

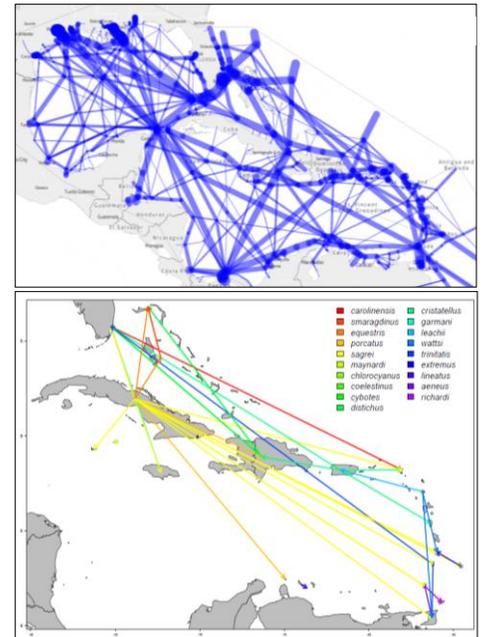
Tracing the spread of exotic species using genetic markers

This project provides an opportunity for a student to learn molecular genetic laboratory techniques that are useful for a multitude of biological fields including evolution, ecology, physiology, conservation, pharmacology, and medicine.

Project Description

Humans are greatly transforming natural landscapes by spreading species far from their place of origin. These exotic species can impact natural biodiversity and ecosystem functioning, and island ecosystems are especially susceptible to the impacts of exotic species.

Our work focuses primarily on terrestrial Caribbean herpetofaunal species (amphibians and reptiles) that are often transported passively from one island to another in cargo shipping containers (top figure shows shipping network). In the Caribbean, there are high rates of endemism such that each island has unique species that are found nowhere else. The first time these species are relocated to a new island, it is obvious where they came from. However, in many cases, these species are relocated in a stepping-stone pattern from island to island making it impossible to know *a priori* whether the exotic species on a particular island originated from its native island or another exotic population. For example in the bottom figure, all of the lines leaving Florida (top left) represent species that are exotic to Florida and are being spread further across the Caribbean (stepping-stone pattern). By using genetic markers, it is possible to identify potential sources of exotic populations. Once the sources of exotics are identified, it is then possible for island nations to enact policies for heightened screening of shipments coming from likely source locations.



The student project will involve conducting genetic analyses using a combination of mitochondrial and nuclear markers on DNA samples that have already been collected for species within their native and exotic ranges. Then the student will use R statistical software to analyze the results and link exotic populations to their likely source populations for each species. Finally, these linked exotic and source populations across several species will be combined to build a genetic invasion network.

Project Goals:

- Conduct molecular genetic analyses on DNA samples from exotic and native populations.
- Use statistical software to link exotic populations to likely source populations for each species.
- Combine results for multiple species to build genetic invasion network.

Student Responsibilities

- Learn appropriate molecular laboratory techniques to analyze DNA samples.
- Use and learn basic methods in R statistical programming to analyze molecular data.
- Maintain organized and consistent lab notebook and data management scheme.

Location

Lab work and statistical analyses will be conducted at the Center for Biodiversity molecular lab at Temple University, Philadelphia, PA, USA

Supervisor Information

Dr. Jocelyn Behm
j.e.behm@vu.nl

Prof. Dr. Jacintha Ellers
j.ellers@vu.nl