like a scientist when encountering everyday things like the strawberries in the experiment. Dogwood Elementary School 1400 Cedarwood Pkwy, Kearney, MO 64060

### **Show-Me Research Week**

April 18<sup>th</sup> 2023

Presented the genetics of cattle evolution and outlined our designs to uncover selection on polygenic traits to a diverse multidisciplinary community of researchers, community members, students and educators. Fielded questions on population genetics methods and discussed applications for agricultural, industrial and anthropological studies.

## Seminar and Journal Club Presentations

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2024-Present

### **MUGenomics Journal Club**

Developed a new format of graduate student only journal club, bringing together students from diverse research disciplines related to genomics. Designed a goal oriented purpose to journal paper discussion to maintain student engagement and increase exercises in literacy of technical papers. Incentivized participation through the shared goal of writing a literature review on reference genomes and their future in cattle genomics.

2023-Present

### **MU Genetics Discussion group**

Weekly discussion of broad topics in genetics and genomics with faculty and student participation. Presented papers related to archaic hominid genomics,

mammoth population genomics, nuclear insertions of mitochondrial DNA, evolution of dynamic metapopulations, key innovation hypotheses.

2022

### **Evolutionary Biology Seminar**

Presented on history and development and limitations of GWAS and quantitative genetics, and the biological reasoning and statistical pitfalls of measuring heritability, distributions of selection, complex traits and non-mendelian inheritance. October 25<sup>th</sup> 2022

Selected literature for and presented on utility of different species concepts, elaborated on consideration of population dynamics, and levels of selection. September 6<sup>th</sup> 2022

### **MUGenomics Journal Club**

Led discussion on a comparative genomics study of mammalian lifespan variability GWAS studies of hyper-complex phenotypes, and limitations thereof. February 8<sup>th</sup> 2022

2021

### **MUGenomics Journal Club**

Showcased recent publication on signatures of domestication in the genomes of Chinese Donkeys, for a methodological comparison to work in other domestic species. October 4<sup>th</sup> 2021

### **Temple Center for Computational Genetics and Genomics (CCGG) Journal Club**

Highlighted state of the art sequencing and imaging technologies used to uncover the origin of Monotreme sex chromosomes, and discussed the implications for placental mammals January 19<sup>th</sup> 2021

Brought forward a paper challenging conventional molecular frameworks and delved into considerations for the underexplored realm of microproteins November 3<sup>rd</sup> 2020

## **Leadership & Involvement**

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### **Tea Institute at Penn State**

January 2015 – December 2016

*Director of Research*, Penn State University, University Park, PA

Conducted interdisciplinary research on the development of tea material and culture. Organized and led weekly lessons for groups of 20 students. Coordinated international exhibitions with tea scholars from overseas.

# Languages and Skills

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**English-** Native

**Spanish-** Proficient (10+ years experience)

## **Computer Skills**

**Computational/Programming skills:** LINUX, Slurm, Python, R, MySQL, Perl, Minitab

**Software skills:** Eigensoft, Plink, TreeMix, Admixtools, VMD, Adobe Photoshop,  
SolidWorks, Microsoft Office