Genomics of hybridisation in British native flowering plants

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Introduction

(1) Hybridisation can play a critical role in plant evolution and has various outcomes, from promoting diversity to causing extinction.

Species A

hybridises with

Species B

Phenotypic traits.

The genetic admixture of a hybridising population at one point.

Fertile hybrid

Inferable/less fertile hybrid

(i) No impacts

(ii) Reinforcement

(iii) Hybrid zone

(iv) Reverse speciation

(v) Introgession

(vi) Hybrid speciation

(2) The British flora is among the most well-studied floras, with extensive hybrid records – an ideal system to understand natural hybridisation.

Study system

Selected from 909 accepted hybridising pairs in the UK (Stace, Preston & Pearman, 2015).

(Hybrids) largely sterile

(965)

Carduus nutans

Verbascum thapsus

Primula veris

Geum urbanum

Linaria vulgaris

(90)

Carduus crispus

Verbascum nigrum

Primula vulgaris

Viola hirta

Viola odorata

(26)

Linaria repens

(10)

Primula vulgaris

Viola hirta

Geum rivale

Viola odorata

Linaria repens

Linaria vulgaris

(43)

Total

134

365

N/A

Why select them?

Within each pair, both species:
- Widely hybridise with each other
- Overlap in their species distribution
- Genome size < 2 Gbp
- At the same ploidy level
- No great identification difficulties in the field

Materials & Methods

1. Sampling design
   - Minimum 5 populations for each species
   - Avoid early generation hybrids
   - Geographically widespread

2. Data source
   - Re-sequencing data
     - Illumina 150bp paired end reads, 15X
     - Reference genomes from the Darwin Tree of Life project (DToL)

3. Analytical approaches
   - Genetic structure
   - Demographic inferences

Research questions

What are the genetic consequences of postglacial introgression in British native flowering plants?

Q1. What is the extent of introgression revealed with whole genome sequences among the selected species?

Q2. What kind of genetic regions are introgressed?

Q3. How much does the fertility of the hybrids affect the extent of introgression?

Progress – fieldwork collection

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Scanning code to view collected sites in Google Maps

Next steps

- Future work
  - Detecting postglacial gene flow in the target hybridising species pairs, using resequencing data and demographic inferences.

- Discussion – hypotheses
  - For Q1, we anticipate that cryptic hybridisation will be detected with genomic data.
  - For Q2, we predict that introgressed linkage blocks underlie functional changes.
  - For Q3, We expect a positive correlation between hybrid fertility and the extent of parental species’ introgression.

Acknowledgements

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References

Fraïsse, et al., 2020. DILS: demographic inferences with linked selection by using ABC, Molecular Ecology Resources.