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Analyzing Genetic Diversity of Eastern White Pine (*Pinus strobus*) in the St. John's Abbey Arboretum

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Introduction

- Eastern White Pine (*Pinus strobus*) are found through the North Eastern US and South Eastern Canada¹ (Fig 1)
- They provide food source for birds and mammals in addition to erosion control; white pine blister rust (*Cronartium ribicola*) is a known pest¹
- There are five planted tree stands in the St. John's Abbey Arboretum (Fig 3)³
- High genetic diversity will increase chances of survival of environmental stressors like high temperatures or pests²



Figure 1. Native range of the eastern white pine (*Pinus strobus*). Map from www.usgs.gov

Methods

- GPS mark each white pine to create stand maps and stand population and total population counts
- Collect representative sample of needles from each stand by hand, pole saw, or shotgun
- Extract needle DNA with Qiagen DNAeasy Plant Kit
- Amplify DNA with touchdown PCR; use 4 multiplex reactions to amplify 10 microsatellite loci
- Analyze fragments with capillary electrophoresis (ABI3730xl) and fragment size analysis to determine genotype from microsatellite size

Table 1. Observed and expected heterozygosity frequencies for 8 loci amplified by touchdown PCR for needles collected from 48 trees in Stand 202 and 20 trees in Stand 118, St. John's Abbey Arboretum, Collegeville, MN.

Locus	Stand 202		Stand 118	
	Observed H _e	Expected H _e	Observed H _e	Expected H _e
RPS1b	0.08	0.53	0.18	0.68
RPS2	0.27	0.83	0.10	0.80
RPS39	0.14	0.72	0.00	0.61
RPS84	0.22	0.70	0.88	0.70
RPS118b	0.16	0.87	0.06	0.42
RPS25b	0.20	0.88	0.53	0.86
RPS34b	0.28	0.80	0.20	0.65
RPS127	0.17	0.90	0.14	0.68
St. Dev.	0.07	0.12	0.29	0.14

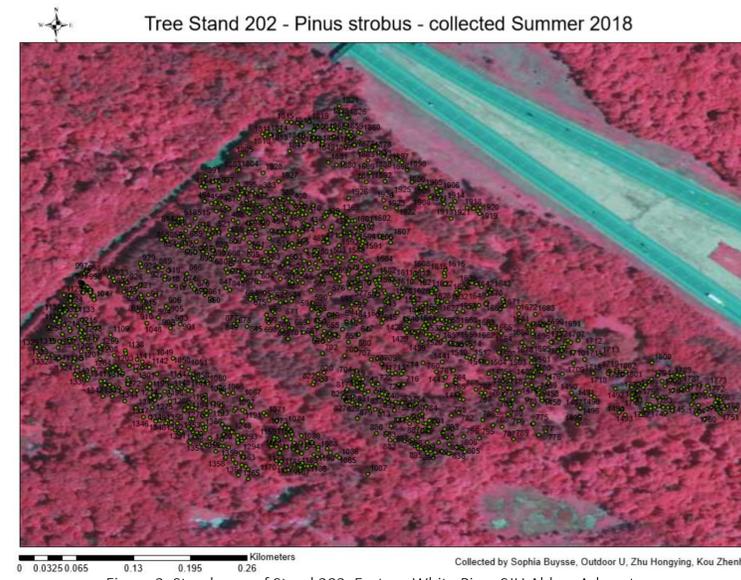


Figure 2. Stand map of Stand 202, Eastern White Pine, SJU Abbey Arboretum.



Figure 3. Map of Eastern White pine (*Pinus strobus*) tree stands in the SJU Abbey Arboretum. Map data from <https://gis.co.stearns.mn.us/Landuse-Restriction/default.aspx#>.

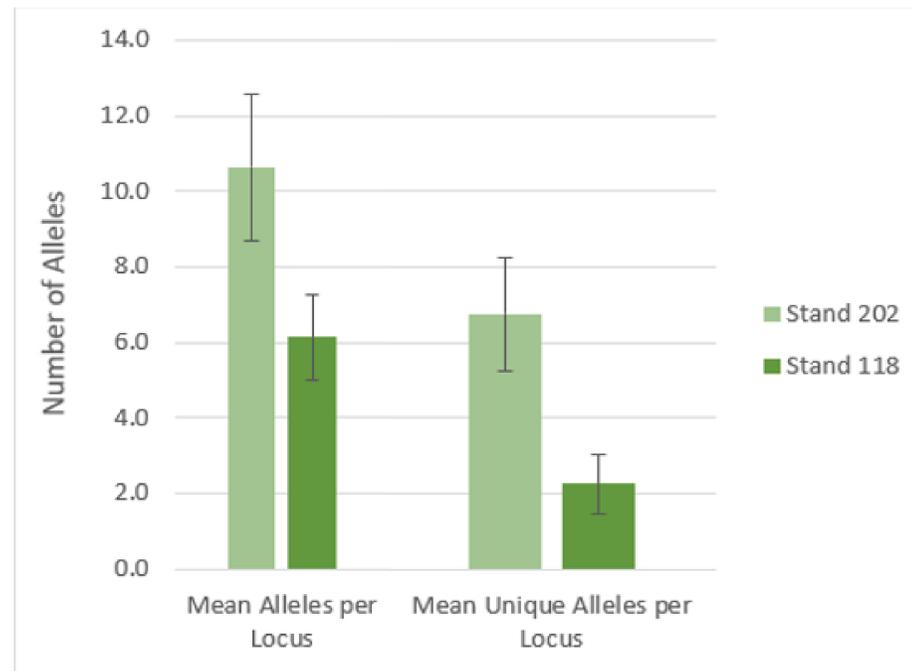


Figure 4. Comparison of mean alleles per locus and mean unique alleles per locus for 8 microsatellites from 48 trees in Stand 202 and 20 trees in Stand 118. Error bars are standard deviation.

Literature Cited

- ¹Dickerson, John. USDA Natural Resources Conservation Service. Plant Fact Sheet: Eastern White Pine [online document]. (2002).
- ²Rajora OP, Rahman MH, Buchert GP, Dancik BP (2000) Microsatellite DNA analysis of genetic effects of harvesting in old-growth eastern white pine (*Pinus strobus*) in Ontario, Canada. *Molecular Ecology*. 9: 340.
- ³Geissler, John. St. John's Abbey Lands Database, Tree Stand Maps (2009).

Results

- GPS mapped over 3000 trees in Summer 2018 and Spring 2019
- Extracted DNA from 137 trees
- Fragment analyzed 68 trees, 8 loci amplified for each tree
- Alleles appeared outside the range reported by previous literature for each locus²
- The stands shared 31 of 103 alleles and 28 of 114 genotypes
- Stand 202 shows more alleles per locus and unique alleles per locus; mean observed heterozygosity is greater in Stand 118.

Discussion

- Only 1 locus shows observed heterozygosity greater than expected heterozygosity (Table 1)
- The genetic diversity is high in terms of unique alleles in each stand but low in terms of observed heterozygosity.
- Alleles in common between stands may be from gene flow or from similarities in the original stand seedling sources
- The SJU Abbey Arboretum should be concerned about the genetic diversity of these tree stands if white pine blister rust is found or other environmental stressors become evident.