

Multi-Taxa Assessment of Genetic Diversity and Differentiation in Invasive and Non-invasive Populations

Claire Blackwell Thrower

Supervised by: Dr. Chloé Schmidt

Introduction

- Invasive species are organisms that have established and spread outside of their native ranges, often causing major ecological and economic damage
- The **genetic paradox of invasion** asks how populations are able to persist despite severe bottlenecks and reduced genetic diversity following introduction
- Genetic diversity is strongly linked to fitness and adaptive potential across taxa
- Here we examine genetic diversity and differentiation patterns in invasive and non-invasive populations using **microsatellite data**
- We hypothesize that invasive populations will exhibit lower genetic diversity, marked by a decrease in **gene diversity**, **allelic richness**, and **effective population size (Ne)**, as well as an increase in population differentiation marked by greater **population-specific fst**

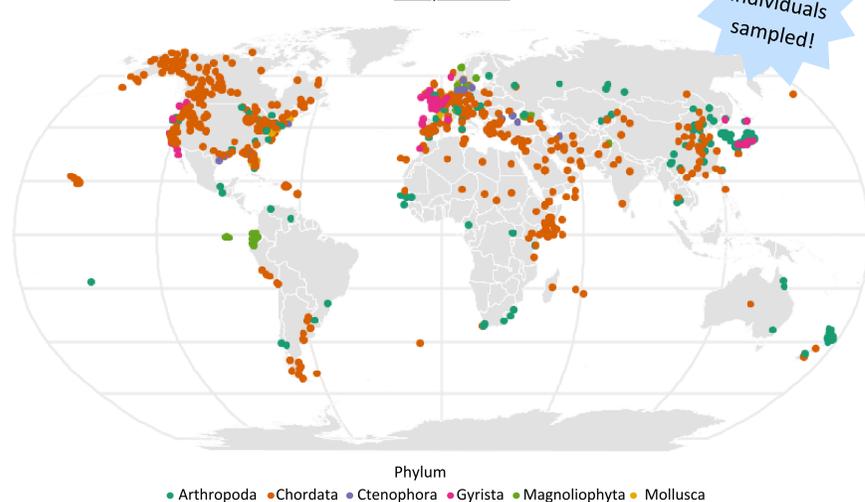


Examples of invasive species within the dataset. From left to right: *Erinaceus europaeus* (European hedgehog), *Heracleum mantegazzianum* (Giant hogweed), *Aedes aegypti* (Yellow Fever Mosquito), *Psittacula krameri* (Rose-ringed parakeet)

Methods

- A dataset was created using a programmatic search of the **Dryad data repository** for **microsatellite data** of invasive species from the Global Invasive Species Database (GISD)
- We used **Bayesian generalized linear mixed models (BGLMMs)** with genetic metrics as response variables and invasion status as a fixed effect to test whether invasion status predicted metrics of genetic diversity and differentiation across species
- We included **random slopes and intercepts** to account for **species-level differences** in baseline genetic diversity
- In addition to testing the overall effect of invasion status, we evaluated whether this relationship varied among habitat types, dispersal method, mass, and number of paths of the species at the time of invasion

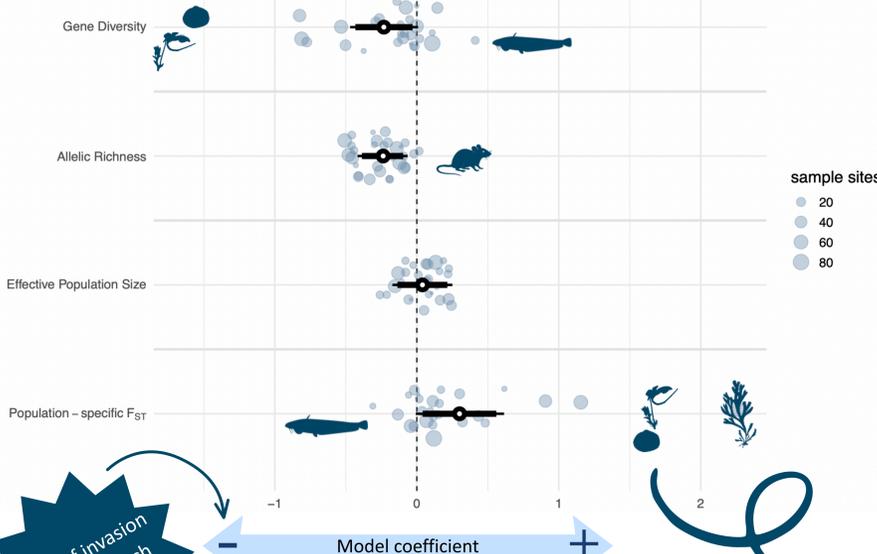
Sample Sites



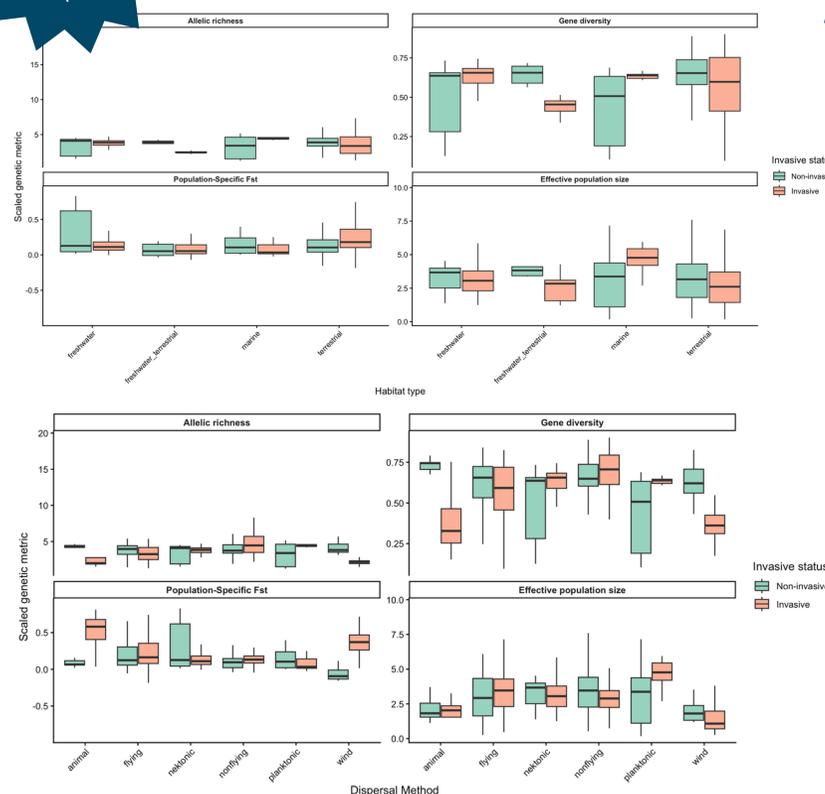
Results

Main Effects of Invasion Status

Overall, there was a strong negative effect of invasion status on gene diversity ($p = 97.08\%$) and allelic richness ($p = 99.62\%$); the two measures of genetic diversity. There was a slight negative effect of invasion status on N_e ($p = 64.93\%$). There was a strong positive effect of invasion status on population-specific F_{ST} ($p = 97.17\%$).



Effects of Dispersal Method and Habitat



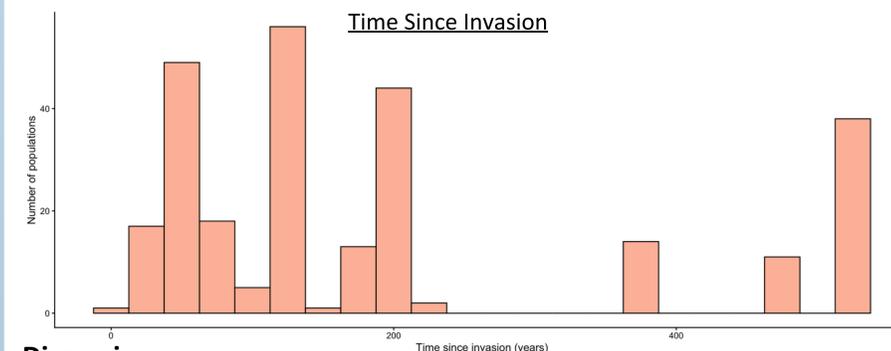
Number of Invasion Pathways

- Within the dataset, there are six potential pathways; **release, contaminant, corridor, stoaway, escape and unaided**. Each species may use one or multiple pathways to establish in a new range.
- We found no significant effect of the number of pathways, nor any interaction with invasion status on gene diversity, allelic richness, N_e or population-specific F_{ST} .



Silurus glanis, the Wel's Catfish, was introduced outside of its native range both deliberately, for sportfishing, and accidentally via escape from aquaculture.

Time Since Invasion



Discussion



Psidium guajava, the **green guava**, native to Ecuador, was introduced to the Galapagos in 1850 as a food resource. It has since spread extensively and now shares habitat with the endemic *P. galapageium* (Valdebenito 2018). Here, green guava shows stronger effects of invasion status on gene diversity (lower) and population-specific F_{ST} (higher), indicating less genetic diversity and greater divergence from the source population. This effect may be amplified as the invasive guava populations in the dataset occur only on islands.

- Overall, invasive populations show **reduced genetic diversity** and **increased genetic differentiation** compared to native populations, supporting our hypotheses
- Successful invasion occurred despite reduced diversity, indicating that invasion ability does not rely on high genetic diversity, supporting the idea that successful invasions are a result of a species coincidentally reaching a new range that is suitable for their expansion
- Habitat type and number of pathways are not reliable predictors for patterns of genetic diversity and differentiation between invasive and non-invasive populations

Conclusions and next steps

- By synthesizing genetic data across multiple invasive species, this study identifies broad, cross-species patterns that may not be detectable in single-species studies
- Next steps
 - Investigate specific introduction pathways within dataset
 - Test whether recent invasions differ genetically from historic invasions