Genomic analyses of claw health traits in Holstein cattle

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Genomic analyses of claw health traits

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Context

Claw lesions: major health issue in dairy cattle
- Welfare
- Economic losses

Objectives

Determine best evaluation approach
Identify QTL

Conclusions

Most suitable method: SSGBLUP
More insight on genetic architecture of claw health traits

Picture: CFPPA

Material and methods

Data

Data collection: April 2014 -> February 2017
Genotypes: Illumina SNP50 BeadChip
Phenotypes recorded on 46 787 Holstein cows (7 333 genotyped)
2 360 sires with genotypes

7 lesion traits: 3 infectious (digital dermatitis, heel horn erosion, interdigital hyperplasia), 4 non-infectious (sole hemorrhage circumscribed, sole hemorrhage diffused, sole ulcer, white line fissure)
Lesion phenotype: 0/1
+ trimming status 0/1 to account for preselection

Evaluation model

$$y_{ijkl} = \mu + (hv_i) + (p_j) + (c_k) + a_l + \varepsilon_{ijkl}$$

Herd*visit → Parity → Lactation stage

Evaluation approaches
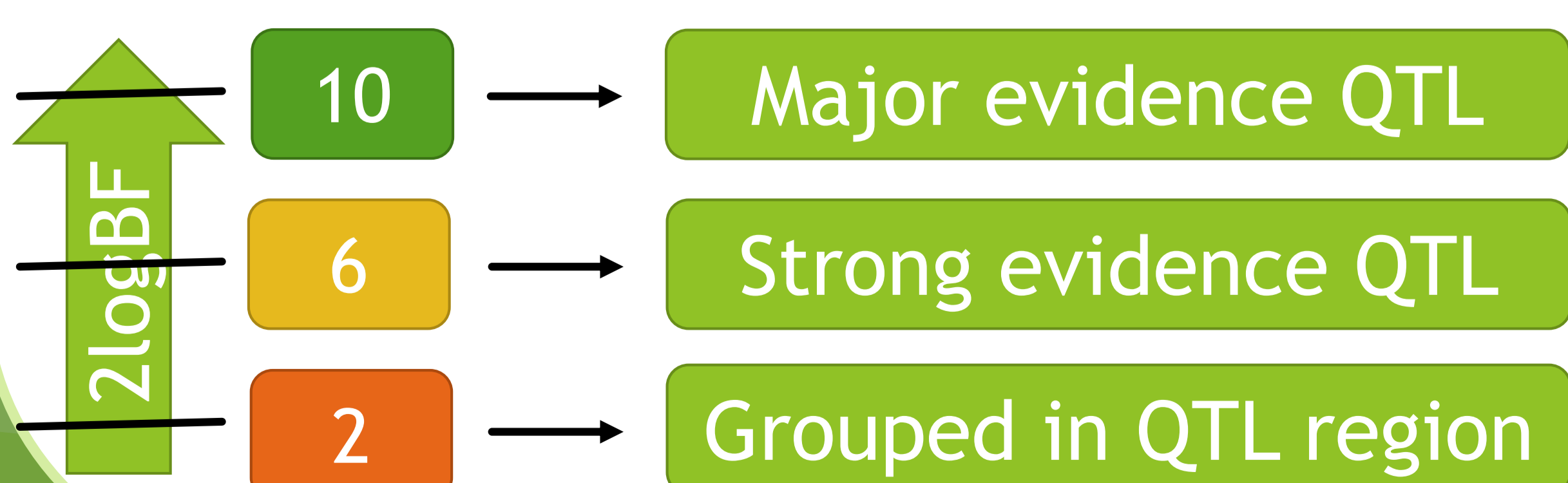
BLUP vs GBLUP vs BayesC vs SSGBLUP
Comparison: cross-validation study

QTL detection

Method: BayesC (∏=1%)
QTL selection: Bayes factor (2logBF)

2logBF

10	→ Major evidence QTL
6	→ Strong evidence QTL
2	→ Grouped in QTL region

Results

Comparison of evaluation approaches

Accuracy	Digital Dermatitis	Sole Ulcer
BLUP	0.05	0.07
GBLUP	0.08	0.12
BayesC	0.09	0.10
SSGBLUP	0.12	0.12
Max expected ($\sqrt{h^2}$)	0.26	0.22

Accuracy: correlation between female preadjusted performances and EBVs

Bias	Digital Dermatitis	Sole Ulcer
BLUP	0.47	0.92
GBLUP	0.38	0.53
BayesC	0.53	0.66
SSGBLUP	0.74	1.03

Bias: slope of the regression of female preadjusted performances on EBVs

QTL detection

5 major evidence QTL

6 overlapping QTL regions on two of the traits

LogBF / Position en mégabase