



Genome-wide association study for calving performance using HD genotypes in dairy & beef cattle

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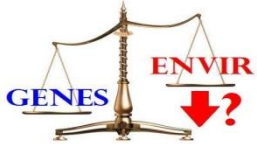
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Calving Performance

Lowly
Heritable



Complex
Quantitative
Traits

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + \alpha A^{-1} \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{a} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$



Dystocia

(Calving Difficulty)

Important
Economic
Traits



National
Breeding
Objectives



Objective: To elucidate the **genomic variation** behind calving difficulty in dairy & beef cattle

Materials & Methods

- High density genotypes (**777,962**) available on **2,660** dairy and beef sires

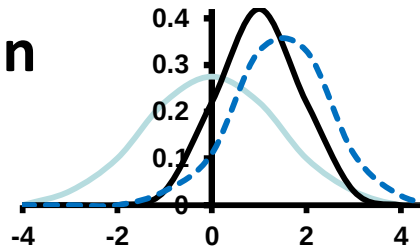


N=	927	770	963
SNPs	602,372	605,718	600,980

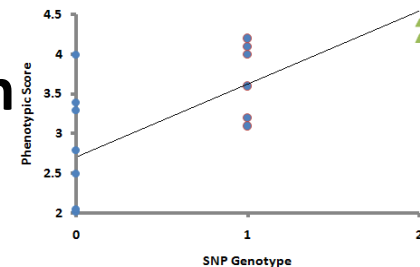
- EBVs obtained from ICBF
 - Deregressed & >30% reliability

- Two GWAS methods

1. Bayesian

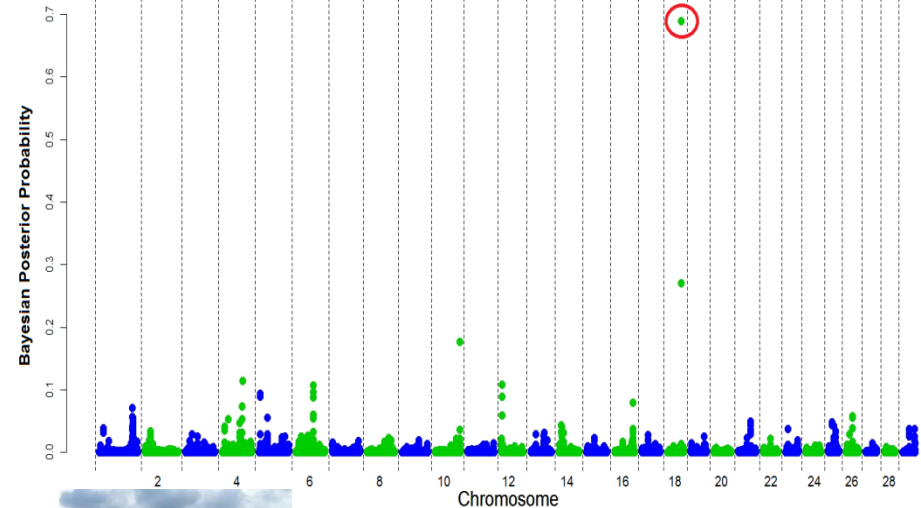
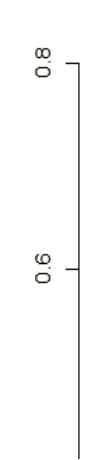


2. Single SNP Regression



- Meta-analysis

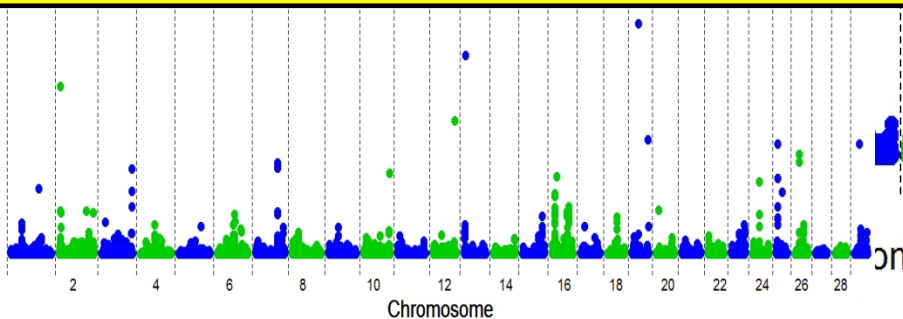
Multibreed GWAS



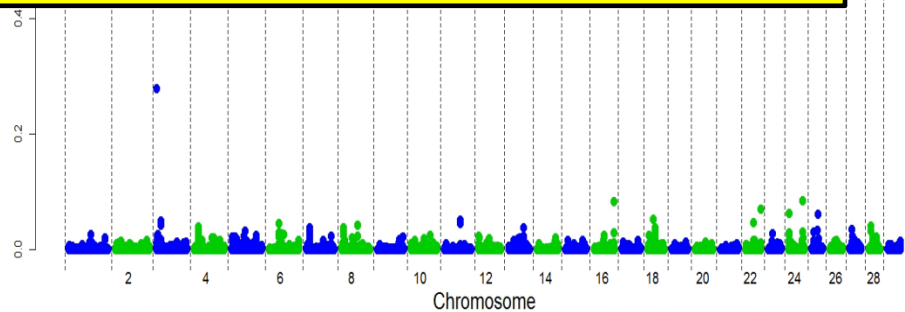
Dairy



Different breed effects

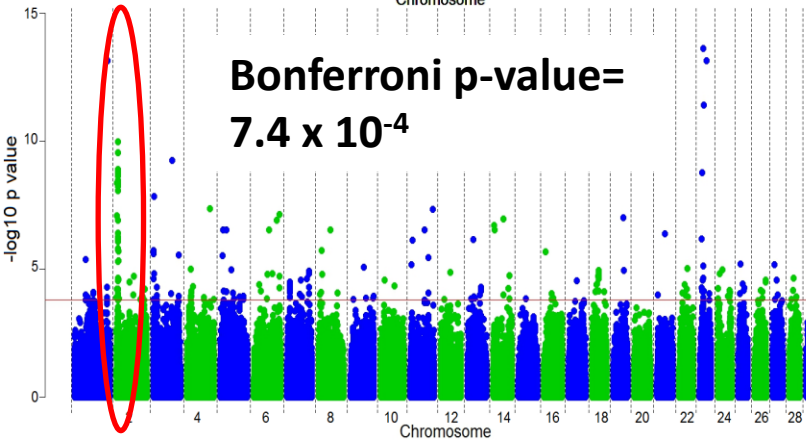
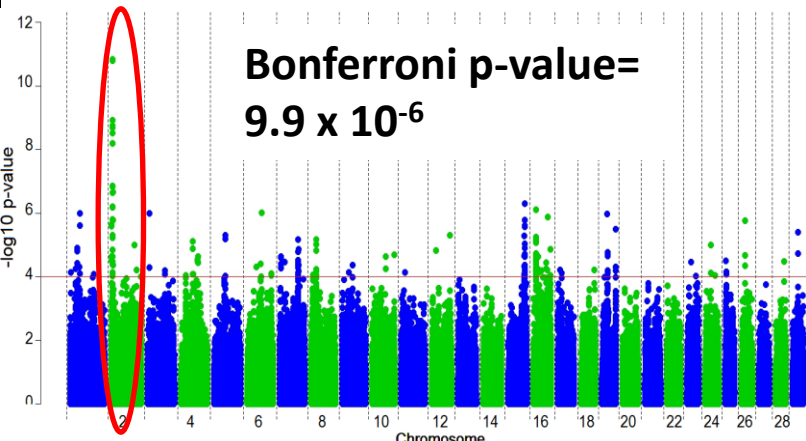
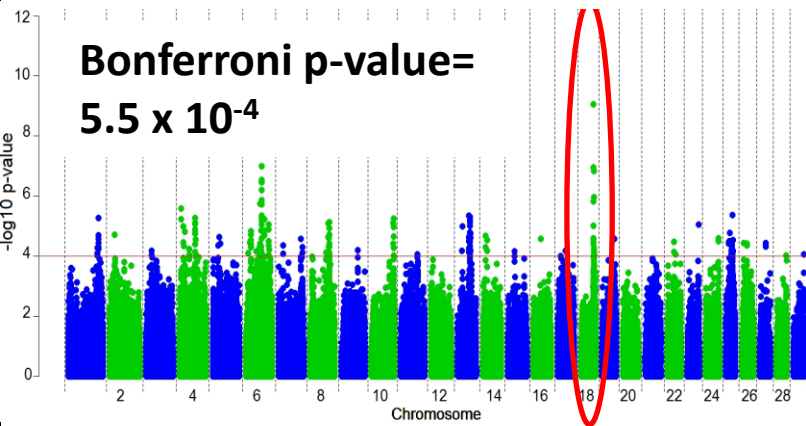


Charolais

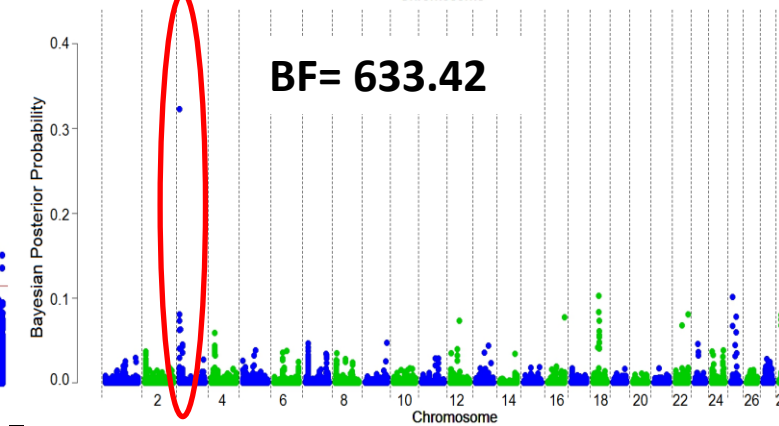
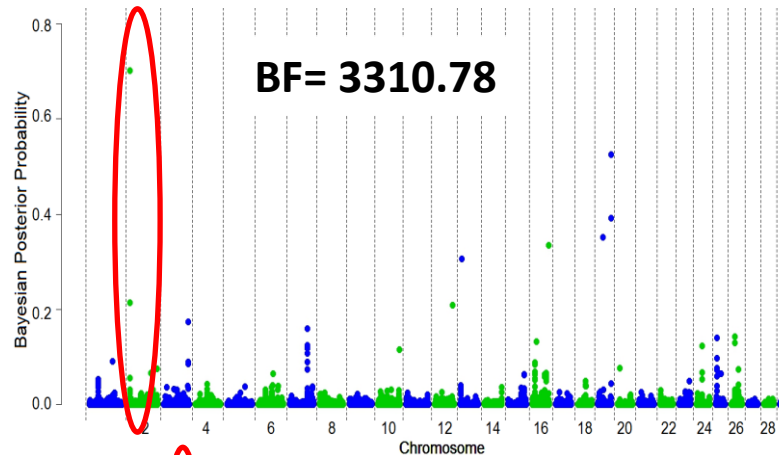
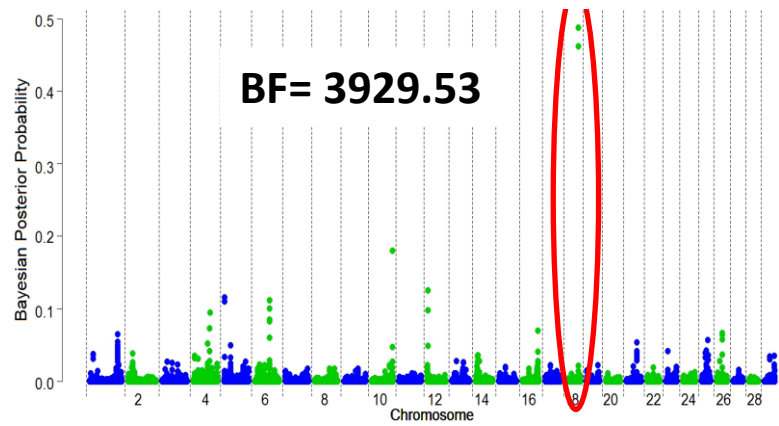


Limousin

Single SNP Regression



Bayesian



Hol-FR

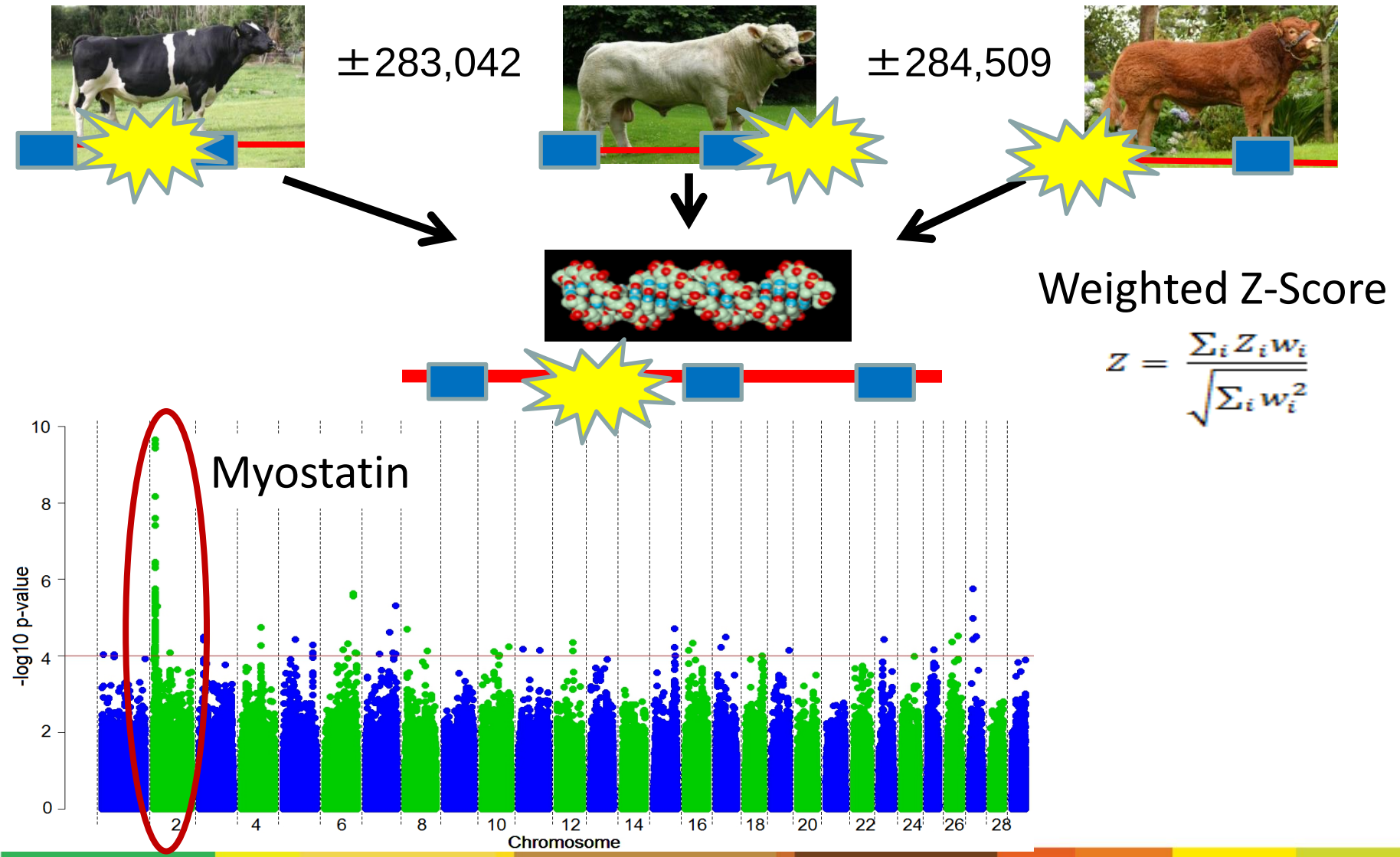


Charolais



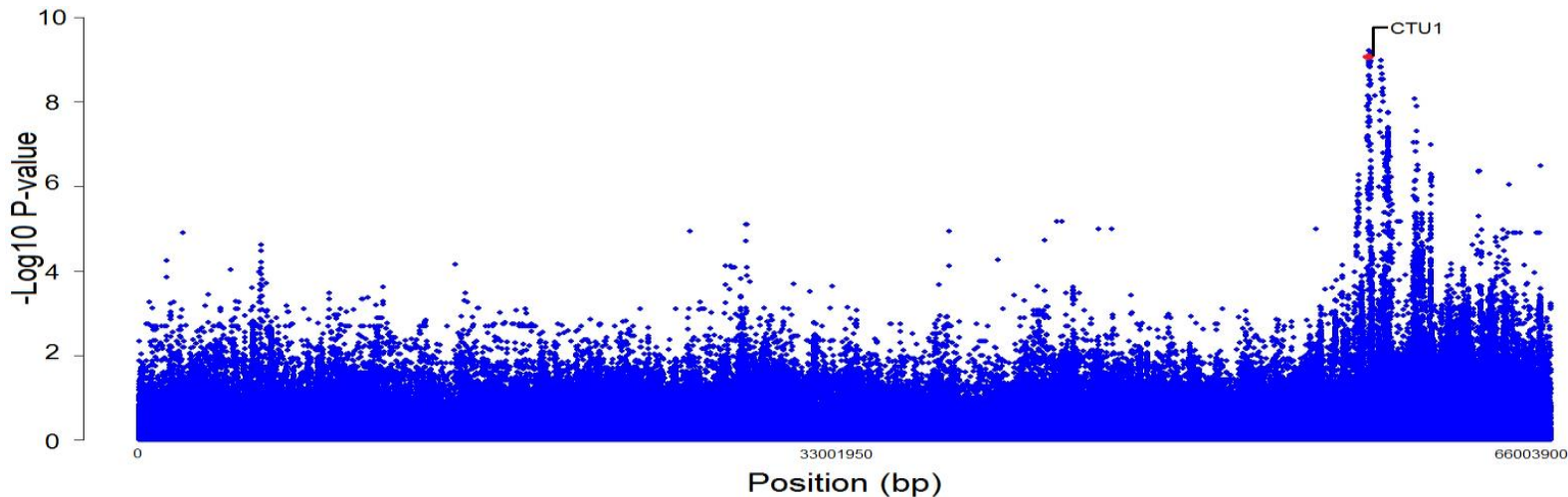
Limousin

Meta-Analysis for direct calving difficulty



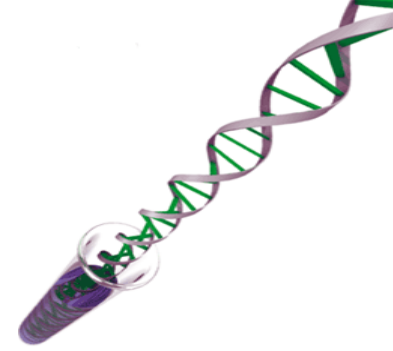
Refinement of genomic associations

- ❑ **1147 whole genome sequence** data available from 1000 Bulls genomes project
 - ❑ 27 breeds, 11.0X genome coverage, 35.2 million SNP variants
 - ❑ Imputed BTA18 in the Holstein-Friesians to sequence density
 - ❑ FImpute: 18,669 SNPs to 912,289 SNPs



- ❑ 16 gene/gene-products
- ❑ 4 highly significant **missense variants** ($p < 2.5 \times 10^{-8}$)
- ❑ CTU1 possibly damaging (**SIFT=0.06; Polyphen=0.95**)

Conclusions



1. Associations **differed** per breed
 - ❑ Impacting across-breed genomic selection??
 - ❑ Proportion of **genetic variance common** across breeds
2. Multiple **strong associations** detected for direct calving difficulty
 - ❑ Possibly change how genetic evaluations are computed
3. QTL on **chromosome 18** most promising for dairy breed
 - ❑ 3.1% of the genetic variation
 - ❑ CTU1 possible candidate gene
4. QTL on **chromosome 2 impacting beef breeds**
 - ❑ 3.13% of the genetic variation
 - ❑ Myostatin

Acknowledgements

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Thank you for your attention

Questions?