How to GWAS - ConGen 2022

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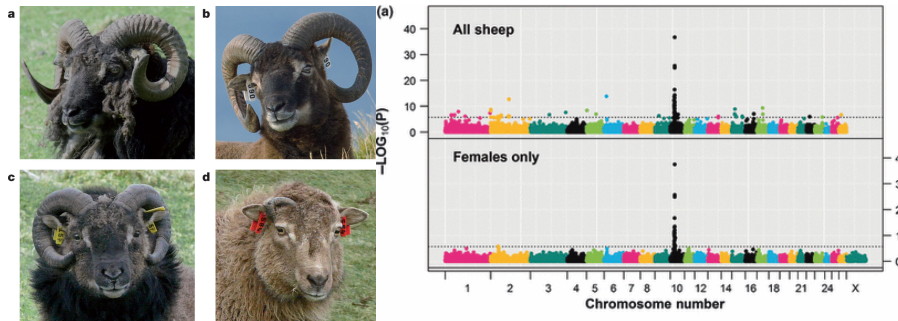
What is GWAS?

Genome Wide Association Study

- $y = a + bx + g + e$
- y: phenotype
- b: fixed effect
- x: the SNP predictor coded as 0, 1, 2
- g: the polygenic random effect (e.g. Kinship matrix)
- e: the error term
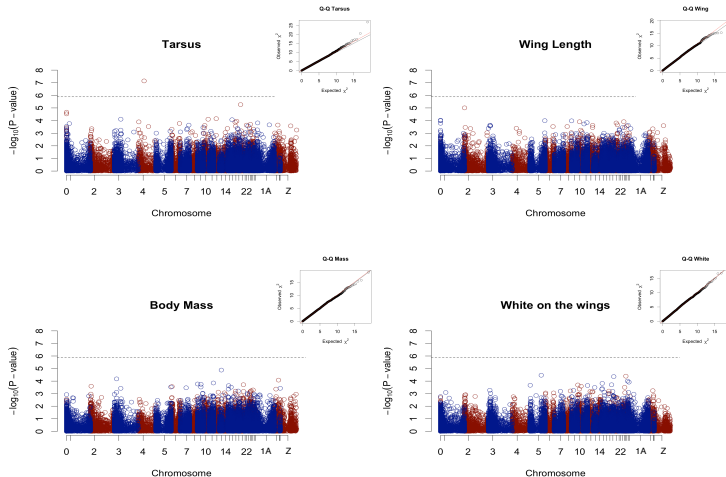
Soay Sheep Horns RXFP2 genotype

Johnson et al. 2011 Mol Ecol, Johnson et al. 2013 Nature

- 486 sheep
- 35 831 SNPs
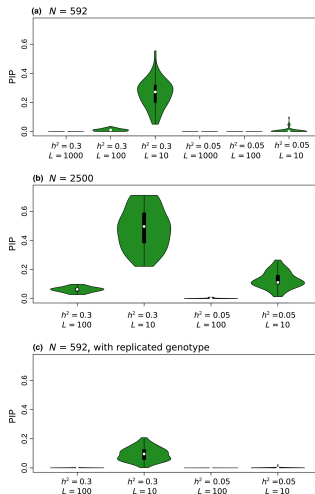- one huge effect locus, explains 76% of the variation in horn size

What are the expectations for a GWAS?

- ▶ No significant SNPs for morphological traits
- ▶ 3 SNPs explaining ~3% of the variation in clutch size

Some considerations for GWAS

- heritability of the trait
- genetic architecture of the trait (unknown!)
- Linkage Disequilibrium
- number of individuals sampled

Kardos 2015 MER, Gompert 2017 Mol Ecol

Some solutions

- Sample more individuals!
- replicated samples of individuals (RepeatABEL, RIP)
- Admixture mapping instead of within population GWAS

What is Admixture mapping?

Deer Case study