1) INTRODUCTION: Human translocation of species and anthropogenic climate change are resulting in some of the fastest rates of species distribution changes ever seen[1,2], causing many native and non-native species to be brought together. While the ecological consequences are often well-documented, the evolutionary impacts of hybridization and gene flow between native and non-native species are usually less visible. Yet gene flow between native and non-native species could profoundly affect future evolutionary adaptations and diversification, potentially impacting on species conservation, responses to climate change and the spread of invasive species[3,4]. The long-term outcomes of gene flow between native and non-native species can vary from genetic swamping or genetic rescue of native species by introgressed genes from non-native species, to introgressed genes from native species allowing non-native species to persist or spread, and even the generation of new hybrid species[5,6].

Previous studies have only focussed on gene flow between a few exemplar species[7,8]. So we lack a general understanding of the prevalence and impact of interspecific gene flow across the tree of life, and specifically of how human activities may be altering these rates of gene flow. This placement contributes to a larger project (Dasmahapatra NERC Standard grant 2022-28, Adaptive Introgression in the Anthropocene) investigating human-induced introgression across 45 British flowering plant genera.

The British flora is perfectly suited for this purpose because the distributions of plant taxa in the British Isles are extremely well-characterised, the hybrid flora has been recently synthesized[9], and we have good estimates of when non-native plant species were first recorded in the wild. For each species data exists on ecological traits relevant to interspecific gene flow (pollination syndrome, self-compatibility, flowering times, hybrid fertility and generation times)[10]. Thus the flora of the British Isles is an ideal model system to build predictive models exploring ecological and genetic factors affecting the rates and effects of gene flow between native and non-native species.

2) OBJECTIVES

A) Build phylogenetic trees for each of the 45 target genus: For each genus, use genomic data of all available species in the NCBI Short Read Archive to build genus-level phylogenies using the Viking HPC to identify appropriate outgroup taxa for introgression tests using genomic data.

B) Test the correlation between ecological traits and propensity to hybridise: Collect trait data (range/habitat overlap, pollination syndromes, breeding system, flowering times, ploidy differences, genetic distance) for each hybridising species pair, and investigate whether these are correlated with propensity to hybridise.

3) SUMMARY OF PROPOSED EXPERIMENTAL WORK AND TIMELINE

Week 1: Induction, background reading and bioinformatics training
Week 2: Bioinformatics training and how to use the Viking HPC
Week 3: Locate and download genomic datasets from NCBI
Week 4-5: Phylogenetic tree reconstruction
Week 5-6: Collect trait data for each hybridising pair from various public databases[10]
Week 7: Analyse the trait data
Week 8: Write up, project presentation at lab group meeting, and hand over.

4) RESEARCH TRAINING FOR THE STUDENT: The student will be fully integrated within the PI's research group, and provided with desk space and computer for the research. Training will be provided by the project supervisors, Dasmahapatra and postdoc researcher Meng Lu, in:
i) Bioinformatics (working with command-line and the Viking HPC); ii) Genome sequence alignment and genotyping; iii) Phylogenetic analysis; 3) Statistical analysis using R.

5) REFERENCES [1] Thomas & Palmer *PNAS* 112:4387–4392 (2015); [2] Ottenburghs *Evol. Appl*. 14:2342–2360 (2021); [3] Chunco *Ecol. Evo*l. 4:2019–2031 (2014); [4] Mable *Heredity* 110:95–96 (2013); [5] Vallejo-Marín & Hiscock *New Phytol*. 211:1170–1187 (2016); [6] Lowe & Abbott *Heredity* 92:386–395 (2004); [7] Dasmahapatra et al. *Nature* 487:94–98 (2012); [8] Valencia-Montoya *Mol. Biol. Evol*. 37:2568–2583 (2020); [9] Preston & Pearman *Biol. J. Linn. Soc. Lond*. 115:555–572 (2015); [10]. Brown et al. *PNAS* 120:e2220261120 (2023).