

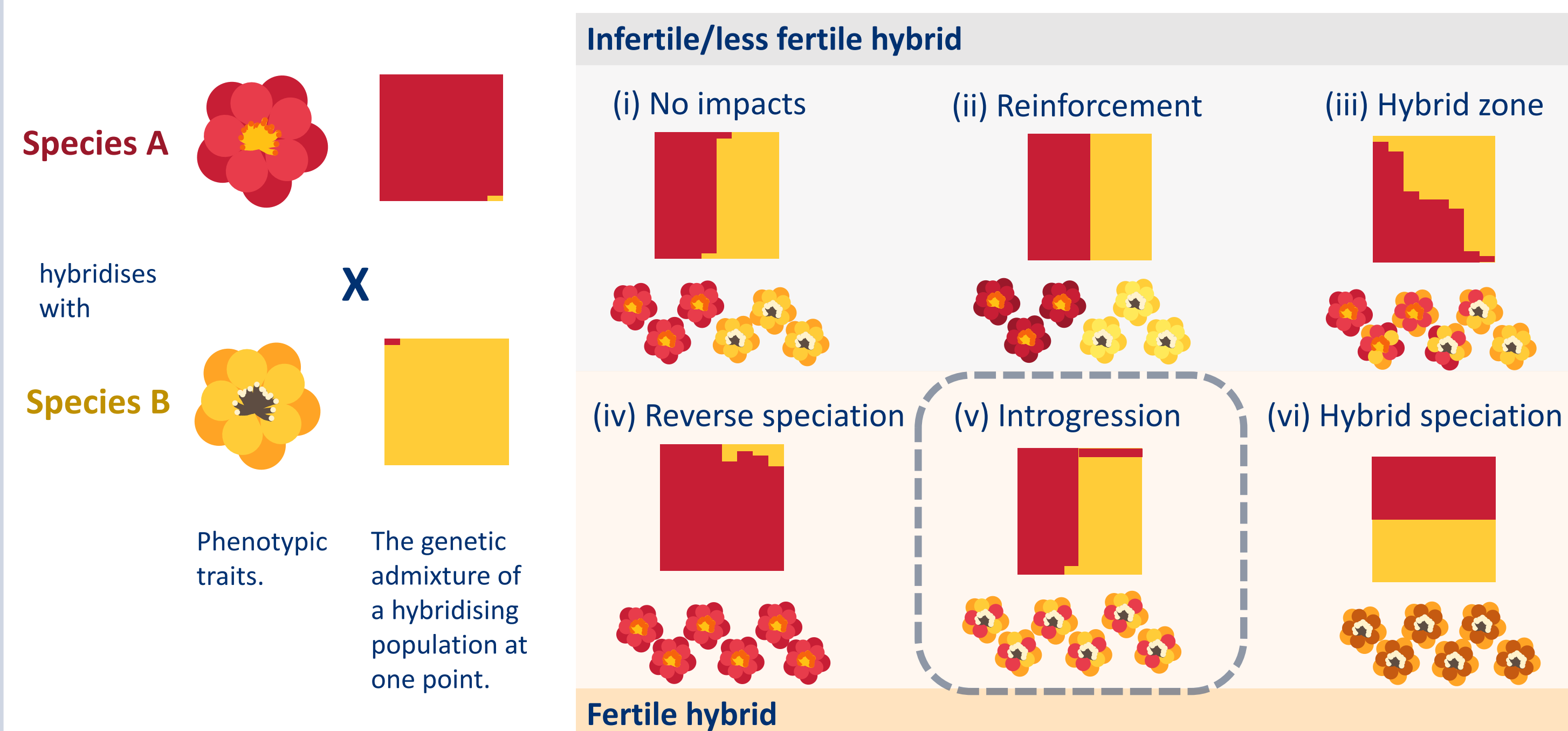


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Introduction

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



(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).



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

Research questions

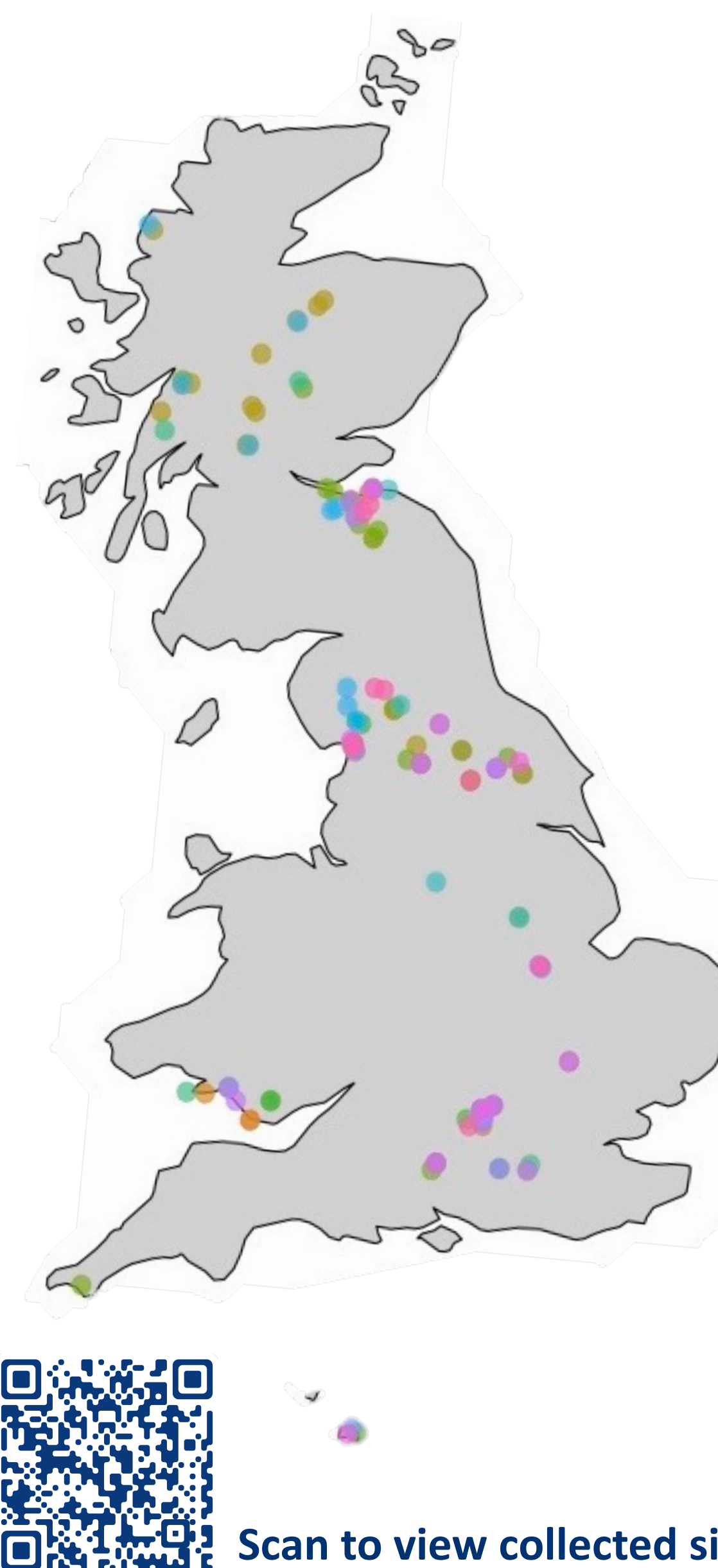
What are the genetic consequences of postglacial introgression in British native flowering plants?

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



Species	#Pop	#Indiv	Category
<i>Carduus nutans</i>	6	35	Hybrids largely sterile
<i>Carduus crispus</i>	10	32	
<i>Verbascum nigrum</i>	6	25	
<i>Verbascum thapsus</i>	12	44	Hybrids variably fertile
<i>Primula veris</i>	11	142	
<i>Primula vulgaris</i>	13	90	
<i>Viola odorata</i>	9	77	Hybrids largely fertile
<i>Viola hirta</i>	10	92	
<i>Geum rivale</i>	16	148	
<i>Geum urbanum</i>	26	187	Hybrids largely fertile
<i>Linaria repens</i>	7	50	
<i>Linaria vulgaris</i>	8	43	
Total	134	965	N/A



Scan to view collected sites in Google Maps

Materials & Methods

1. Sampling design

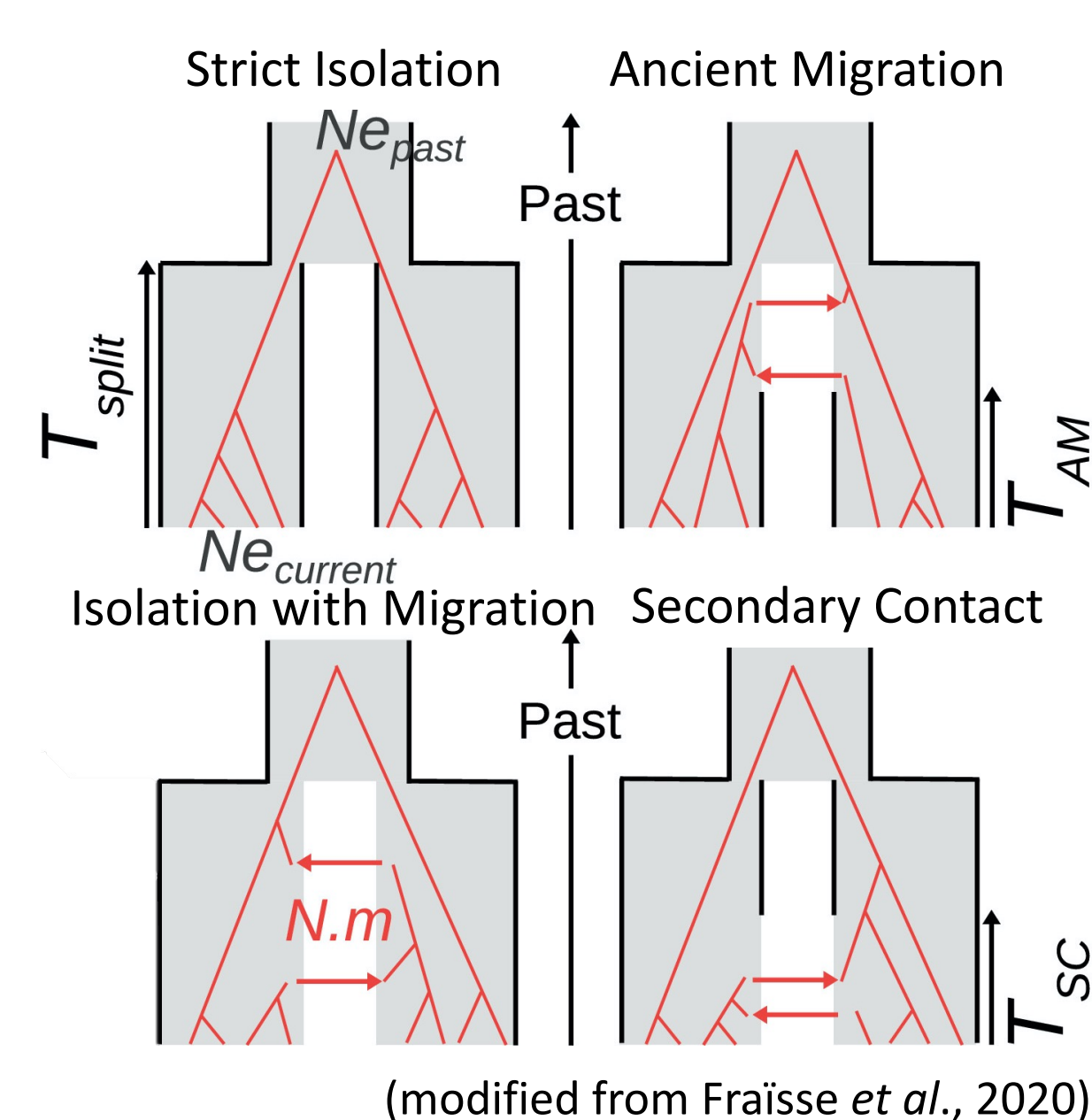
- > Minimum 5 populations for each species
- > Avoid early generation hybrids
- > Geographically widespread

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



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*.
- Stace CA, Preston CD, Pearman DA, 2015. Hybrid flora of the British Isles. *Bristol: Botanical Society of Britain and Ireland*.