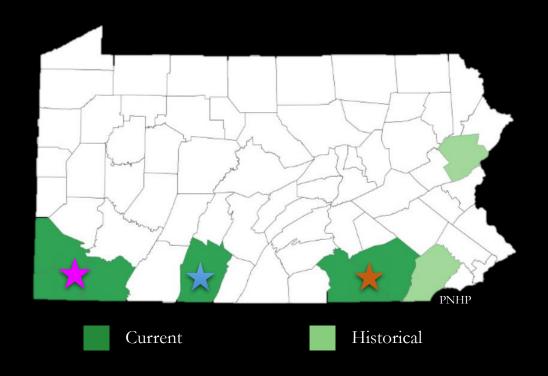
Chasmanthium latifolium in Pennsylvania Critically Imperiled (S1)

- Declining populations
 - Habitat elimination
 - Agriculture, Industry, Housing
 - Damming of rivers
 - Alteration of flood patterns
 - Invasive species
- Disjunct populations
- Edge of range (northeastern edge)



Monongahela (West)

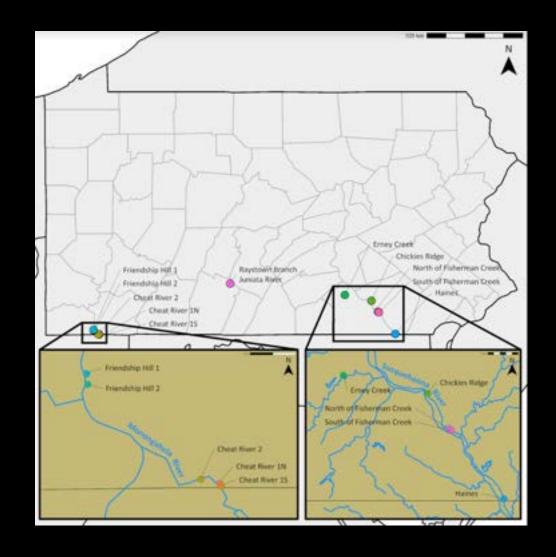
Juniata (Central)

Susquehanna (East)



Sample Collections

- Field collections (Scott, Rachel, Tanisha)
 - 11 populations
 - 7-16 individuals per populations
 - 155 individuals total



Methods

• DNA extraction

• Digestion: ApeKI enzyme

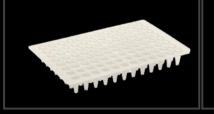
 Genotyping by sequencing (GBS)

• Illumina NovaSeq 6000

• Single nucleotide polymorphisms (SNPs)



Extraction, quantification, adding restriction enzyme, adaptors, and barcodes



Pooling samples and PCR



Sequencing



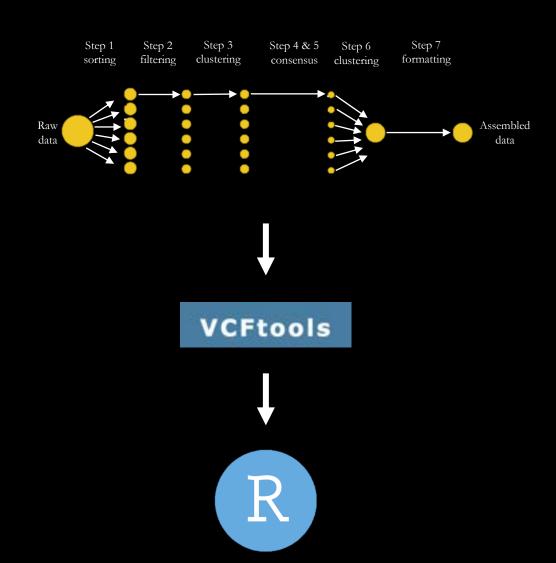




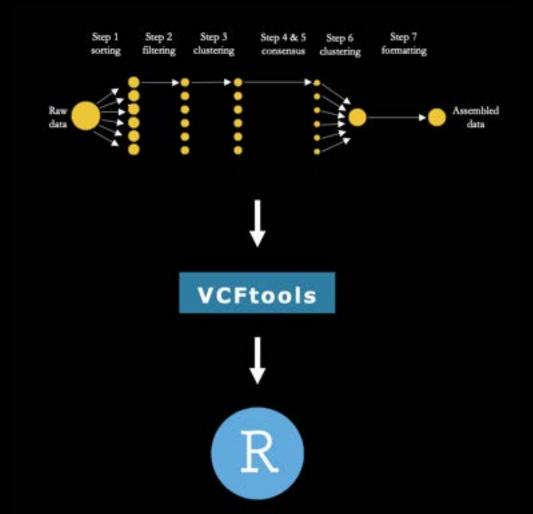
Methods

• Sequences assembled using ipyrad

- Hard Filtering: VCFtools
 - Removed samples with
 - <200,000 raw reads
 - Missingness ≥ 55% of loci across 75% of samples
- All populations genetics analyses done in R



Methods





Dr. Angela McDonnell



Workshop on population and speciation genomics (Czech Republic)





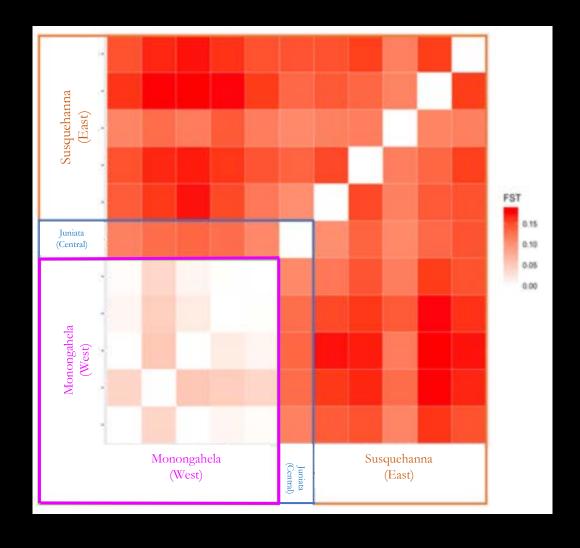
- 133 individuals across 11 populations
- 2 million reads per sample (average)
- 1,000 loci
 - 1,998 SNPs



- Overall F_{ST}
 - $F_{ST} = 0.1130$

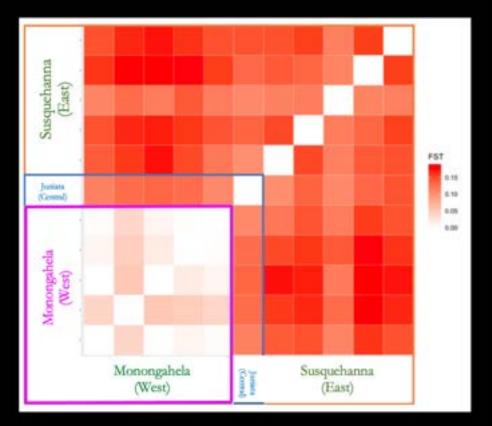


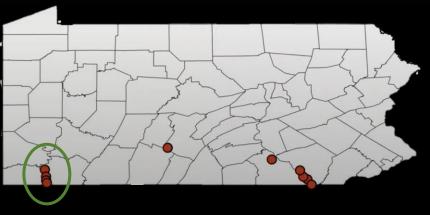
• Pairwise F_{ST}





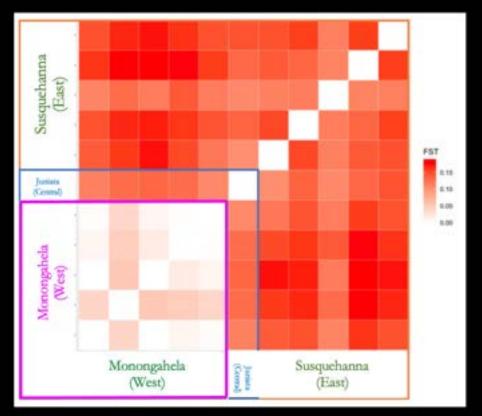
- Pairwise F_{ST}
 - A lot of gene flow between western pops

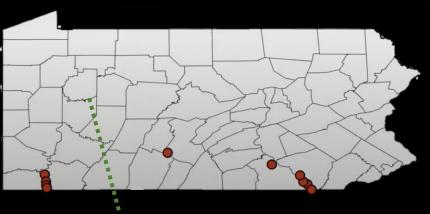






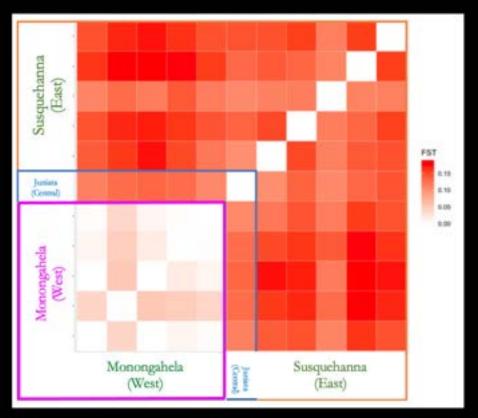
- Pairwise F_{ST}
 - A lot of gene flow between western pops
 - Very little gene flow between western and central-eastern

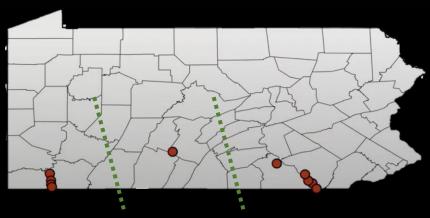






- Pairwise F_{ST}
 - A lot of gene flow between western pops
 - Very little gene flow between western and central-eastern
 - Very little gene flow between central and eastern pops







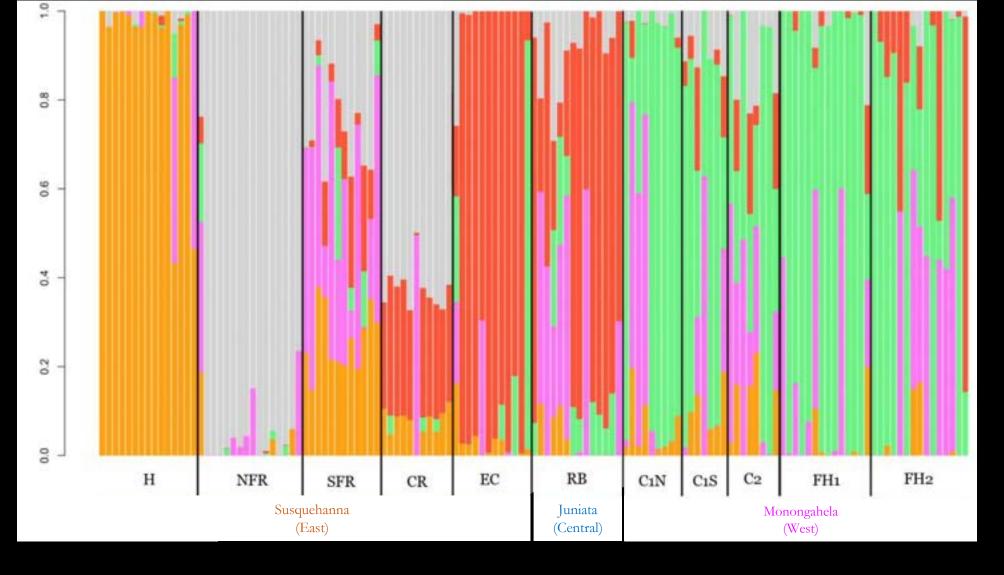
- Heterozygosity
 - Overall:
 - H_O: 0.6590
 - H_E: 0.3969
 - Every case $H_O > H_E$

Region	Population	H_0	H_{E}	Bartlett's K ² *p < 2.2e ⁻¹⁶
	Haines	0.7103	0.3837	421.6*
unna)	North of Fisherman Run	0.7355	0.3944	457.0*
Susquehanna (East)	South of Fisherman Run	0.5154	0.4097	372.1*
	Chickies Ridge	0.7388	0.3926	454.6*
	Erney Creek	0.7400	0.3985	482.0*
Juniata (Central)	Raystown Branch Juniata River	0.6440	0.4047	401.3*
	Cheat River 1N	0.6969	0.3958	423.1*
la	Cheat River 1S	0.6212	0.4147	475.5*
igahe est)	Cheat River 2	0.5507	0.3863	355.5*
Monongahela (West)	Friendship Hill 1	0.6847	0.3909	396.4*
	Friendship Hill 2	0.6119	0.4035	355.8*



- Inbreeding (F_{IS})
 - Overall:
 - $F_{IS} = -0.6219$

Region	Population	F_{1S}	FIS [95% CI]
Susquehanna (East)	Haines	-0.8512	[-0.8615, -0.8408]
	North of Fisherman Run	-0.8649	[-0.8754, -0.8526]
	South of Fisherman Run	-0.2580	[-0.2905, -0.2238]
	Chickies Ridge	-0.8817	[-0.8911, -0.8713]
	Erney Creek	-0.8569	[-0.8694, -0.8434]
Juniata (Central)	Raystown Branch Juniata River	-0.5915	[-0.6087, -0.5746]
Monongahela (West)	Cheat River 1N	-0.7608	[-0.7789, -0.7412]
	Cheat River 1S	-0.4978	[-0.5246, -0.4692]
	Cheat River 2	-0.4258	[-0.4577, -0.3963]
	Friendship Hill 1	-0.7517	[-0.7648, -0.7387]
	Friendship Hill 2	-0.5166	[-0.5360, -0.4976]



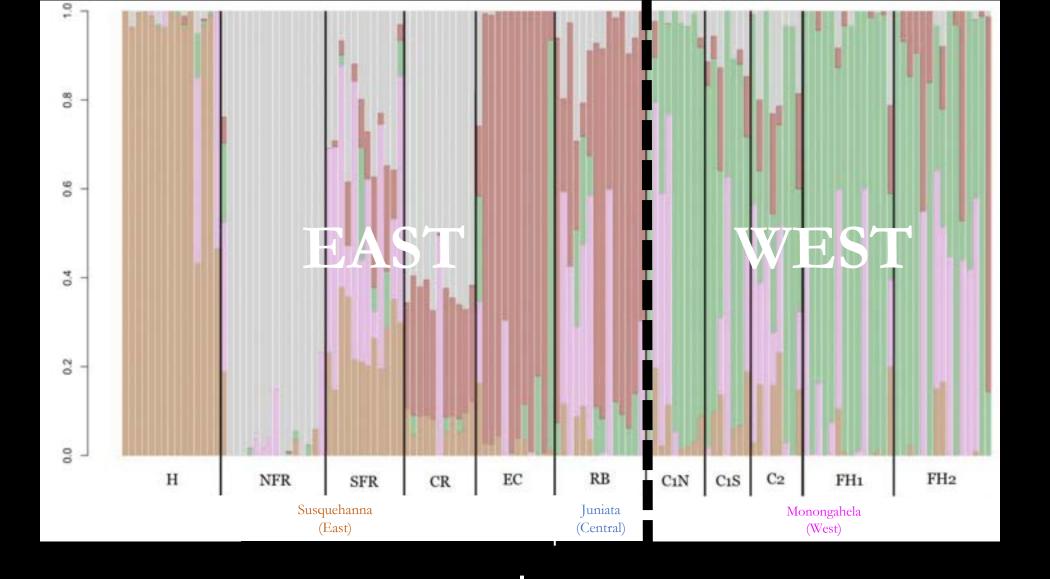
STRUCTURE Analysis

K = 5 ancestral clades

Eastern: Lots of genetic differentiation

Western: Genetically similar

Central: Clustering with EC



STRUCTURE Analysis

K = 5 ancestral clades

East-West Disjunction



Conclusions

- Currently, all populations are genetically healthy
- Western pops are genetically similar
- Eastern and central populations are genetically isolated from each other and western pops

Global F_{ST}: moderate differentiation

Pairwise F_{ST}:
high gene flow only in
western pops

F_{IS}: no inbreeding is occurring

Heterozygosity: higher than expected

STRUCTURE & DAPC:

western pops similar, while generally centraleastern pops are genetically different

Conservation Implications



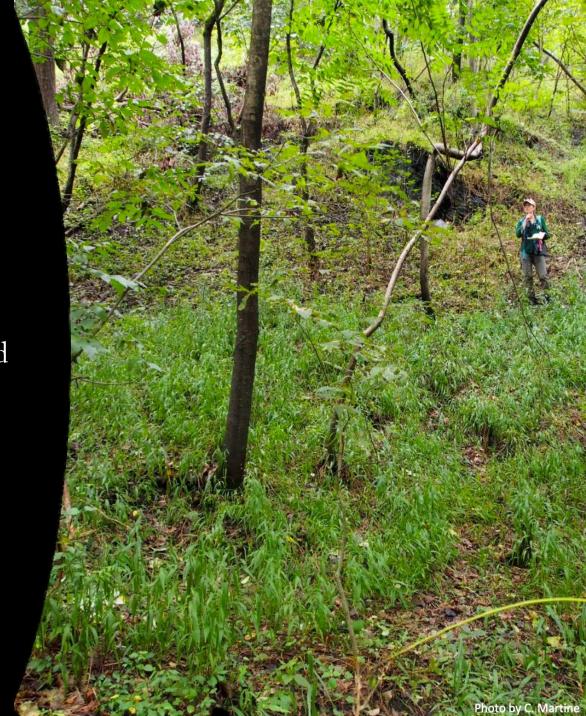
Limited and declining state distribution

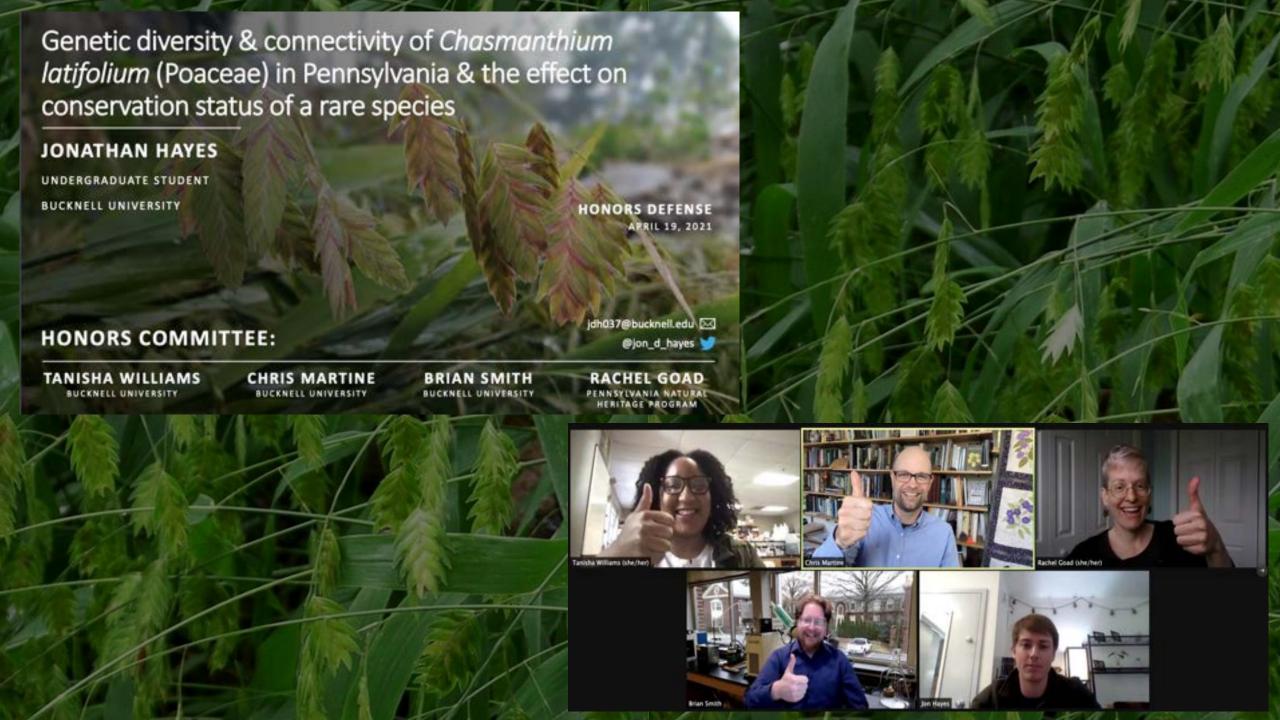


Populations appear to be massive and healthy



Western populations appear genetically secure, while eastern and central populations are of greater concern







Thanks to...

Funding

- David Burpee Endowment
- PA DCNR Wild Resource Conservation Program
- Sigma Xi
- Torrey Botanical Society
- Botanical Society of America

















Thanks to...



Rachel Goad





Dr. Angela McDonnell



Dr. Scott Schuette



Ariel Antoine



Dr. Chris Martine



Jon Hayes









Cheyenne Moore

Population Genomics and Climate Change Vulnerability of an Appalachian Endemic Plant in Pennsylvania



Research seeks to clarify the conservation and protection status of bog Jacob's ladder (*Polemonium vanbruntiae*), a species of conservation concern, using a combination of traditional herbarium and field-based assessments, modern population genetics methods and climate modeling. This will be a model for rare plant conservation work that uses comparative plant population genomic techniques and climate change modeling methods, in combination with traditional natural heritage methods.

















David Burpee Endowment

Wayne Manning Internship Fund

Bucknell University

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National Science Foundation

Western Pennsylvania Conservancy

Pennsylvania Natural Heritage Program

San Francisco State University

Chicago Botanica Garden





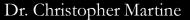














Dr. Angela McDonnell



Dr. Jason Cantley



Peter Jobson

CHICAGO BOTANIC GARDEN















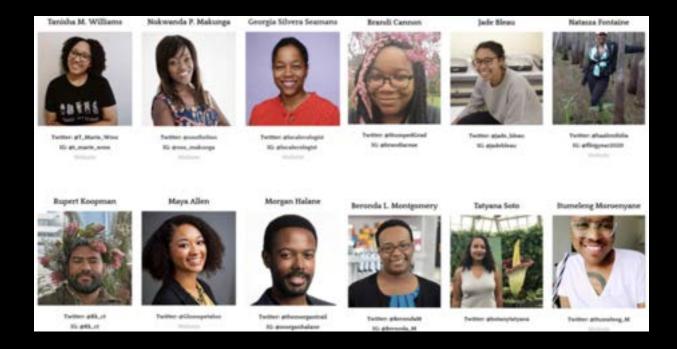
One last thing...

Black Botanists Week



Started in 2020 to promote, encourage, create a safe space for, and find more Black (and BIPOC) people who love plants!

Black Botanists Week









www.blackbotanistsweek.weebly.com

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Special Issue on Conservation

From Theory to Practice: New Innovations and Their Application in Conservation Biology

- Best practices
- Novel conceptual frameworks
- Software of database
- Best practices for managing ex situ collections
- New techniques to combat poaching
- Abstracts due April 4, 2023



