How to GWAS - ConGen 2022

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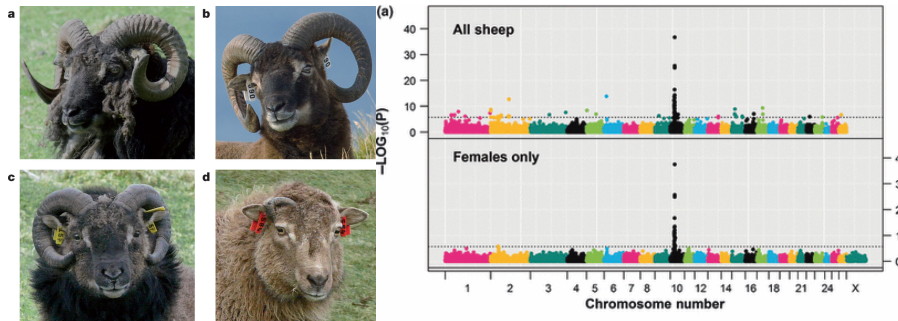
What is GWAS?

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)
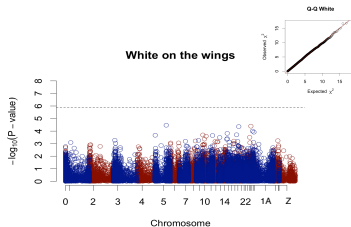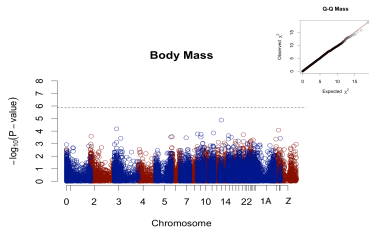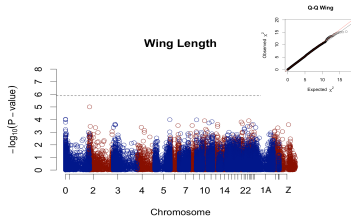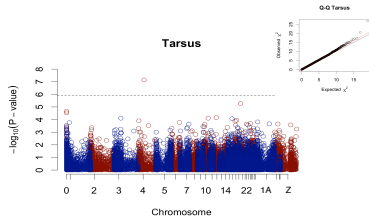- e: the error term

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

Slide with R Output

```
summary(cars)
```

```
##      speed           dist
##  Min.   : 4.0   Min.   :  2.00
##  1st Qu.:12.0   1st Qu.: 26.00
##  Median :15.0   Median : 36.00
##  Mean   :15.4   Mean   : 42.98
##  3rd Qu.:19.0   3rd Qu.: 56.00
##  Max.   :25.0   Max.   :120.00
```

Slide with Plot