Determining minimum sample sizes for IUCN Red List endangered oaks through simulation

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Background

- Botanic gardens sample seed from the wild to form ex situ collections.
- A sufficient amount of genetic diversity is required for conservation (95% of alleles).
- Generic 'rules of thumb' have long been used to guide sampling; however, this may not be effective for all species.
- Recent work has shown that taxonomic similarity isn’t predictive of the minimum sample size required (Hoban et al., 2020).
- The genus Quercus was an exception, with one minimum sample size applying to all species tested (Hoban et al., 2020).

Study species

- IUCN Red List endangered species of genus Quercus (oaks).
- Oaks are keystone species for many ecosystems and are 'exceptional species'.
- Many oaks are threatened by climate change, habitat loss, and agriculture.
- We chose 12 species of IUCN Red List endangered oaks with adequate population information to simulate and sample from.

Objectives

- Determine minimum sample sizes to conserve 95% of the genetic diversity for 12 species of IUCN Red List endangered oaks.

Methods

- Prepare simulations: We wrote parameter values to represent our species and used the software Simcoal 2 to run backwards in time genetic simulations.
- Simulations & output: The simulation output represents individual genotypes. We ran 1000 replicates of each species simulation.
- Sampling: We wrote R code that represents random sampling in the wild. We sampled from 1 to 500 individuals for every species.
- Analyses: We calculated the proportion of alleles captured to determine the conservation success of each sample strategy for each species.

Results

- Genetic diversity captured for varying sample sizes across 12 oak species.
- Figure 1: Photos of several IUCN Red List endangered oaks.
- Figure 2: Known species ranges for several IUCN Red List endangered oaks of interest, with localities shown as orange dots.
- Figure 3: Results for sampling from 12 species of oaks. The x-axis shows the number of individuals sampled, from 1 to 500. The y-axis shows the proportion of alleles captured, which represents the genetic conservation success. Each species of oak we simulated is represented by a different color line. Note that some species have total population sizes less than 500, so we stopped sampling when the total population was sampled. The proportion of alleles captured across replicates for a given sample size were averaged.

Key findings

- One sampling strategy doesn’t fit all rare oaks.
- The sample sizes required to capture 95% alleles spans ranges from 30 to 270 individuals.
- However, most species require a sample size of 150 individuals.
- Why is this result different from the empirical study?
- We simulated 12 oak species, while 3 oak species were studied in Hoban et al. study.

Simulations represent idealized versions of the world, but can help us to understand and model complex processes that would be difficult impossible to do empirically.

The results of this project may contribute to practical sampling guidelines for these oak species and aid in conservation efforts.

Acknowledgements

References:
https://www.iucnredlist.org/