

# Genetic architecture of clinical mastitis traits in dairy cattle

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**GWAS identifies 61 regions affecting mastitis resistance in dairy cattle**

A limited number of genomic regions explain a substantial fraction of genetic variation in mastitis risk.

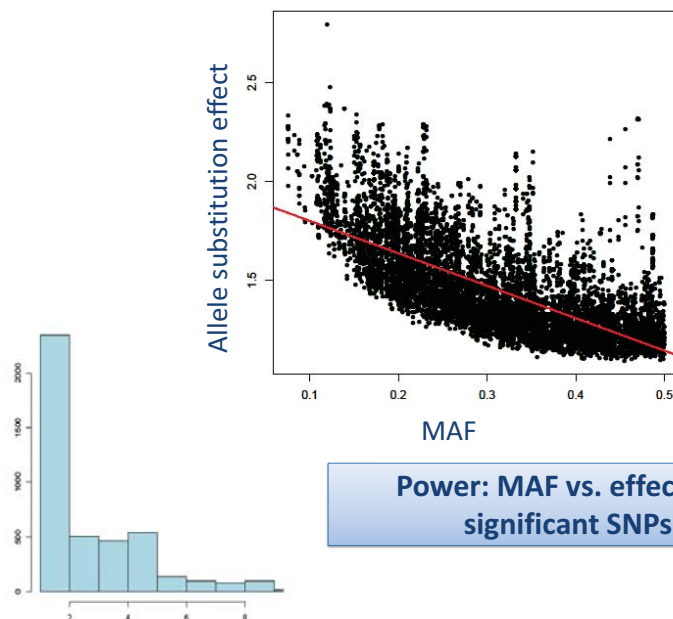
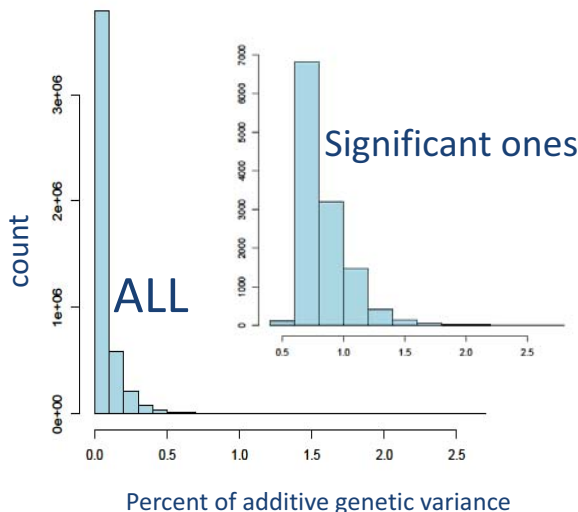
**Method**

- 4,200 Nordic Holstein
- 648,219 SNP
- Nine mastitis traits
- Linear mixed model

**Results in brief**

- 12,372 SNP-by-trait genome-wide significant associations
- 45% of significant SNPs were associated with  $\geq 2$  traits
- ‘Clustered’ into 61 regions

Variance explained by individual SNP



Power: MAF vs. effect, for significant SNPs

No. of traits associated with one SNP