

Decreased genetic diversity and higher inbreeding in an ex situ population of Hibiscus Waimeae subsp. Hanneriae

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Introduction

- High levels of genetic diversity and low rates of inbreeding allow for populations to be resilient to environmental changes
- Seed banking is one way to conserve genetic diversity of endangered plants, but exceptional species must be managed as living in ex-situ populations
- Effective sampling of in situ populations to establish an ex situ population can safeguard their genetic diversity for reintroduction
- Ex situ populations should have high genetic diversity, low inbreeding, and representation from all genetic clusters to capture most of the species' genetic variation.

Objectives and Predictions

- Determine how much genetic structure there is between in situ and ex situ groups
 - There will be low genetic structure between ex situ and in situ groups because individuals in both were collected from similar geographic areas, which will limit their genetic differentiation
- Determine if there is a difference in genetic diversity and inbreeding between ex situ and in situ individuals
 - Genetic diversity will be higher in the in situ populations because there are more individuals from multiple populations in the wild
 - Inbreeding will be higher in the ex situ populations because fewer individuals can be bred together

Study System

Hibiscus waimeae subsp. *hanneriae*

- is a member of the Malvaceae family native to Kaua'i's northwestern valleys of Hanakapi'ai, Limahuli, and KalihiWai
- There are fewer than 200 individuals left in the wild
- It is a rare species due to hybridization, habitat loss, and competition from introduced plants

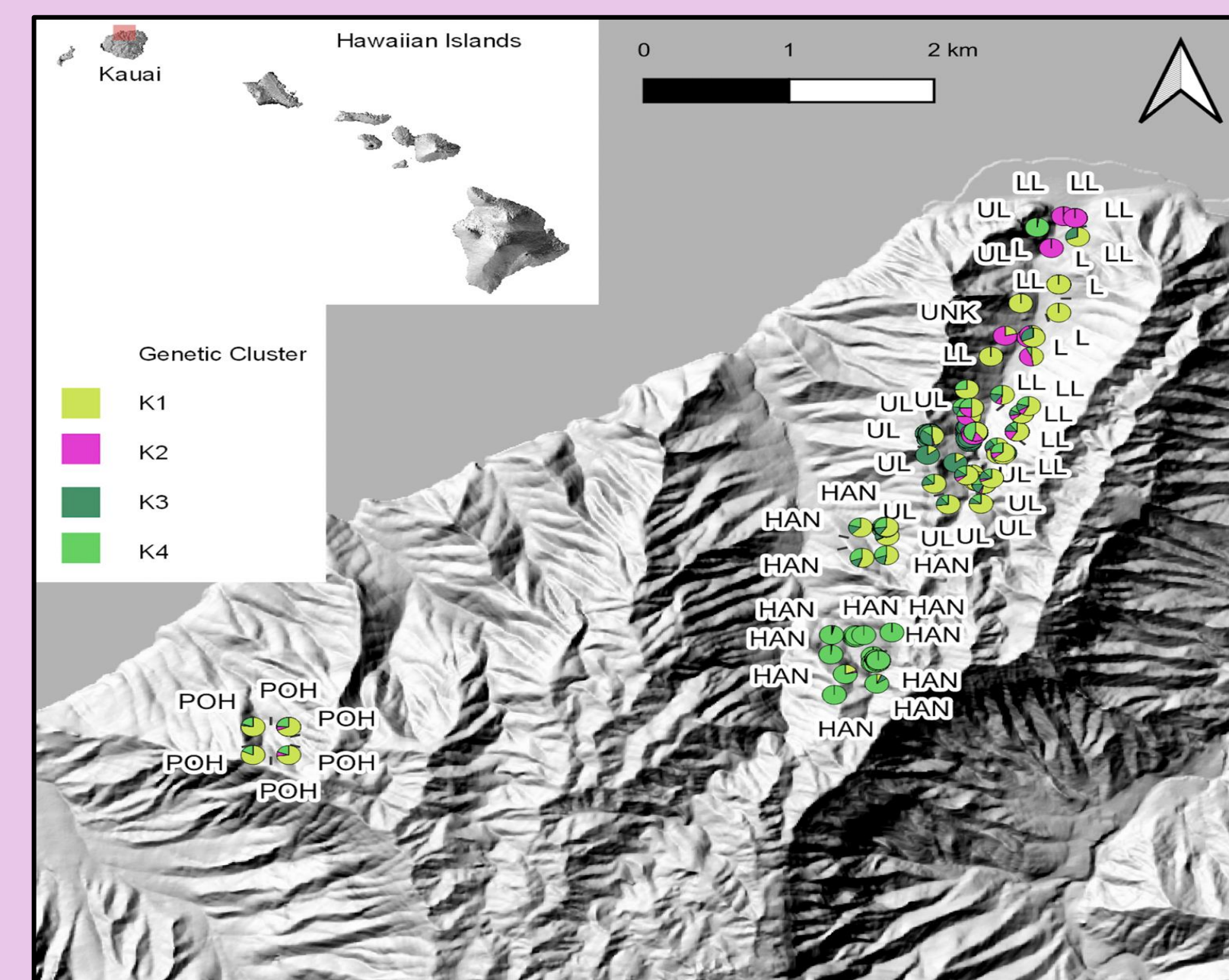


Figure 1

Location of each of the in-situ populations that were studied or sampled for the ex-situ populations. Pie charts reflect genetic structure results.

Figure 2

Genetic diversity (Pht) in and inbreeding (F) in in-situ and ex-situ populations.

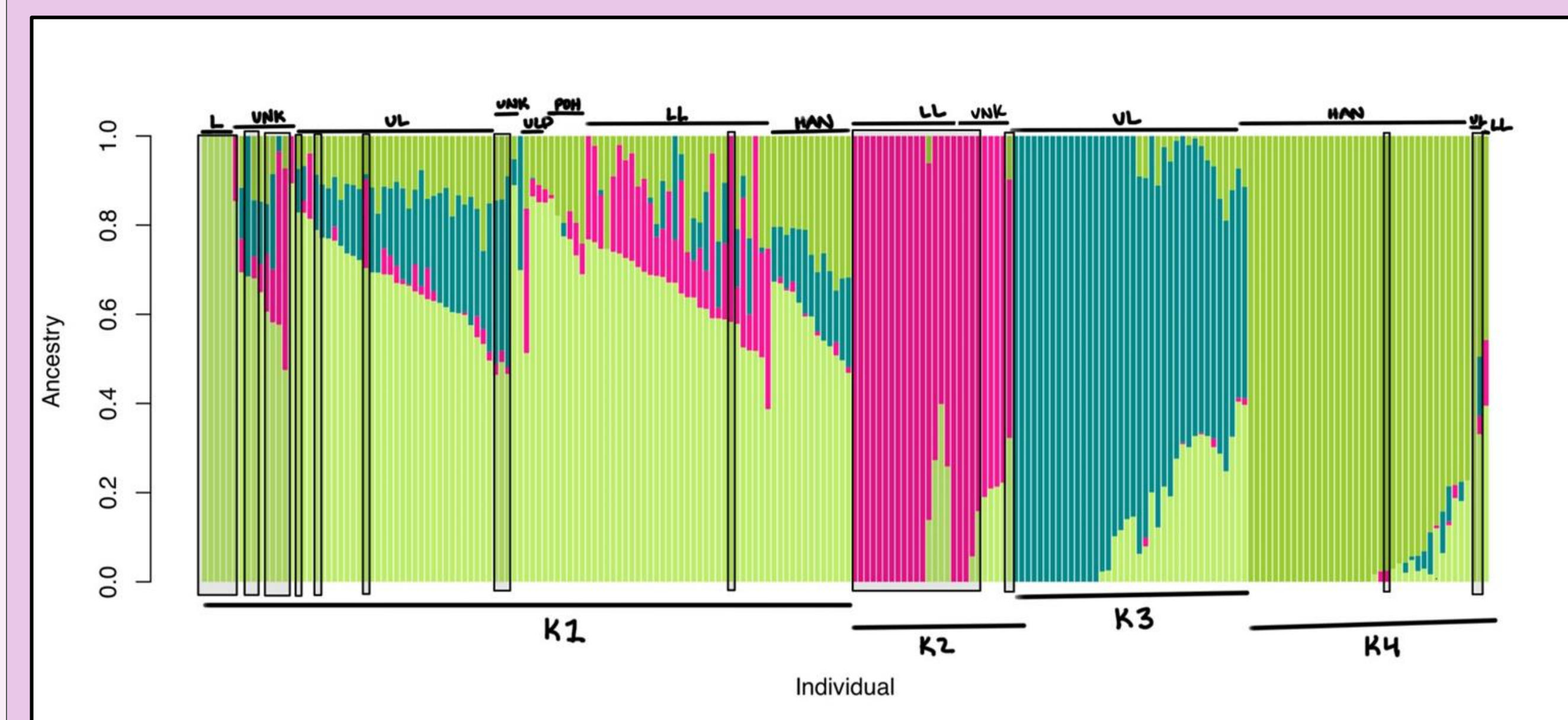
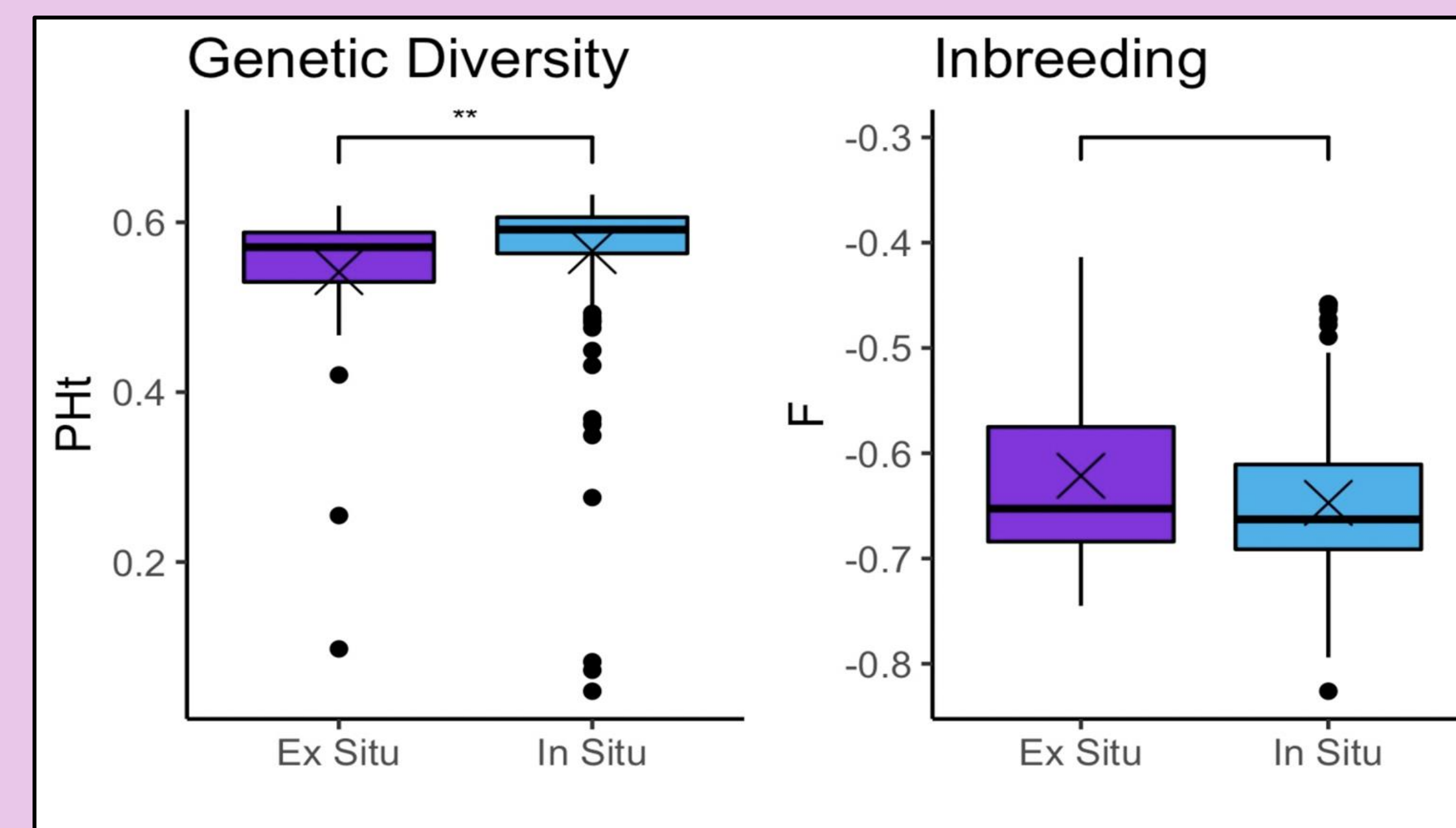


Figure 3

ADMIXTURE ancestry plot where each bar is an individual and the color corresponds to the percent identity to each genetic cluster. Lower labels indicate the genetic cluster and upper labels indicate the wild origin. Black boxes indicate ex situ individuals

Results

- I identified four genetic clusters as the optimal number of genetic clusters. There was high amounts of genetic structure between clusters but no genetic structure between in situ and ex situ populations.
- I found significantly higher genetic diversity ($W = 0.56639$, $p\text{-value} < 0.0001$) and significantly lower inbreeding ($W = 0.95009$, $p\text{-value} < 0.0001$) in in-situ populations compared to ex-situ populations.

Methods

- Extracted DNA: 209 samples, 42 ex-situ, 159 in-situ, 8 unknown status
- Created 2bRAD genomic library and sequenced on Illumina platform
- Performed denovo STACKS pipeline to call single nucleotide polymorphisms (Catchen, 2013)
- Performed Wilcoxon rank sum test in R (R Core Team, 2020)
- Evaluated genetic structure with ADMIXTURE (Alexander, 2009)
- Estimated genetic diversity with the proportion of heterozygous loci (Pht) using Genhet (Carter, 2022)
- Estimated inbreeding with the inbreeding coefficient (F) in PLINK (Purcell, 2007)

Discussion

- Lower genetic diversity and higher inbreeding ex situ suggest incomplete sampling of the in situ population, which is also supported by the overrepresentation of some genetic clusters and the lack of representation of others.
- Ex situ individuals were 'born' in the wild, which is likely why there is low genetic structure between the groups – there has not been adequate time for genetic differentiation to arise through a lack of gene flow or genetic drift.
- This work highlights the need for additional sampling of the in situ population in order to establish a conservation collection that captures all the genetic diversity in the wild.
- Using a genetic approach to evaluate how ex-situ populations are established tells us how to better manage exceptional species.

References