

Introduction

- High genetic diversity and low inbreeding are important to population resilience. For example, genetic diversity directly affects evolutionary potential which is the ability to respond to environmental change such as disease and variations in climate.
- Seed banking is one way to conserve the genetic diversity of endangered species but there are many species whose seeds cannot survive the drying and freezing process of seed banking or they produce little to no seeds to preserve. These are exceptional species that must be managed as living, ex situ populations.
- The establishment of ex situ populations involves collecting seeds from the in situ population. To ensure we have an ex situ population whose individuals can successfully be reintroduced, ideal sampling of in situ individuals will include seeds that: come from a variety of wild origins, are unrelated, have high genetic diversity, and have low inbreeding.
- In this project, I compare the genetic structure, diversity, and inbreeding between the ex situ and in situ populations of a critically endangered Hawaiian plant to lend insight into the collection needs of the species

Study system: *Phyllostegia Electra*

- A rare mint species from Hawai'i from Kaua'i island
- An exceptional species, little is known about the plant
- NO known pollinator other than an extinct flightless bird called a Turtle jawed moa-nalo
- Include info about the potential and lost dispersers



Objectives

Objective 1: I evaluated the amount of genetic structure between and within in situ and ex situ populations

Prediction 1.1: There will be a higher genetic structure between the populations because most ex situ individuals share the same wild origin (80%), which is a location from which few in situ individuals were collected.

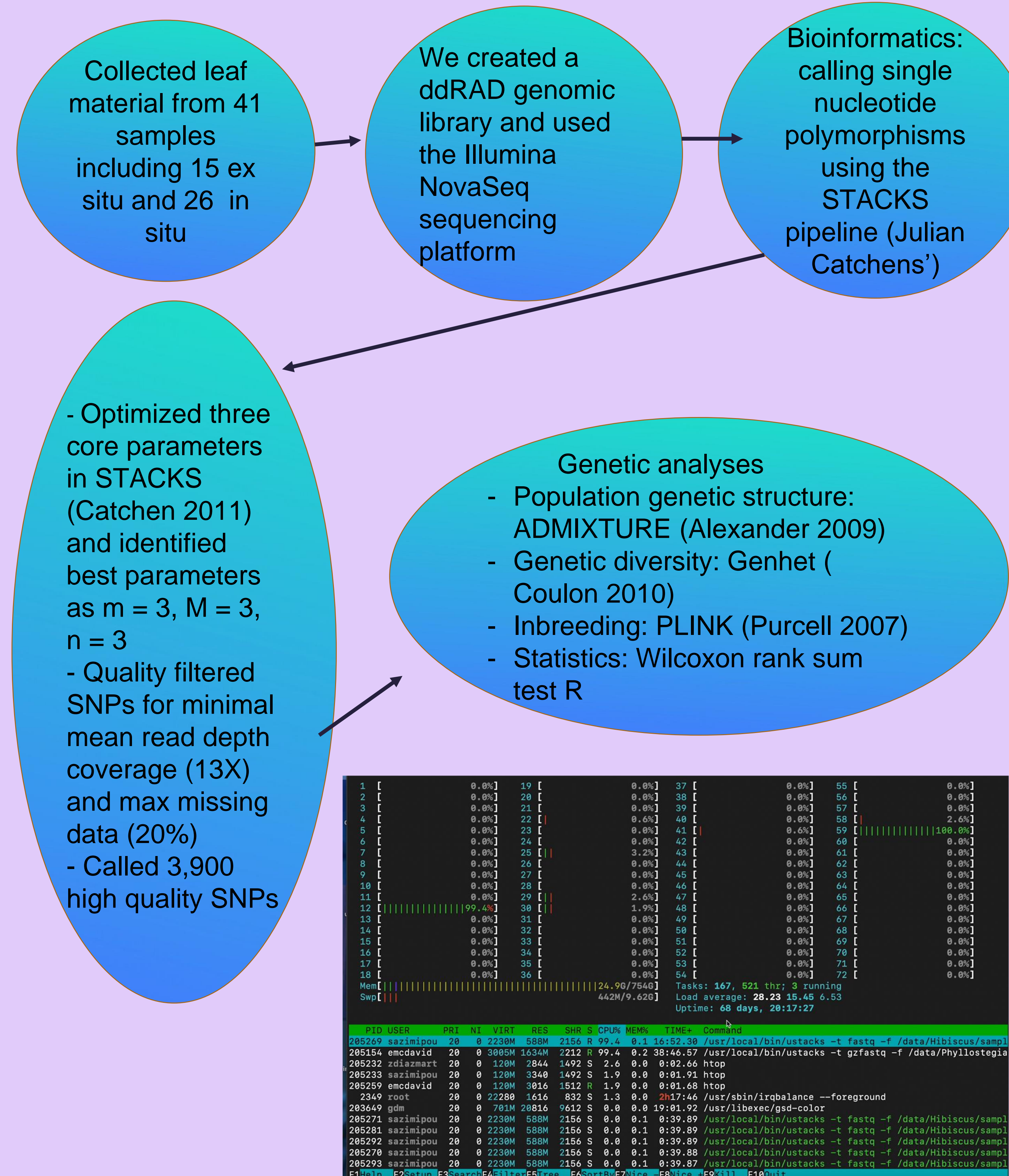
Prediction 1.2: There will be a higher genetic structure in the in situ population because individuals come from a variety of wild origins ($n = 14$) and are likely more genetically isolated compared to the ex-situ population that shares the same three wild origins.

Objective 2: I investigated the difference in genetic diversity and inbreeding between ex situ and in situ individuals

Prediction 2.1: The ex situ population will have higher inbreeding because most individuals share the same wild origin and may be more likely to have been the result of mating between genetically similar individuals compared to the in situ population which has fewer individuals with shared wild origin (54%).

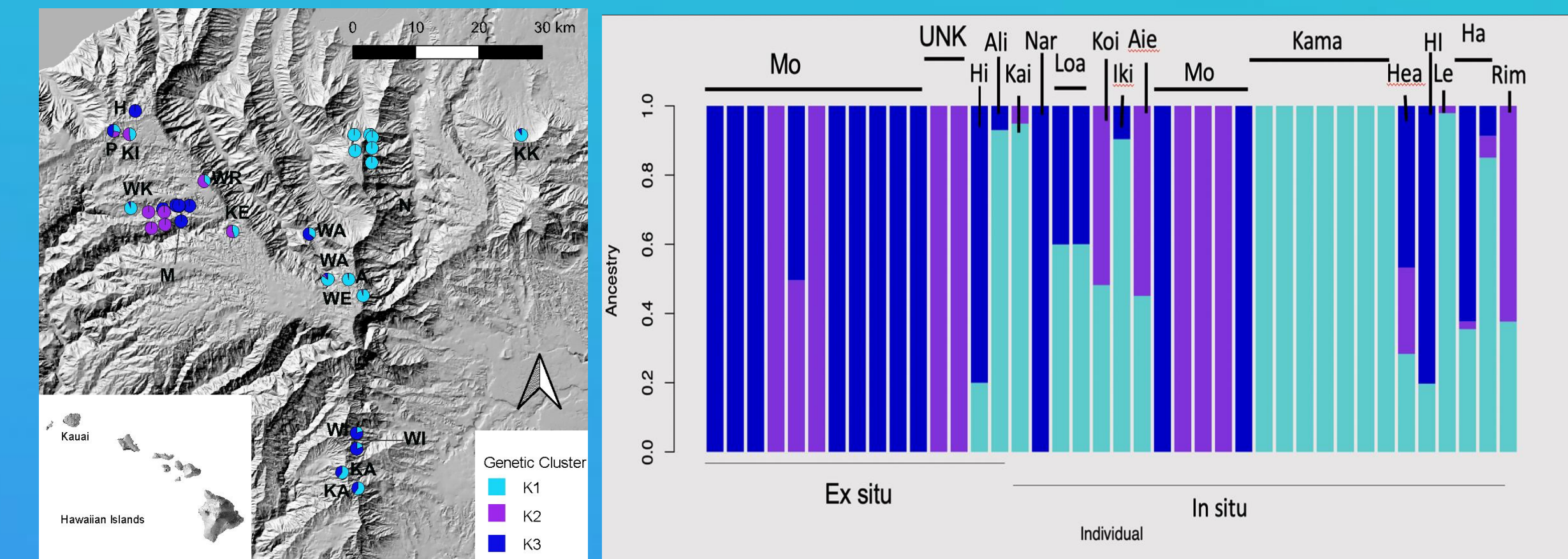
Prediction 2.2: The in situ population will have higher genetic diversity because it has a larger population size and is represented by individuals from several wild origins that may share less ancestry, be locally adapted to different environments, and be genetically isolated.

Methods

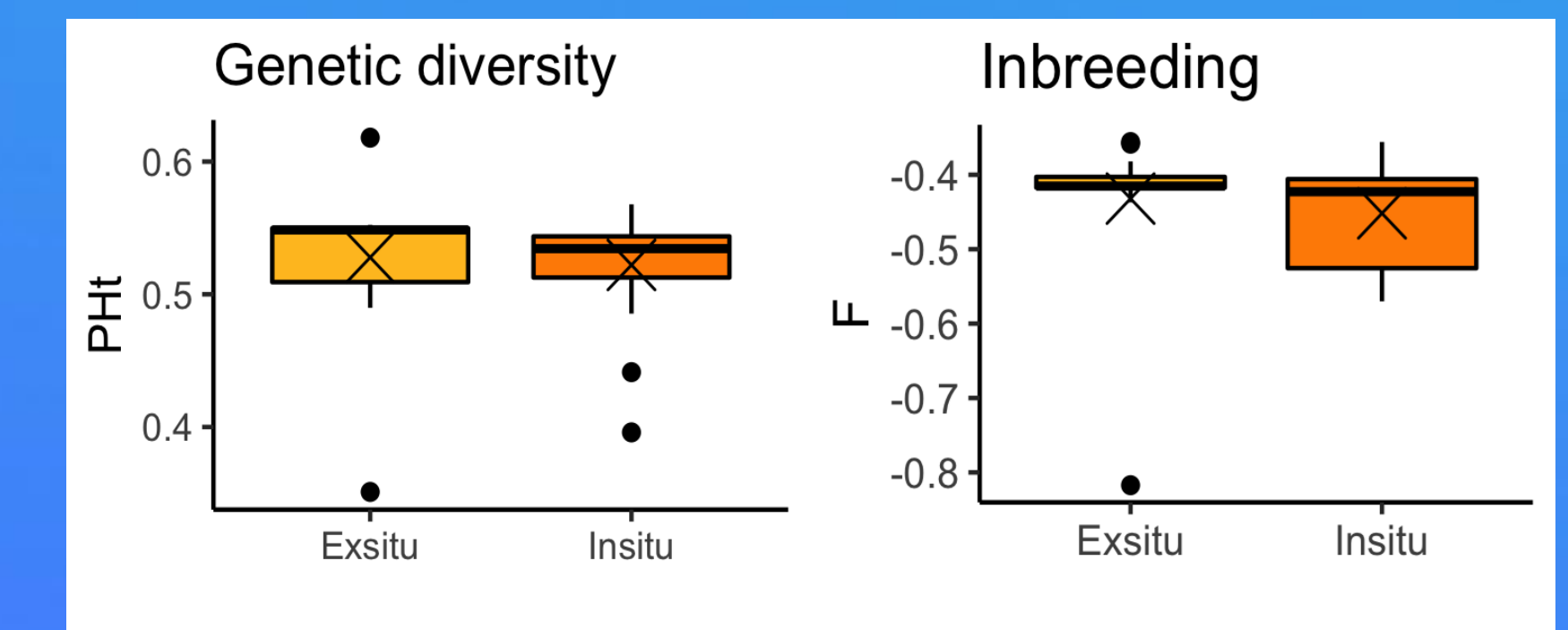


Results

- Genetic structure: I identified three genetic clusters that have minimal admixture between clusters.
- I found that there was moderate genetic structure between ex situ and in situ populations and less genetic structure within the in situ population compared to the ex situ population.



Genetic diversity and inbreeding: there was no significant difference in individual level measures of genetic diversity (W -value = 229.5 , $p = 0.25$) or inbreeding (W -value = 248.5 , $p = 0.09$) between in situ or ex situ populations.



Acknowledgments

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References

- https://en.wikipedia.org/wiki/Turtle-jawed_moa-nalo
- https://commons.wikimedia.org/wiki/File:Phyllostegia_electra_%285491293762%29.jpg
- <https://ntbg.org/news/eye-on-plants-phyllostegia-electra/>

Discussion

- Genetic structure between ex situ and in situ populations are likely due to difference in sampling locations – most ex situ are from Mohihi while in situ individuals are from various locations, including some that are not represented ex situ
- Ex situ individuals were mainly collected from one geographic site limiting within population structure, while in situ individuals were collected from geographically distant sites which increases genetic structure within this population
- Surprisingly, there was no difference in genetic diversity or inbreeding, suggesting that despite being from distinct populations the amount of homo/heterozygous was nearly the same.
- This work suggests that we should sample from additional sites, especially those that come from Namolokama or other sites from the light blue genetic cluster location.
- Even though there is currently low inbreeding ex situ, it could increase in the future because of sampling from the same site highlighting the need for genetic monitoring and informed breeding
- Together, this highlights the importance of proper sampling of in situ populations to establish ex situ conservation collections in order to successfully reintroduce endangered plant species in the future