

**Meng Yuan**

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## RESEARCH EXPERIENCE

**Doctoral Researcher**, University of Toronto *2019 - Present*

- Developed and managed research projects combining experiments and genomics to understand the genome-wide importance of haploid selection in diverse plant taxa
- Managed and implemented bioinformatic pipelines to analyze high-throughput DNA and RNA sequencing data in high-performance computing environments

**Undergraduate Researcher**, University of Toronto *2018 - 2019*

- Designed project on selfish transmission of sex chromosomes using pooled sequencing
- Developed bioinformatic pipelines for alignment and variant calling, used Python and R to visualize and compare sex-linked and autosomal allele frequencies

**Mitacs Globalink Research Intern**, Simon Fraser University *Summer 2018*

- Developed pipeline for RNA Seq-based analyses of economical traits in conifer species
- Conducted gene expression analysis, GO (gene ontology) and KEGG (Kyoto Encyclopedia of Genes and Genomes) pathway analysis, identified candidate genes for defense traits

**Undergraduate Researcher**, Sichuan University *2017 - 2018*

- Developed bioinformatic pipelines for chloroplast genome assembly and annotation

## EDUCATION

**University of Toronto**, Toronto Canada *2019 - 2024 (expected)*

Ph.D. in Evolutionary genomics

Supervisors: Drs. Stephen Wright, John Stinchcombe

**Sichuan University**, Chengdu China *2015 - 2019*

Honours B.Sc. in Biological Sciences (major), B.E. in Software Engineering (minor)

Courses: Object-oriented Programming (Java), Data Structure & Algorithm, Database System (SQL), Operating Systems, Computer Networking, Software Development Environment & Tools

## PUBLICATIONS

Hibbins MS, Rifkin JL, Choudhury BI, Voznesenka O, Sacchi BM, **Yuan M**, Gong Y, Barrett SC, Wright SI. Phylogenomics resolves key relationships in *Rumex* and uncovers a dynamic history of independently evolving sex chromosomes. *bioRxiv*. 2023:2023-12.

Rifkin JL, Hnatovska S, **Yuan M**, Sacchi BM, Choudhury BI, Gong Y, Rastas P, Barrett SC, Wright SI. 2022. Recombination landscape dimorphism and sex chromosome evolution in the dioecious plant *Rumex hastatulus*. *Philos Trans R Soc Lond B Biol Sci*. 377(1850):20210226.

**Yuan M**, Stinchcombe JR. 2020. Population genomics of parallel adaptation. *Mol Ecol*. 29(21): 4033-4036.

Zhang Z, Dong H, **Yuan M**, Yu Y. 2020. The complete chloroplast genome of *Oenanthe javanica*. Mitochondrial DNA Part B. 5(3):3151-3153.

## PRESENTATIONS AND INVITED TALKS

### Talks

- Yuan M**, Kollar LM, Sacchi BM, Carey SB, Choudhury BI, Barrett SCH, McDaniel SF, Wright SI & Stinchcombe JR. 2024. *Evolutionary genomics of plant gametophytic selection*. Dept of Evolution, Ecology & Paleontology, University of Lille, online. **Invited**
- Yuan M**, Kollar LM, Sacchi BM, Carey SB, Choudhury BI, Barrett SCH, McDaniel SF, Wright SI & Stinchcombe JR. 2023. *Evolutionary genomics of plant gametophytic selection in an angiosperm and a moss species*. Evolution, Albuquerque, NM, US.
- Yuan M**, Kollar LM, Sacchi BM, Carey SB, Choudhury BI, Barrett SCH, McDaniel SF, Wright SI & Stinchcombe JR. 2023. *Evolutionary genomics of plant gametophytic selection in an angiosperm and a moss species*. European Meeting for PhD Students in Evolutionary Biology (EMPSEB28), Scotland, UK. **Best oral presentation runner-up**
- Yuan M**, Kollar LM, Sacchi BM, Carey SB, Choudhury BI, Barrett SCH, McDaniel SF, Wright SI & Stinchcombe JR. 2023. *Evolutionary genomics of plant gametophytic selection in an angiosperm and a moss species*. Atwood Colloquium, University of Toronto, Toronto, ON, Canada.
- Yuan M**, Rifkin JL, Kim D, Jarvis-Cross M, Barrett SCH, Wright SI & Stinchcombe JR. 2021. *Testing for genome-wide balancing selection due to antagonistic pleiotropy between life-stages*. Evolution, online.

### Posters

- Yuan M**, Sacchi BM, Choudhury BI, Rifkin JL, Barrett SCH, Stinchcombe JR & Wright SI. 2022. *Genome-wide characterization of genetic variation for pollen expression in Rumex hastatulus*. Congress of the European Society for Evolutionary Biology (ESEB), Prague, Czech Republic.
- Yuan M**, Rifkin JL, Kim D, Jarvis-Cross M, Barrett SCH, Wright SI & Stinchcombe JR. 2021. *Testing for genome-wide balancing selection due to antagonistic pleiotropy between life-stages*. Society for Molecular Biology and Evolution (SMBE), online.

## SCHOLARSHIPS AND AWARDS

SGS Conference Travel Grant, U of T. \$910	2023
EEB Rustom H. Dastur Graduate Scholarship, U of T. \$3,200	2022, 2023
EEB Harold H. Harvey Travel Award, U of T. \$800	2022, 2023
Mitacs Globalink Graduate Fellowship, Mitacs Canada. \$15,000	2019 – 2020
Outstanding Undergraduate International Exchange Scholarship, China Scholarship Council. \$6,500	2018

## TEACHING AND MENTORING

<b>Teaching Assistant</b> , University of Toronto	
Intro Computation & Data Science for Life & Physical Sciences (EEB125)	Winter 2023
Biostatistics for Biological Science (EEB225)	Fall 2021, 2022, 2023

Adaptation and Biodiversity (BIO120)

*Fall 2019, 2020, 2021*

From Genomes to Ecosystems in a Changing World (BIO220)

*Winter 2021*

### **Undergrad and Grad Mentoring**

Undergrad Thesis Project Supervision (Bioinformatics): Mykhailo Sukmaniuk (2022-23)

Undergrad Thesis Project Supervision (Greenhouse work): Olena Voznesenska (2022-23)

EEB Grad Peer Mentorship Program: Hatena Osawa (2020-21), Xiaozhuo Tang (2021-22)

Undergrad Work-Study Program Supervision: Kieran Guimond, Katie Monat, Anya Gopaul

## **COMMUNITY OUTREACH**

Preprint Editorial Team, Proceedings of the Royal Society B  
Bioinformatics Section

*2020 - Present*

EEB Mental Health Committee Co-Chair, U of T

*2022 - 2023*

EEB Student Journal Club Co-Chair, U of T

*2021 - 2022*

Executive Committee, Chinese Genomics Online Meet-up

*2020*

Peer Review of Academic Journals

- Co-reviewed a manuscript for *Evolution Letters* in 2021 with Dr. John Stinchcombe

Founder and President, Botany Association at Sichuan University

*2016 - 2018*

## **SKILLS**

**Bioinformatics:** Proficient in developing bioinformatic pipelines for analyzing high-throughput sequencing data, specializing in Whole Genome Sequencing (WGS), variant calling, RNA-seq analysis, differential expression analysis, and population genomics

- Tools: Snakemake, Juicebox, LASTZ, BWA, STAR, Picardtools, SAMTools, BCFTools, PLINK, pixy, featureCount, DFE-alpha, Geneious, R packages (Deseq2, ggplot, qtl), etc.

**Programming and Statistics:** Advanced skills in R, Python, Bash, and Linux. Experienced in data wrangling, data visualization, statistical analyses, git version control, and high-performance computing

**Science Communication:** Proficient in public speaking through conference talks and poster presentations. Experienced in academic writing for publications and fostering collaborations within the academic community

**Leadership and Organization:** Demonstrated leadership through teaching undergraduate courses, mentoring undergraduate projects, managing teams, and coordinating students and technicians

**Research Design and Project Management:** Skilled in designing research projects and executing greenhouse experiments (plant crossing and maintenance) and molecular experiments (DNA and RNA isolation)