

# Genetic Distance in Relation to Floral Color Variation of *C. sessiliflora* Populations

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## Introduction:

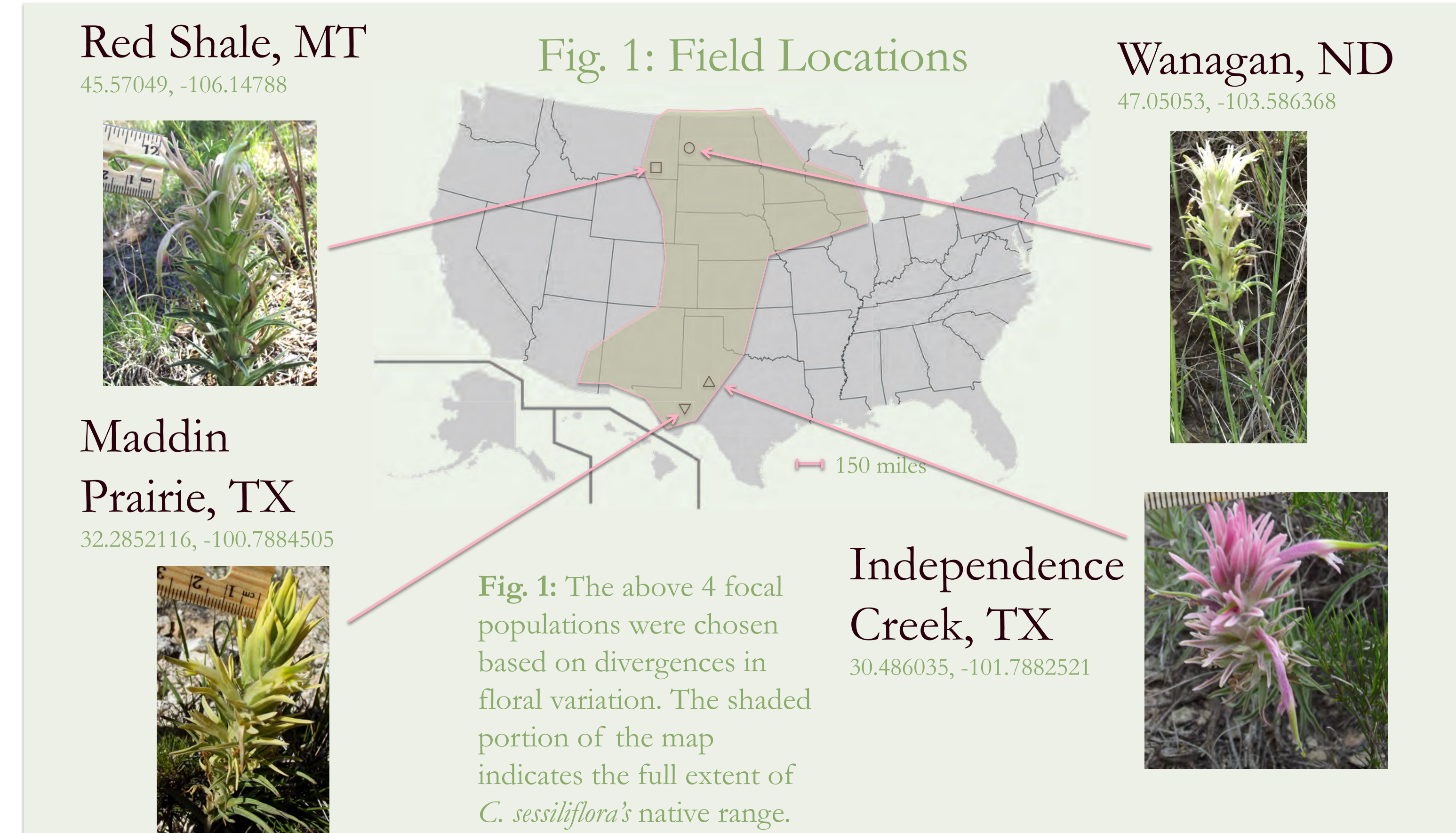
Geographic differentiation of floral traits is often associated with locally differing pollinator assemblages<sup>1</sup>. The movement of pollen controls gene flow within and among populations, and controls the degree of genetic differentiation among populations.<sup>2</sup> *C. sessiliflora* displays **white to yellow to pink** inflorescences across its native range. This species is known to be pollinated by bees and hawkmoths<sup>3,4</sup>, although how these pollinators may vary across its range are unknown. Understanding genetic dynamics of populations has become integral to the study and conservation of native plant species. This project examines the genetic makeup of two pairs of populations (from the southern and northern range extents, respectively) that display different levels of floral color divergence. Using leaf tissue samples we will compare the genetic composition of these populations with the aid of microsatellite markers developed for *C. sessiliflora*<sup>5</sup>.

## Hypothesis:

We expect the populations from the southern range, which show **greater variation in floral color** will likely show **greater genetic differentiation**, as opposed to the northern populations which display similar floral morphology.

## Methods:

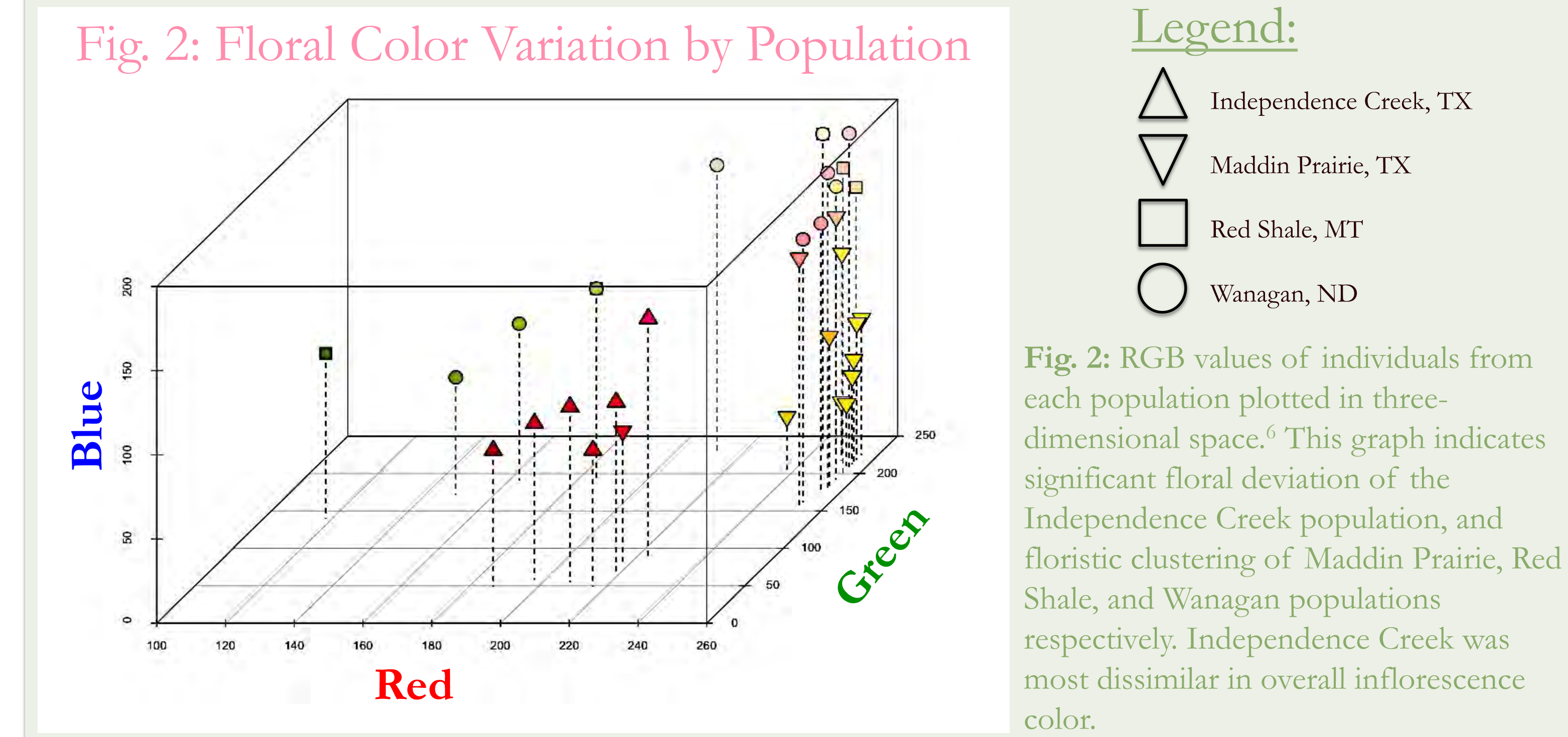
- 4 focal populations were chosen based on observed divergences in floral variation, following a range wide survey of floral variation.
- Paired samples were located ~140-160 miles apart.
- 30 leaf tissue samples were collected from each location.
- Overall inflorescence color was recorded for every flowering individual and compared based on Red-Green-Blue values.
- DNA was extracted from leaf tissue and the genetic makeup of populations was assessed using 7 microsatellite primers.



## DNA Extraction & Genetic Analysis:



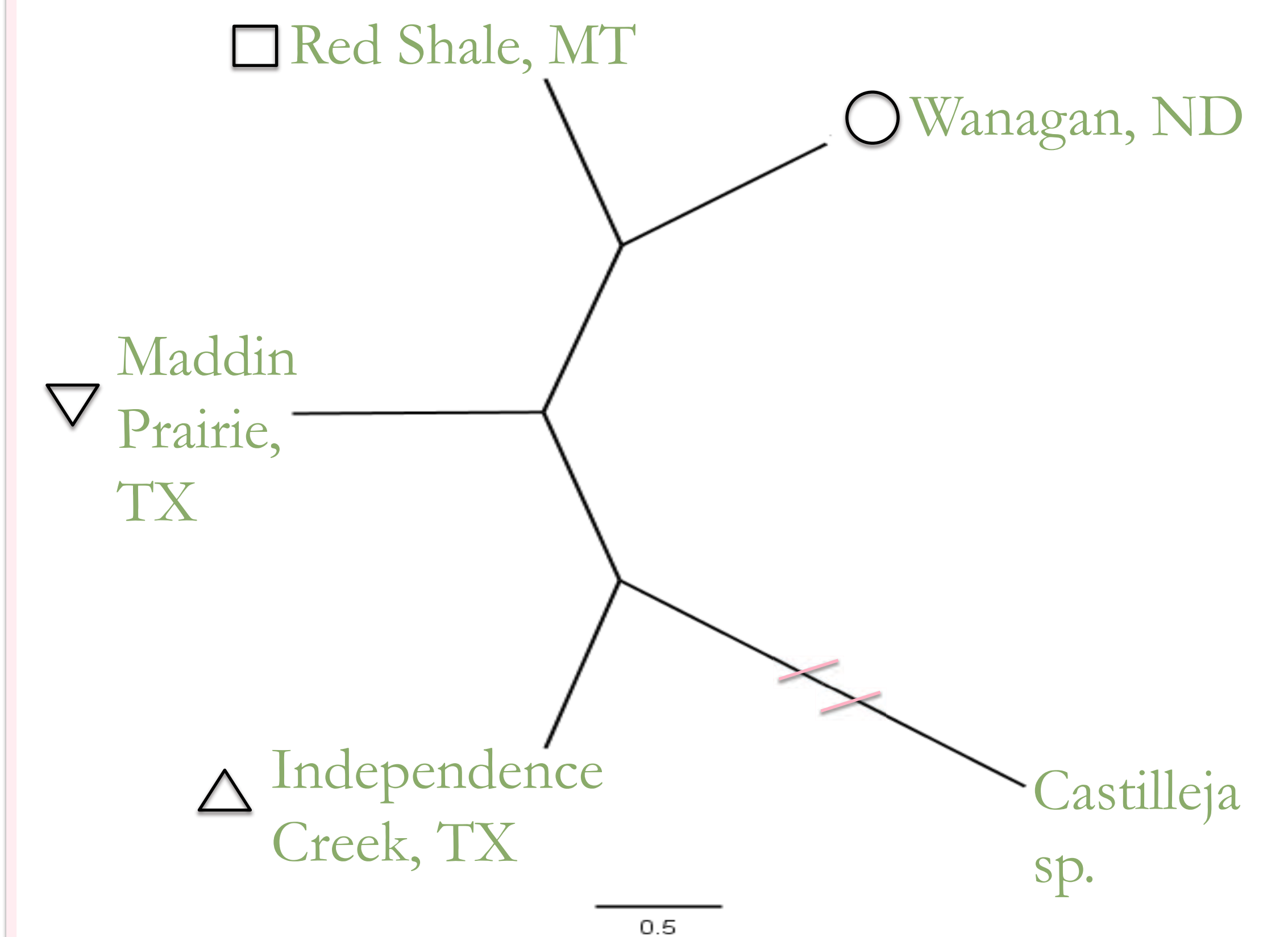
## Results:



## References:

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## Fig. 3: Genetic Distance Among Populations



**Fig. 3:** A distance tree showing structural relatedness of all four populations. The above indicates phylogenetic divergence of the Independence Creek population – a possible reflection of local adaption to pollinator assemblages based on floral variation.

## Table 1: Genetic Analysis of Populations

| Pop. | Sample Size | No. Alleles | No. Effective Alleles | Observed Heterozygosity | Expected Heterozygosity | Fixation |
|------|-------------|-------------|-----------------------|-------------------------|-------------------------|----------|
| IC   | 20,500      | 5,000       | 2,929                 | 0.510                   | 0.626                   | 0.204    |
| MP   | 18,750      | 5,625       | 3,392                 | 0.425                   | 0.592                   | 0.305    |
| RS   | 20,375      | 5,250       | 2,578                 | 0.475                   | 0.558                   | 0.139    |
| WA   | 21,125      | 5,625       | 2,777                 | 0.545                   | 0.531                   | -0.019   |

**Table 1:** The above represents the genetic structure of each population. *Expected Heterozygosity*, measures the amount of heterozygotes in the population. An increasing number of heterozygotes indicates greater genetic diversity.

## Conclusion:

- Independence Creek, TX. displays both floral and genetic differentiation compared to the other three populations.
- Independence Creek and Maddin Prairie are geographically separated by about 140 miles, despite being genetically distant.
- This genetic dissimilarity is paralleled by their divergence in floral color, which suggests a similar process could be driving both factors – for example, geographically differing pollinator assemblages.
- Sample size indicates that these results are not conclusive enough to make larger scale judgments about this species overall.
- **Future work:** 1) Increase the number of populations to cover the complete range for this species and 2) characterize local pollinator assemblages to understand potential drivers of morphological and genetic patterns.

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