

THE UNIVERSITY of EDINBURGH



**Botanic Garden** Edinburgh

# Resolving taxonomic complexity in diploid and tetraploid British eyebrights (Euphrasia)

**Presenter: Yangian Ding** Supervisors: Alex Twyford & Pete Hollingsworth







local



- Taxonomically complex groups (TCGs) are difficult to assign to discrete and unambiguous species due to the following reasons (see left <<)
  - Understanding genetic structure is the basis for TCG conservation, because inappropriate preservation will trigger a series of problems (like the 'butterfly effect', right >>)

## Study system

### Data analyses

- Genotyping by sequencing
- TASSEL pipeline for SNP calling (ref genome: *E. anglica* & *E.* arctica) Population genetic statistics; PCA, fastStructure, isolation by distance

### Euphrasia

- Phenotypic plasticity;
- Recent speciation;
- Extensive hybridisation;
- Diverse in polyploidy, mating system, ecology 862 samples from 4 diploid species, 14 tetraploid species, 35 putative hybrid combinations









## Questions

- What are the most distinctive clusters in all British eyebrights?
- Do clusters correspond to species or geography? 2.
- Is there evidence of genome-wide differentiation 3. across species?

## Hypotheses

- 1. Diploids vs tetraploids is the primary axis of divergence
- Geography drives clusters due to local hybridisation
- Low species-level differentiation with a few outlier 3. regions



Туре	Outlier SNP	Mean Fst
intra-species	17 50/	0 1 2 5
inter-cluster	12.5%	0.125
intra-species	0 70/	0.001
intra-cluster	8.2%	0.091
inter-species	F 10/	0.020
intra-cluster	5.4%	0.036

## Summary

- 1. In the UK, northern *E. micrantha* is genetically distinctive, indicating a different colonization history 2. Across the UK, geography plays an important role. We hypothesized that it related to selfing / hybridisation, this needs follow-on study to find out details
- 3. In closely related species, genome scans showed low species-level differentiation with a few outlier regions, these regions might underlie species differences

## Acknowledgements



Thanks to Hannes Becher for suggestions that improved this work. The sample collections are from the 'Eye for eyebright' project in collaboration with the **Botanical Society of Britain & Ireland.** 

## Reference

Ennos, R. A., et al. 2005. Conserving taxonomic complexity. Trends in Ecology & Evolution 20: 164–168.

French, G.C. 2003. Conservation genetics of the critical plant genus *Euphrasia* L. in Britain. Elshire, R.J., et al. 2011. A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. PLoS One, 6, 1–10. Raj, A., Stephens, M. & Pritchard, J.K. (2014). FastSTRUCTURE: Variational inference of

population structure in large SNP data sets. Genetics, 197, 573–589.

🄰 @YanqianD