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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

$$y_{ijkl} = \mu + \underbrace{h_{v_i}}_{\text{Herd*visit}} + \underbrace{p_j}_{\text{Parity}} + \underbrace{s_k}_{\text{Lactation stage}} + a_l + \varepsilon_{ijkl}$$

### Evaluation approaches

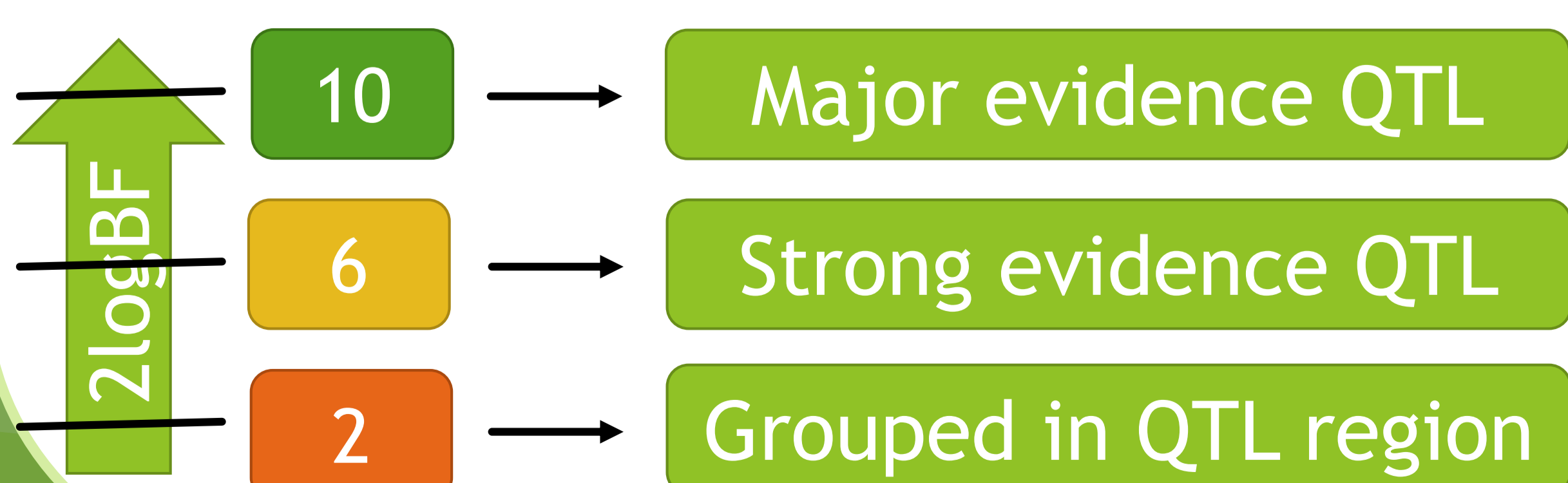
BLUP vs GBLUP vs BayesC vs SSGBLUP

Comparison: cross-validation study

### QTL detection

Method: BayesC ( $\pi=1\%$ )

QTL selection: Bayes factor ( $2\log\text{BF}$ )



## 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

