

CHICAGO BOTANIC GARDEN



#### Introduction

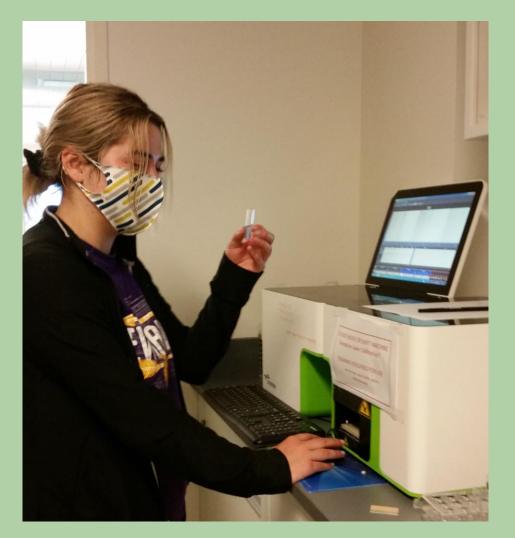
- Studying polyploidy is extremely beneficial to help understand climate change and phenotypic plasticity regarding climate change
- Research has shown that chromosome variation can be important for species to tolerate different climates. Understanding intraspecific ploidy variation (IPV) is important for managing species in areas where they compete and overtake other native species (1/3 of restoration species have IPV)
- Previous studies suggests that different landscapes on a regional scale have diploid populations of *Solidago altissima* tends to be more drought tolerant than polyploids
- Polyploids could have mutated due to the difference in conditions at each location. The woods have less light and higher competition from woody species. The prairie locations are more open, have higher sunlight, and the competition of mostly herbaceous plants

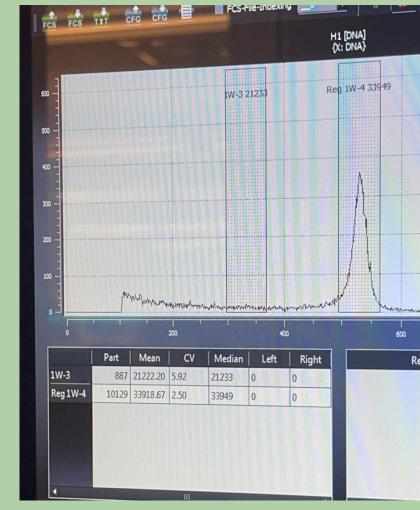
#### Hypothesis

There will be variation in ploidy within a site and it will be related to the habitat. Due to the drier nature of the prairie the samples from the prairie would tend to be made up of more diploids than polyploids

#### Methods

- 10 S. altissima samples haphazardly collected from woods and prairie at two SW Cook County sites (40 total samples)
- 2. Quantified relative genome size of all samples using the flow cytometer and the Pea as a standard
- We used a linear model to model Genome size as a factor 3. (predicted by) habitat, site, and the interaction between habitat and site
- 4. We evaluated the model using type 3 ANOVA





# **Understanding Ploidy Variation in Solidago altissima to Inform Prairie Restoration and Management**

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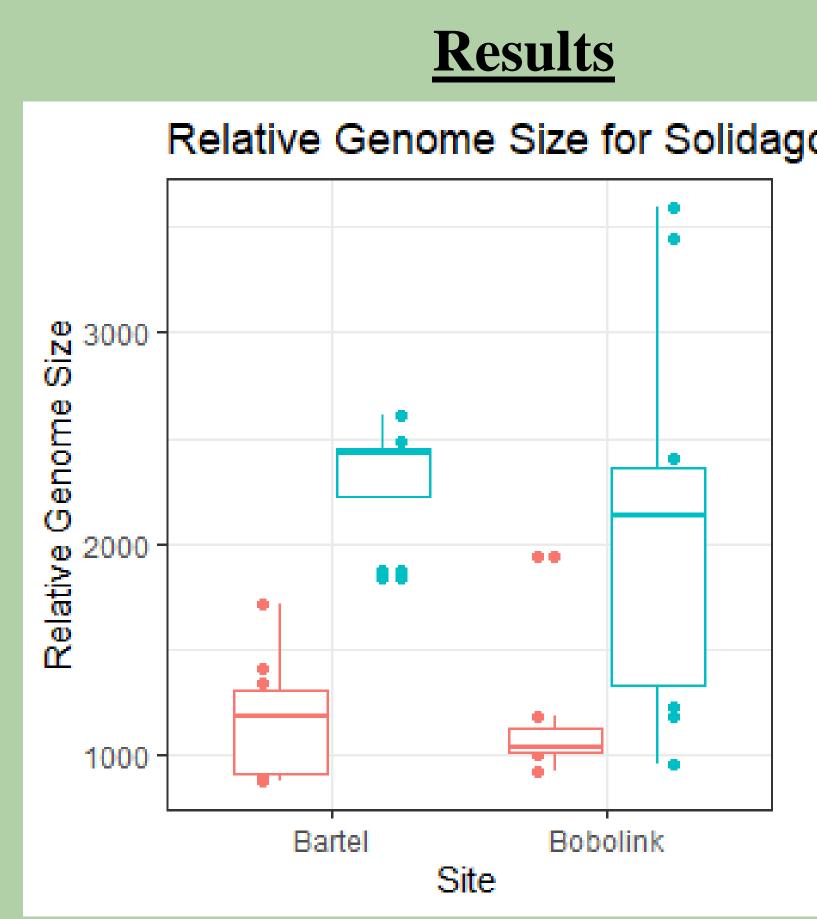
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A map of the Bobolink Family Area on Google Earth showing where samples were collected. Not shown is the Bartel Grasslands site





- My research shows that both sites have intraspecific
- Overall, the average relative genome size was higher compared to the prairie samples at both sites. We estin polyploids have much higher relative genome sizes co diploids
- It is estimated that almost all of the woods samples w a few polyploids being in the prairies
- This is telling us that Genome size was significantly influenced by habitat type (F=19.21, p<0.001), but not by site or the interaction



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#### **Project Limitations**

- Limited sample sizes
- Solidago altissima is difficult to work with on flow cytometer
- Time constraints did not allow for chromosome squashes

#### Discussion

- Tall Goldenrod is an aggressive native species that will never be used in restoration, but many other Asteraceae could have varying ploidy levels so this information benefits restoration projects
- Differences in ploidy are present as expected. Future research could be done to see how ploidy affects management and restoration. Do disturbances lead to polyploidy?
- Questions remain about variation within a site. Future research could be done to help understand what this means for managing species with differing ploidy levels
- Future research can be done to get the exact ploidy levels. Chromosome squashes would need to be done on those with higher relative genome sizes to know for sure if the plant is a triploid, hexaploid, or tetraploid



Alexis B. (L) and Lauryn C. (R) at Bobolink

### Acknowledgments

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## **Literature Cited**

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