Using spatial population genetics to simulate the
efficacy of tropical forest restoration efforts

Patricia S. Sujii\(^1\), Micael E. Nagai\(^1\), Pedro H. S. Brancalion\(^2\)
Maria I. Zucchi\(^3\), Patrick M. A. James\(^4\)

Introduction

Deforestation

850 million hectares of
tropical forests were
degraded or deforested in the last century.

Conservation

+ Restoration

Conservation of remnant areas is one solution for the intense
forest and biodiversity loss. Ecological restoration is also required
to speed ecosystem recovery \(^1\). Over the past 30 years, riparian
forest formations have received special attention, due to their
importance to river protection \(^2\).

High genetic diversity

Potential to adapt to
environmental change

To maintain viability and evolutionary potential, it is important to retain the
maximal allelic diversity at all loci within a population, which requires attention to seed selection and
sourcing \(^3\).

Cetrolobium tomentosum

Tree widely used in restoration projects in the Atlantic Rain Forest, because is a
typical gap species, with relatively fast
growth and has symbiotic associations
with nitrogen fixation microorganisms.

Question

What is the effect of the following factors on genetic diversity and
long-term population viability in restoration zones?

- Initial genetic composition (allelic and genotypic frequencies)
- Forest patch size
- Forest patch shape

Model

Individual based model

The model accounts for:
- population demography
- reproductive patterns (pollen flow and seed dispersal)
- germination probability based on inbreeding

Simulations

We simulated an isolated population of C. tomentosum in a restoration area with three experimental treatments:

1. Population initial genetic composition

2. Size of restoration area

3. Shape of restoration area

Repetitions and time span

Each initial condition was simulated at least 200 times.
Populations from small and narrow areas were simulated for 500 years.
Populations from more square like areas were simulated for 250 years, for limitation of computational power.

Results

Among simulated restoration areas that were long and narrow in shape, we found that the larger areas resulted in
smaller effects of genetic drift, measured here as loss of total number of alleles.

- An 12% remaining
- A 5% decrease in sRate \(^7\)
- A 10% increase in FIS

Our square 5 ha restoration areas were as affected by genetic drift as the 10 ha long and narrow areas (Figure 2).

Mean number of individuals observed in each
population after different time spans for each treatment.

- Long and narrow
- Square like
- Small area

Figure 2. Mean number of alleles observed in each
collection after different time spans for each treatment.

Initial genetic composition had a stronger effect on the
inbreeding coefficient in populations from the small and narrow restoration areas. Selection against overall
homozygosity at the germination phase kept the inbreeding coefficient small or moderated, even with
fixation of alleles at some loci (Figure 4).

Figure 4. Mean inbreeding coefficient (FIS) observed in each
collection after different time spans for each treatment.

Poppulations in the smaller areas that were founded by
seeds from only one mother tree had a greater probability of
extinction. However, the shape of the restoration area, and consequently the initial population size, had a
stronger effect on probability of extinction than the initial genetic composition (Figure 5).

Conclusion and perspectives

If the restoration area is long and narrow, as in riparian forests, its length and the initial population size are important characteristics to consider to reduce the risk of strong genetic bottlenecks. The shape of the area has a large effect on mid-term genetic diversity loss and population viability due to the weaker border effect. So, the smaller and narrower the area, the greater should be the concern with the

References

species. Restoration Ecology. 22(6):1071-1080
species. Restoration Ecology. 22(6):1071-1080
fabricação. Dissertação, UFJF
tracking. PloS one, 6(5), e19997.