

Aaron K. Lee

Department of Plant and Microbial Biology
University of Minnesota, Twin Cities
Saint Paul, MN 55108
lee02893@umn.edu || <https://github.com/aaklee>

EDUCATION

University of Minnesota, Twin Cities (UMN), Saint Paul, MN

PhD student in Plant and Microbial Biology, in progress (started Fall 2020)

Advisor: Dr. Ya Yang

The College of New Jersey (TCNJ), Ewing, NJ

BS in Biology with honors, magna cum laude, December 2019
Honors Program

Advisor: Dr. Wendy L. Clement

Honors Thesis: Honeysuckles in the age of genomics: Leveraging big data to study the evolution of organ fusion in a non-model clade

RESEARCH EXPERIENCE

Research Interests

I am broadly interested in plant evolution, and more specifically in connecting the evolution of plant biodiversity to the evolution of its underlying genetic and genomic foundation. I am especially excited about genome and gene family evolution, novel computational and statistical approaches to phylogenetics, and big data applications in plant biology.

Plant Systematics and Evolutionary Biology Lab, TCNJ

PI: Dr. Wendy L. Clement

Mentored Research Student (for-credit), August 2017 – December 2019

Mentored Undergraduate Summer Experience (MUSE), June 2019 – August 2019

Research Technician, January 2020 – July 2020

Dipsacales Phylogenomics. As part of team with collaborators at Yale University, we reconstructed the phylogeny of Dipsacales using the Angiosperms353 bait kit and explored the utility of this approach in evaluating gene tree-species tree concordance, cytonuclear discordance, and species tree dating.

Honeysuckle Phylogenomics. I used genome assembly and identification of orthologous genes from genome skimming and transcriptome data to help develop baits for a targeted enrichment approach to phylogenetic reconstruction of a non-model lineage.

CUC Evolution. I used BLAST-based data mining to recover orthologous *CUP-SHAPED COTYLEDON (CUC)* and related genes from genomic and transcriptomic data of taxa with

sampling focused in the Dipsacales (including *Lonicera*) and extending out to the Asterids. At the bench, I used DNA extraction and cloning to directly sequence these genes in *Lonicera* and relatives, and I used these sequences to support and improve our data mining efforts and gene tree reconstruction.

Herbarium Digitization. I evaluated, accessioned, and digitized 414 120-year-old herbarium specimens from the TCNJ Herbarium (TCNJ) for submission to publicly-accessible museum data repositories.

Evolutionary and Computational Genomics Lab, Michigan State University

PI: Dr. Shin-Han Shiu

Plant Genomics @ MSU (NSF REU), May 2018 – August 2018

Undergraduate Research Assistant (volunteer), August 2018 – December 2019

Tomato Gene Prediction, Mentor: Bethany Moore, PhD Candidate. Through a machine learning approach, I predicted metabolic classifications of enzymatic genes by generating features describing the conservation and duplication of these genes. Following the end of the REU, I generated features describing the genomic clustering of these genes and trained models for pathway-specific gene prediction.

PUBLICATIONS

- **Lee, AK**, I Gilman, M Srivastav, A Lerner, MJ Donoghue, & WL Clement. Reconstructing Dipsacales phylogeny using Angiosperms353: Issues and insights. *American Journal of Botany*, in review.
- Moore, BM, P Wang, P Fan, **AK Lee**, B Leong, YR Lou, CA Schenck, K Sugimoto, R Last, MD Lehti-Shiu, CS Barry, & SH Shiu. 2020. Within and cross species predictions of plant specialized metabolism genes using transfer learning. *in silico Plants*, in press.
<https://doi.org/10.1093/insilicoplants/diaa005>

PRESENTATIONS

Oral Presentations

- **Lee, AK**, M Bhatti, H Rahman-Vyas, DG Howarth, MJ Donoghue, & WL Clement. Honeysuckle (*Lonicera*, Caprifoliaceae, Dipsacales) NAC subfamily Ia evolution and implications for the evolution of organ fusion. *Presented at Botany 2020 (virtual) on 07/30/2020.*
- **Lee, AK**. Honeysuckles in the Age of Genomics: Using Big Data to Study the Evolutionary History of a Non-Model Clade. *Presented in fulfillment of my senior honors capstone at TCNJ (Ewing, NJ) on 12/06/2019.*
- **Lee, AK**. Progress on reconstructing a *CUC* gene tree in Dipsacales and Asterids. *Presented at collaborative NSF grant meeting for NSF DEB-1929670 at Yale University (New Haven, CT) on 11/09/2019.*

- **Lee, AK**, BM Moore, & SH Shiu. Prediction of specialized metabolism genes in *Solanum lycopersicum*. Presented at the Plant Genomics @ MSU Research Symposium (East Lansing, MI) on 07/26/2018.

Poster Presentations

- **Lee, AK**, H Rahman-Vyas, J Walker, MJ Donoghue, SA Smith, DG Howarth, & WL Clement. Exploring the evolutionary history of the *CUP-SHAPED COTYLEDON (CUC)* gene family in the honeysuckles (*Lonicera*, Caprifoliaceae) and relatives. Presented at Botany 2019 (Tucson, AZ) on 08/29/2019, and Evolution in Philadelphia Conference (EPiC) (Philadelphia, PA) on 09/14/2019.
- **Lee, AK**, H Rahman-Vyas, DG Howarth, MJ Donoghue, & WL Clement. Exploring the evolutionary history of the *CUP-SHAPED COTYLEDON (CUC)* gene family in the honeysuckles (*Lonicera*, Caprifoliaceae) and relatives. Presented at the TriBeta NE District 2 Convention (Bloomsburg, PA) on 03/23/2019, and the TCNJ Celebration of Student Achievement (Ewing, NJ) on 05/08/2019.
- Zhang, L*, **AK Lee***, H Rahman-Vyas*, DG Howarth, & WL Clement. Morphological and genomic insights into the evolution of *Lonicera* (Caprifoliaceae). Presented at the Pennsylvania Botany Symposium (State College, PA) on 11/02/2018. Awarded first place, undergraduate poster.
- **Lee, AK**, BM Moore, & SH Shiu. Evolutionary features inform prediction of specialized metabolism genes in *Solanum lycopersicum*. Presented at the Mid-Michigan Symposium for Undergraduate Research Experiences (East Lansing, MI) on 07/24/2018.
- Fertakos, ME*, L Zhang*, **AK Lee***, & WL Clement. Insights from 120 years in the past: Using historical specimens to study plant phenology in Mercer County, NJ. Presented at the TCNJ Celebration of Student Achievement (Ewing, NJ) on 05/02/2018 and the Mid-Atlantic Ecological Society of America (Newark, NJ) on 04/07/2018.

*co-presenters

LEADERSHIP AND SERVICE

2020 – present	Undergraduate Student Mentor, Field Guides UMN (Saint Paul, MN)
2020 – present	K-12 Tutor, EduMate NYC (virtual)
2019 – 2020	STEMNauts Tutor, Children's Home Society of New Jersey (Trenton, NJ)
2019	Awards/Fellowships/Internships Chair, TCNJ Honors Student Advisory (Ewing, NJ)
2019	Course Assistant, Foundations of Biological Inquiry (TCNJ) (Ewing, NJ)
2019	Botany 2019 Student Conference Assistant (Tucson, AZ)
2018 – 2019	BioGuides (TCNJ Biology Department tour guide) (Ewing, NJ)
2018 – 2019	TCNJ Honors Student Advisory Board (Ewing, NJ)
2018 – 2019	Science and Math Peer Tutor, TCNJ Tutoring Center (Ewing, NJ)
2018 – 2019	Secretary, Chi Upsilon Chapter of TriBeta (Ewing, NJ)

2018 – 2019	Science and Math Tutor, HomeFront Family Campus (Pennington, NJ)
2018	Science Fair Judge, Hopewell Elementary Science Fair (Hopewell, NJ)
2017 – 2018	Holiday Co-Chair, Chi Upsilon Chapter of TriBeta (Ewing, NJ)
2017	GED Math Tutor, Trenton Violence Reduction Strategy (Trenton, NJ)

AWARDS AND RECOGNITION

2020	Undergraduate Research Award (American Society of Plant Taxonomists)
2020	Young Botanist Award (Botanical Society of America)
2019	Barry Goldwater Scholarship
2019	Novo Nordisk Student Scholarship (TCNJ)
2019	Mentored Undergraduate Summer Experience Award (TCNJ)
2019	Phi Kappa Phi Student-Faculty Research Award (TCNJ)
2018	First Place, Undergraduate Poster Award (PA Botany Symposium 2018)
2016 – 2019	Merit Scholarship (TCNJ)
2016 – 2019	School of Science Dean's List (TCNJ)
2014 – 2016	Dean's List (RVCC)

SKILLS

Bioinformatics

De novo and reference-based genome/transcriptome assembly, Sequence alignment, Phylogenetic analysis (maximum parsimony, maximum likelihood, Bayesian analysis), Ancestral character state reconstruction, Local BLAST search, and Machine learning (supervised learning in scikit-learn)

Programming Languages

Python 3, R, Bash, Java, and C++

Software

Geneious, Mesquite, Mega, RStudio, Microsoft Office, Adobe Illustrator & Photoshop (working familiarity), and GIMP

Molecular Biology/Benchwork

DNA extraction (Qiagen kit), Cloning, PCR, Quantitative RT-PCR, Gel electrophoresis, DNA quantification (Nanodrop, BioAnalyzer), and *Saccharomyces cerevisiae* and *Drosophila melanogaster* genetics

Languages

Mandarin (native speaker, proficient reader, intermediate writer) and Cantonese (native speaker, intermediate reader/writer)

PROFESSIONAL AFFILIATIONS

American Society of Plant Taxonomists (ASPT)
Beta Beta Beta National Biological Honor Society (TriBeta)
Botanical Society of America (BSA)
Phi Beta Kappa
Phi Kappa Phi