

The Method of Gene Flow Between Two *Oenothera harringtonii* Populations

Peter Sullivan^{1,2}

¹Truman College; ²Chicago Botanic Garden

Introduction

As biodiversity is being threatened all over the world, understanding the mechanisms of gene flow between populations of a species is becoming imperative in order to maintain genetic diversity. The more overall gene dispersal there is amongst the populations, the more likely the species will remain extant¹.

For flowering plants, seed and pollen dispersal are two important components involved in gene flow between populations². Seeds migrate to other populations via several means and interact with the local population to produce offspring. A more effective means of high gene flow between more distant populations is via pollination³.

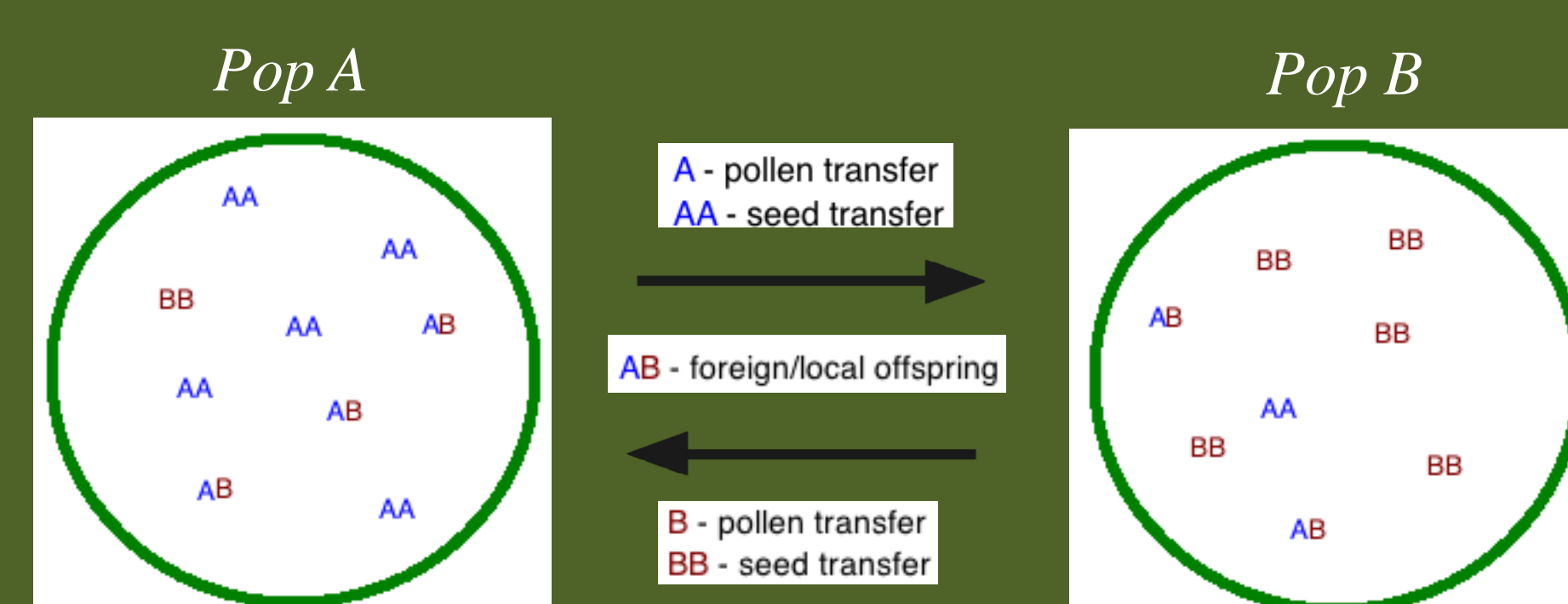
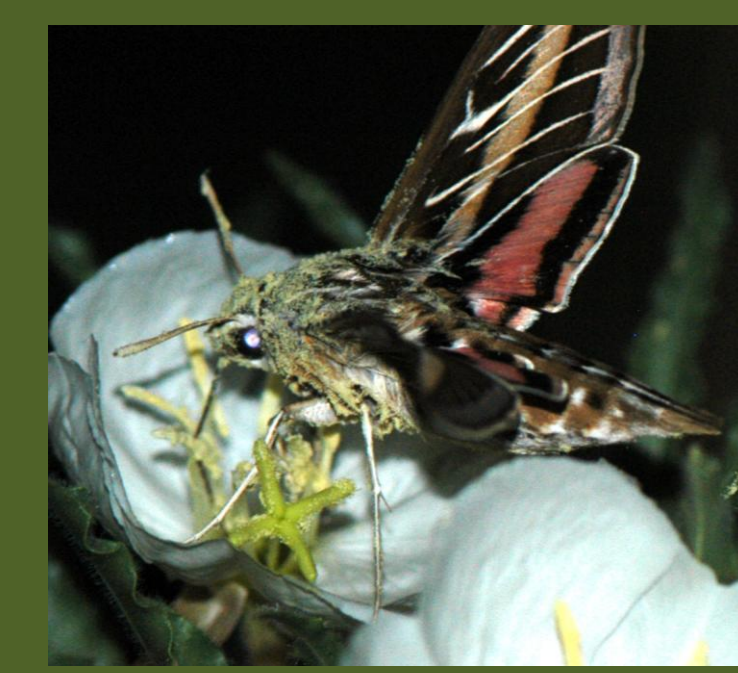


Figure 1: Example of gene flow via seed and pollen dispersal



Picture 2: Hawkmoth – a pollinator



Picture 1: *Oenothera harringtonii*



Picture 3: bumble bee – a pollinator

Study Species – *Oenothera harringtonii*

Oenothera harringtonii, an evening primrose endemic to central Colorado (see map below for location), utilize both hawkmoths and bumble bees for pollination. Hawkmoths have the capacity to travel far distances, up to more than 20 miles⁴. Bumble bees, on the other hand, tend to travel much shorter distances⁵. In this study, we examined two *O. harringtonii* populations, Bear Paw (BP) (sample size = 52) and Florence (FLO) (sample size = 25), located roughly 200 meters from each other and sought to analyze the genetic differentiation between the two.

GOAL

Determine whether or not there is gene flow between *O. harringtonii* populations BP and FLO by either seed or pollen dispersal.

Method

On-Site

- Gathered tissue from 76 *O. harringtonii* individuals located near Florence, Colorado in Fremont County.
 - Two populations roughly 200 m from each other
 - Bear Paw (BP), Florence (FLO)

In the Lab

- Extracted DNA from each of the 76 individuals from both populations following the CTAB protocol.
- Carried out Polymerase Chain Reaction (PCR) method to amplify 11 neutral microsatellite loci for analysis using primers from Skogen, et al (2012)⁶.
- Ran Beckman Coulter CEQ 8000 to determine the alleles of each individual plant.

Statistical Analysis

- GenAlEx⁷ (through Excel)
 - F-statistics (F_{ST}): calculated genetic differentiation between the two populations.
 - Spatial autocorrelation: determined relationship between genetic and geographic distance.
- STRUCTURE⁸
 - Genetic grouping method to determine population structure.

Results/Discussion

Genetic Differentiation

	Value	P-value
F_{ST}	0.014	0.001

Table 1: F_{ST} comparing BP and FLO genetic differentiation

The F_{ST} value provides a numeric estimate of the genetic differentiation between two populations. Low genetic differentiation is negatively correlated with gene flow. The 0.014 value from this study's analysis suggests very low divergence between BP and FLO. However, because the P-value is so low, there is a very high likelihood (99.9%) that the slight differentiation actually exists rather than being observed due to random chance.

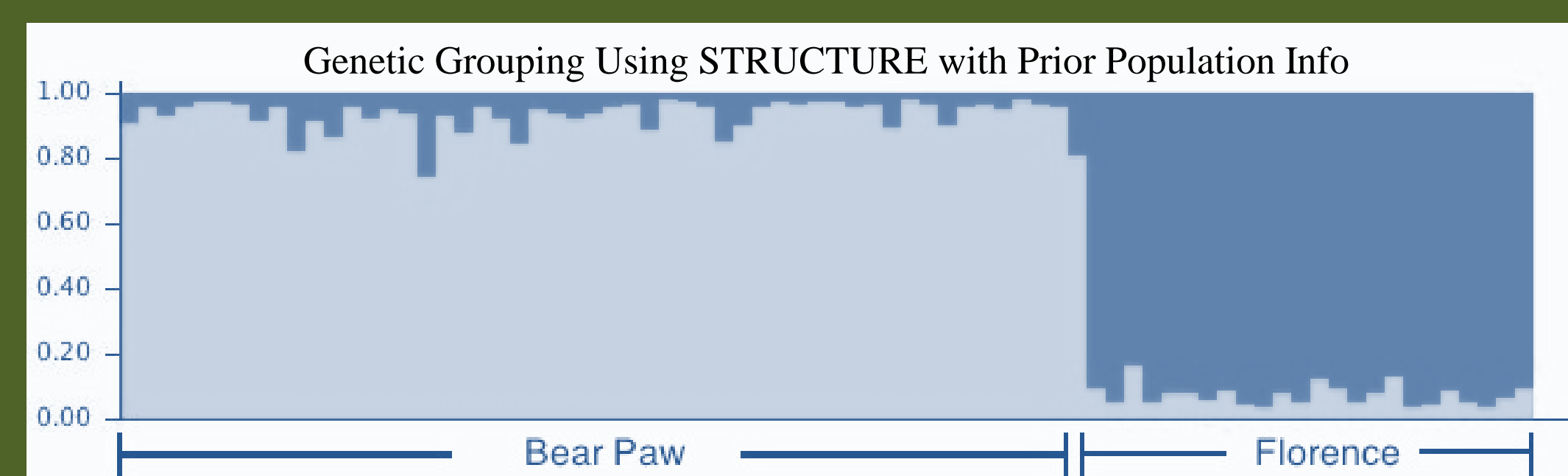


Figure 5: Each vertical line represents an individual within both populations. Prior population information emphasizes the subtle genetic differences between BP and FLO when STRUCTURE analyzes the data. The two colors represent genetic clusters or groups.

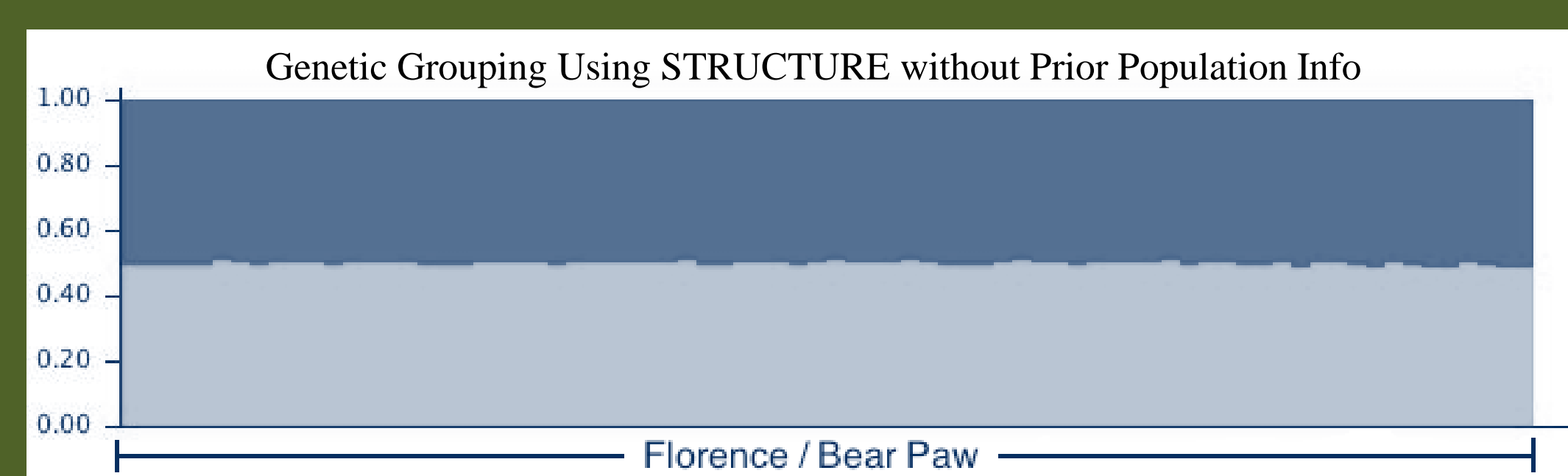


Figure 6: When the populations are not preset, STRUCTURE treats BP and FLO as one whole and does not recognize the weak, but existent genetic structure of the two populations.

Figures 5 and 6 were created using the same genetic data set but offer two different interpretations regarding the genetic structure of BP and FLO. There is significant, but very subtle genetic structure (due to some mating isolation) within each population. Low genetic structure means that there migration between each population is taking place.

Genetic Diversity

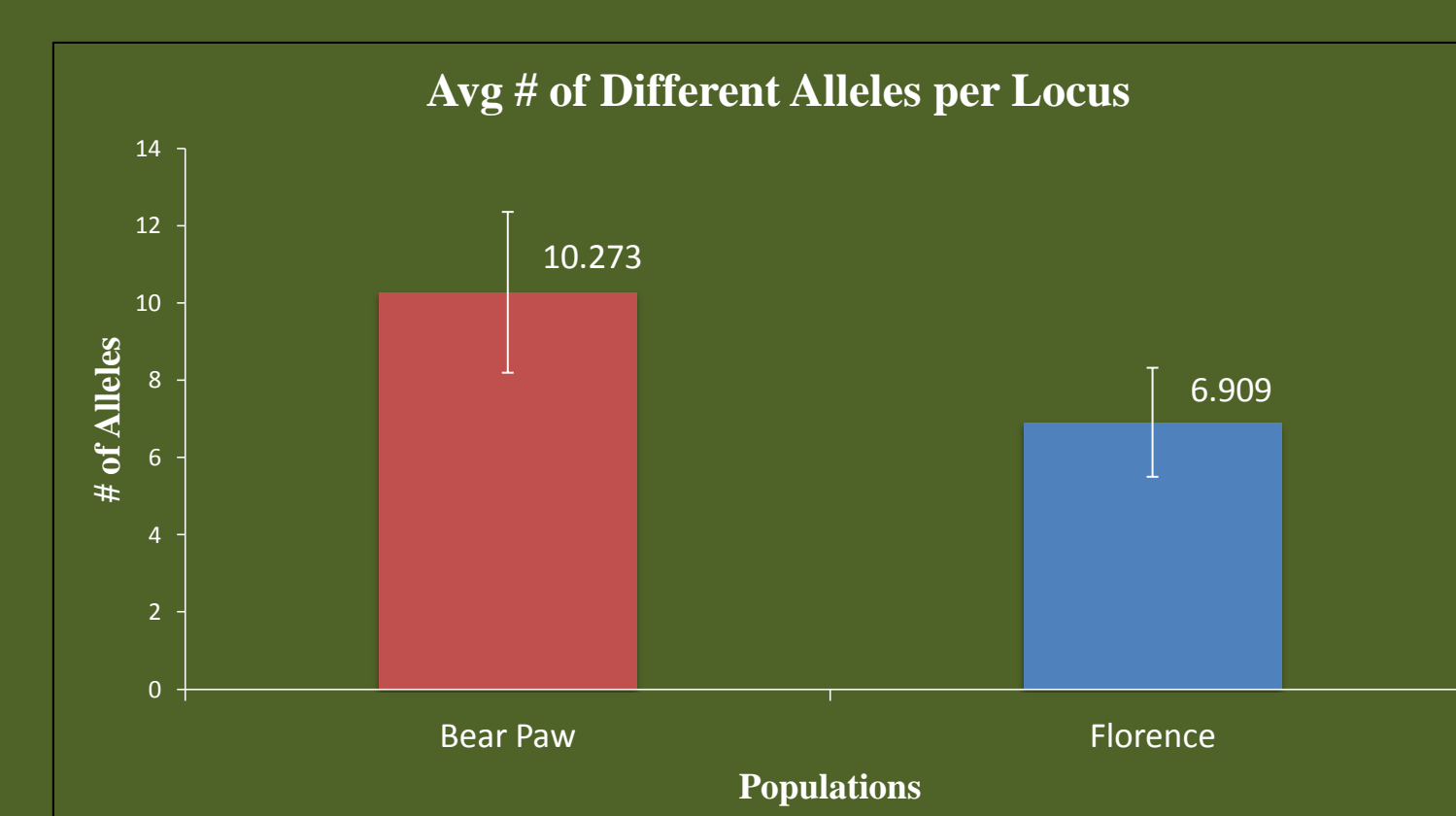


Figure 3: Accumulative average of all 11 loci for each population sample

The BP sample averaged roughly 3 different alleles more per locus than FLO. This could be interpreted as higher genetic diversity, although BP had a sample size of 52 while FLO had only 25. This low FLO sample size could attribute for the difference in average number of alleles. Ultimately, both averages suggest high genetic diversity.

Genetic/Spatial Relationship

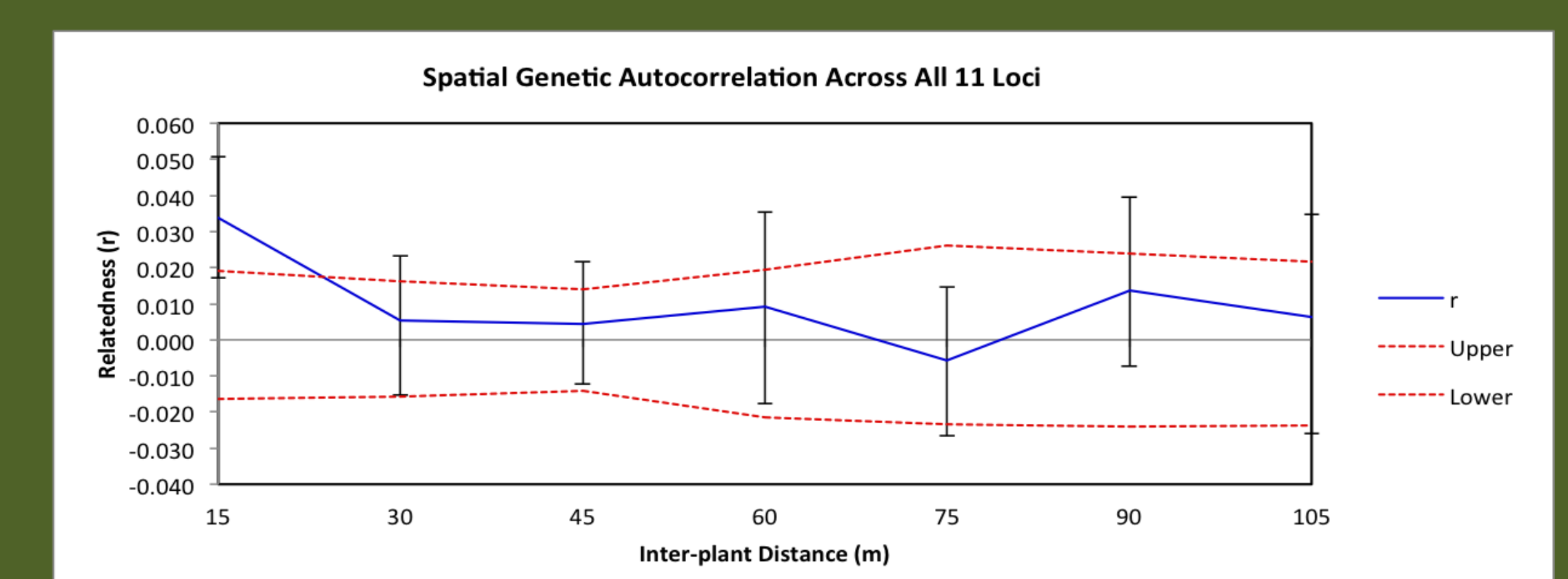


Figure 4: The genetic relatedness between individuals at a particular distance. The dashed red lines represent confidence intervals.

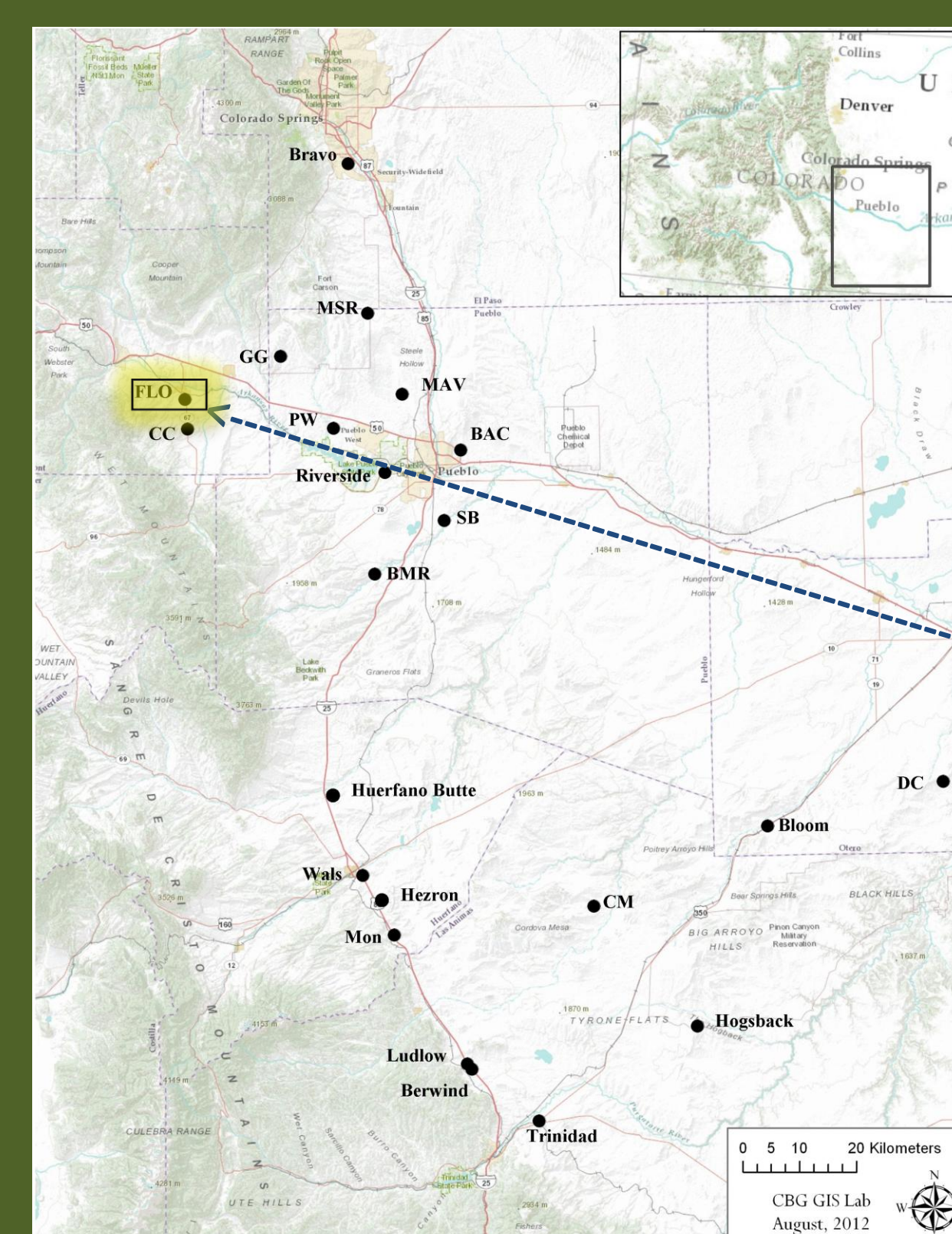
The analysis was done by genetically comparing each individual plant to plants grouped between 0-15 meters from the individual, 16-30 meters, and so on. Significant relatedness means that plants are more closely related, based on their geographic distance, than is expected if random mating was occurring. As the graph shows, there is significant relatedness between individuals within 15 meters of each other. This suggests that seed dispersal is fairly limited. Gravity is likely the primary dispersal agent for the BP and FLO populations.

CONCLUSION

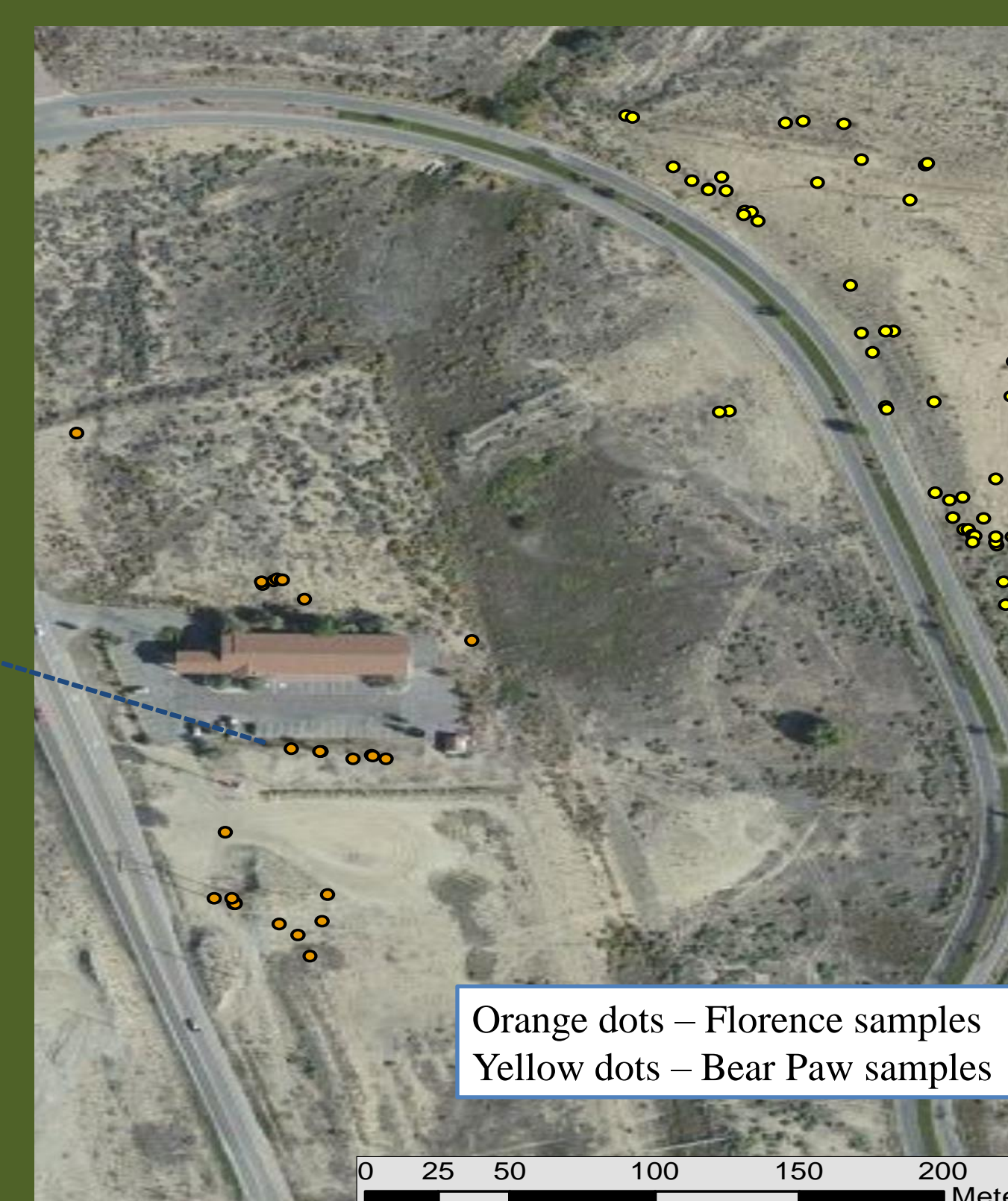
- Relatedness is significant only between individuals in close proximity, which is due to limited seed dispersal.
- Even with slight genetic differentiation, gene flow is occurring by means of pollination.

References

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Map 1: locations of *O. harringtonii* populations in CO



Map 2: locations of Bear Paw and Florence