



Exploring the impact of selection at hair colour loci across different human populations

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BACKGROUND

Phenotypic diversity across geographically distant human populations probably owes a lot to **adaptation** processes (positive selection) to **local environments**. Differences in complex disease prevalence between ethnic groups could be caused by population-specific adaptive patterns in recent prehistory.

We use hair colour as a model phenotype on which to study the possible fingerprint left by these processes on the genome.

1. Hair colour GWAS¹

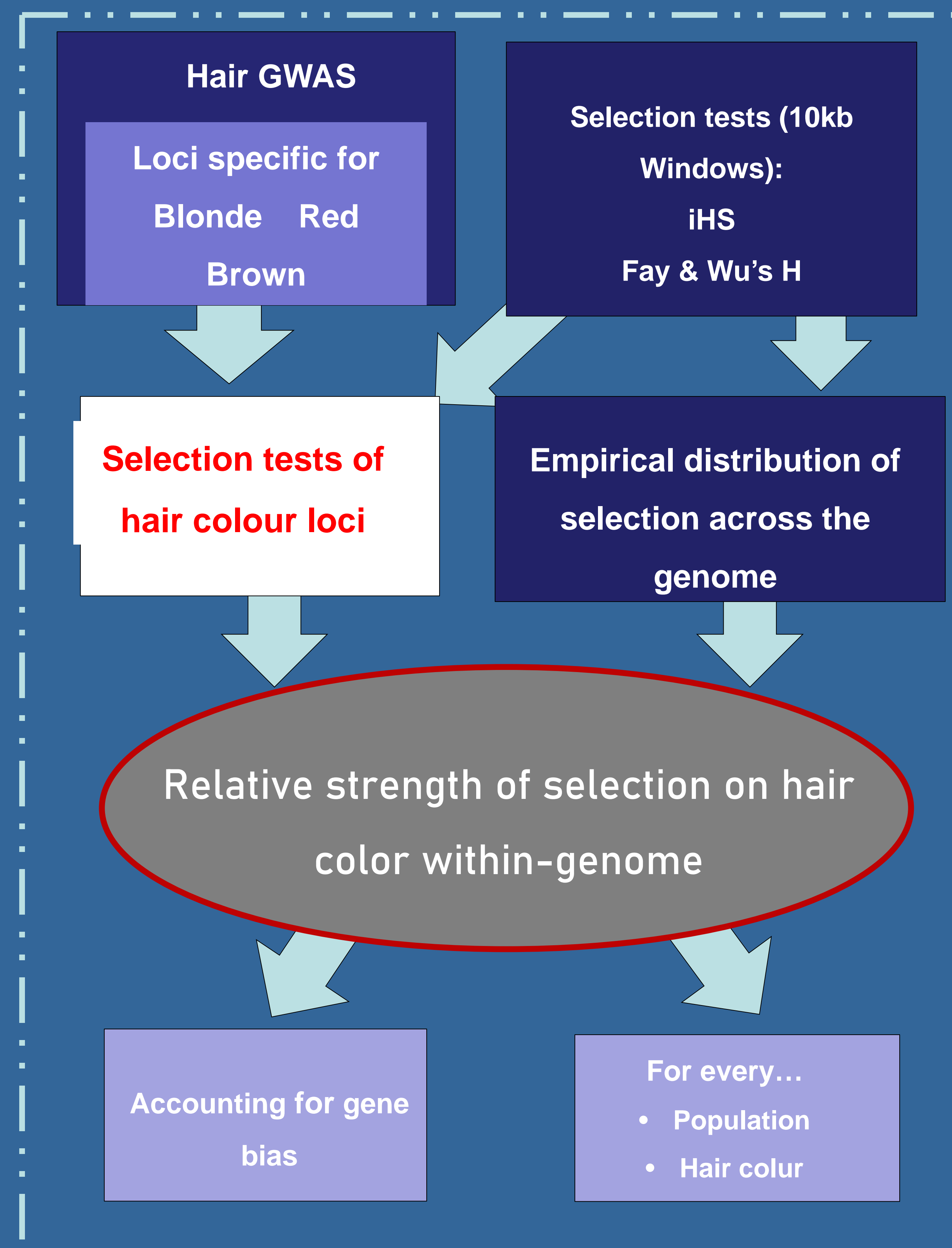
- British Caucasian individuals from UK Biobank
- Identified loci associated with red, blonde & brown hair

2. Tests of recent selection (PopHuman)²

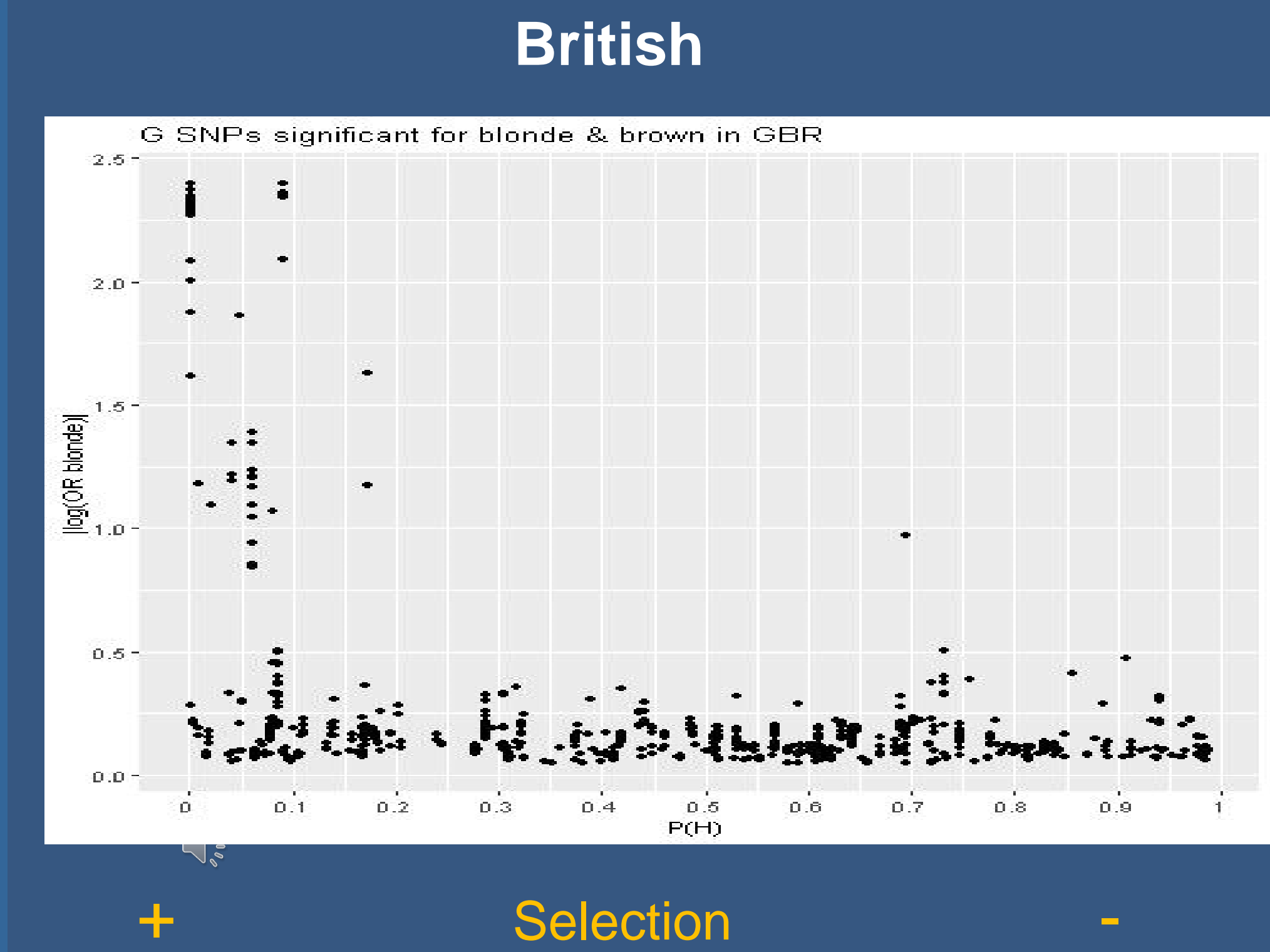
- Genome divided in 10 kb windows
- Sequences from 1000Genomes project³

References

1. Morgan, M. D. et al. (2018) *Nature Communications*, 9(1), 1-10.
2. Casillas, S. et al. (2018) *Nucleic Acids Research*, 46(D1), D1003-D1010.
3. <https://www.internationalgenome.org/data/>
4. Lotterhos, K. E. et al. (2017) *Methods in Ecology and Evolution*, 8(6), 717-727.



Effect size



RESULTS

- Hair colour evolution matches models of out-of-Africa human migration
- Probable moderate selection for lighter hair in Europe
- Black hair colour in East Asia and Africa: same phenotype, different evolutionary history