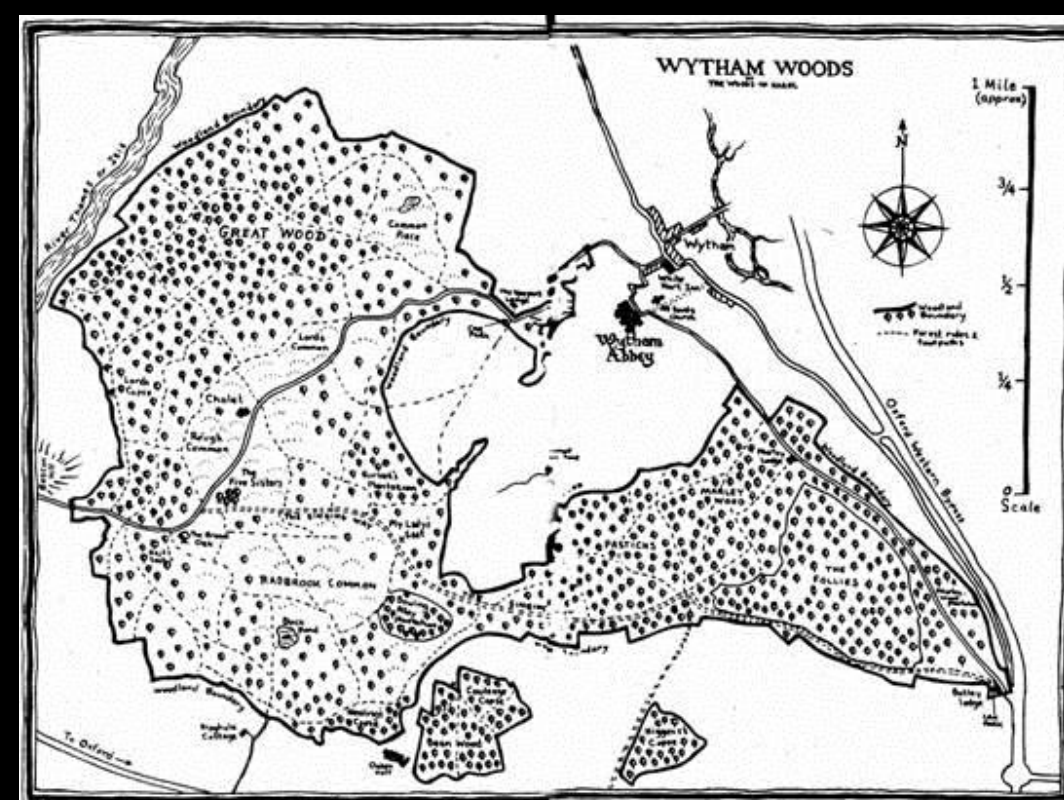


Genetic architecture of a reproductive trait in a wild bird population

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Data from long-term field study of great tits in Wytham woods, Oxford.

Questions:

Can variation in lay date in great tits (*Parus major*) be attributed to underlying genetic variance?

Is lay date an oligogenic or polygenic trait?

(Variation determined by few genes of great effect or many genes of small effect)

Methods

Identifying genomic regions contributing to variation using quantitative genetic techniques:

1. Quantitative trait loci (QTL) mapping

- Using pedigree, single nucleotide polymorphism (SNP) marker and phenotype data in 'animal models'

2. Genome-wide association scan

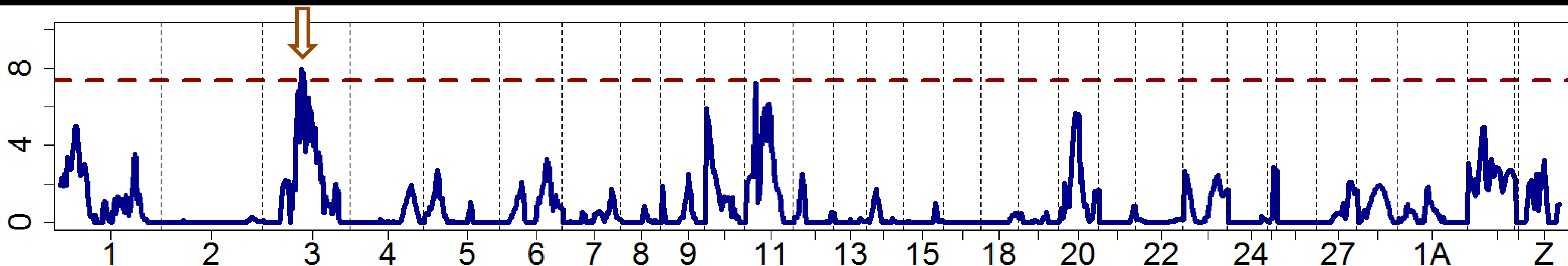
- Measuring the association between SNP markers and lay date

3. Chromosome partitioning

- Genetic variance partitioned across chromosomes by estimating 'the covariance between phenotypic similarity and sharing of alleles'¹

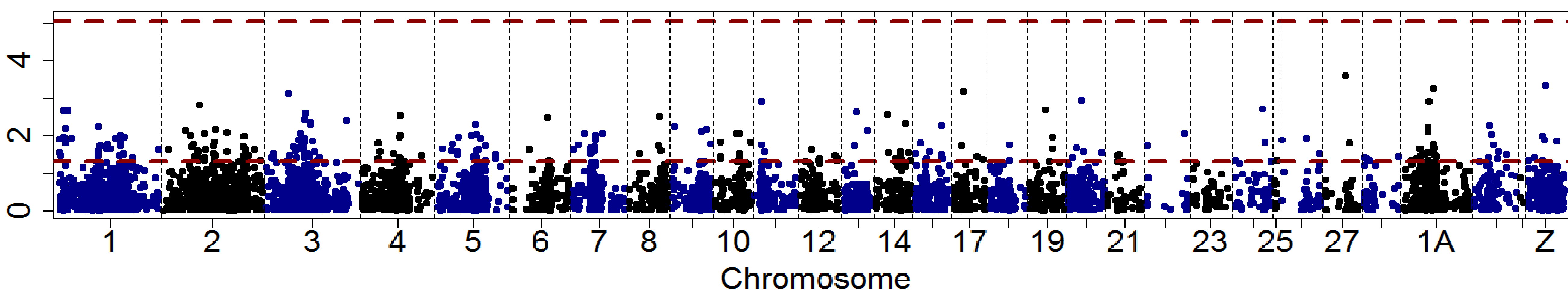
QTL scan

LRT score



GWAS

-log10 pvalue



1. QTL scan

Suggestive QTL peak on chromosome 3

(suggestive threshold - - -)

Heritability of lay date ($h^2 = 0.06$, SE 0.02).

2. GWAS

No genome-wide significant results, 271 SNPs over suggestive threshold (suggestive and significant thresholds - - -)

3. Chromosome Partitioning

Chromosome 7:

Significant contribution to overall genetic variation ($P = 0.04$)

Does not account for all heritable variation (Chromosome 7 $h^2 = 0.02$)

Conclusion:

These analyses suggest a polygenic basis for phenotypic variation in lay date