The effect of single genes – genes with large effect and recessive lethals

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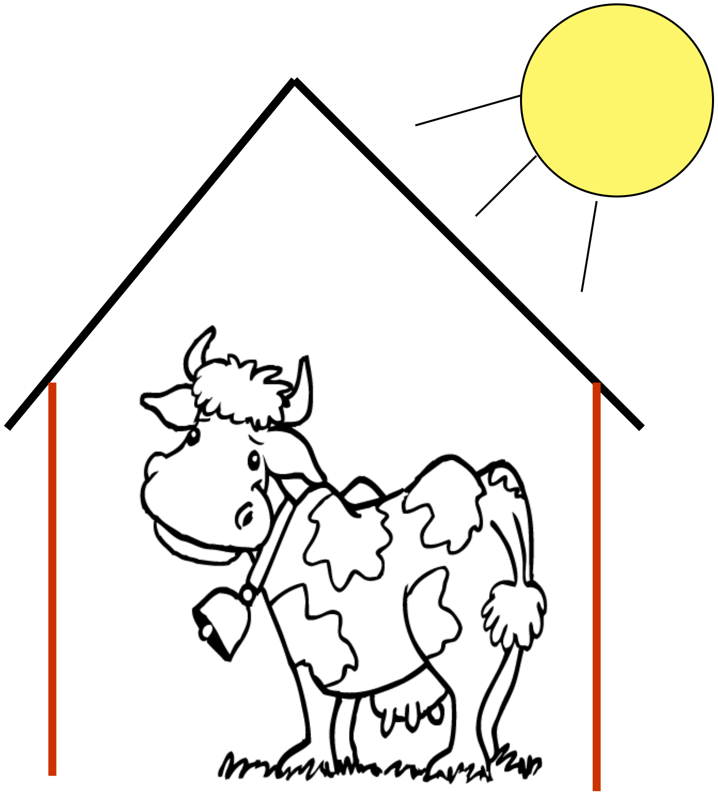
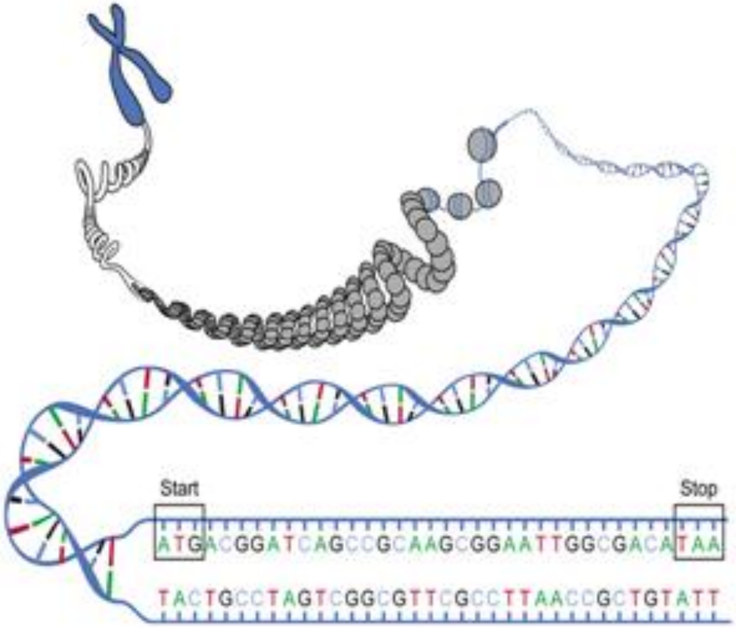
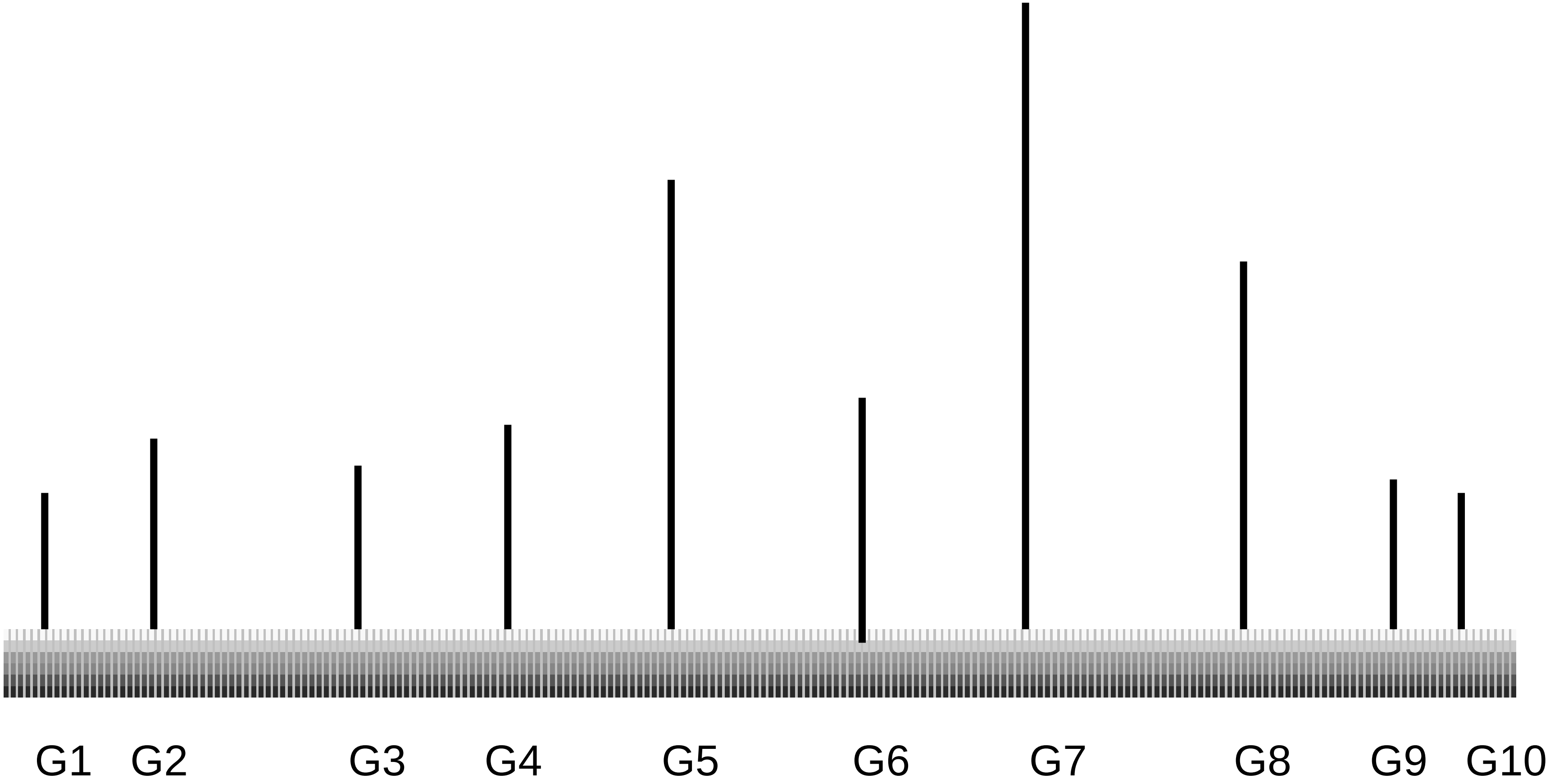
Environment and Genes



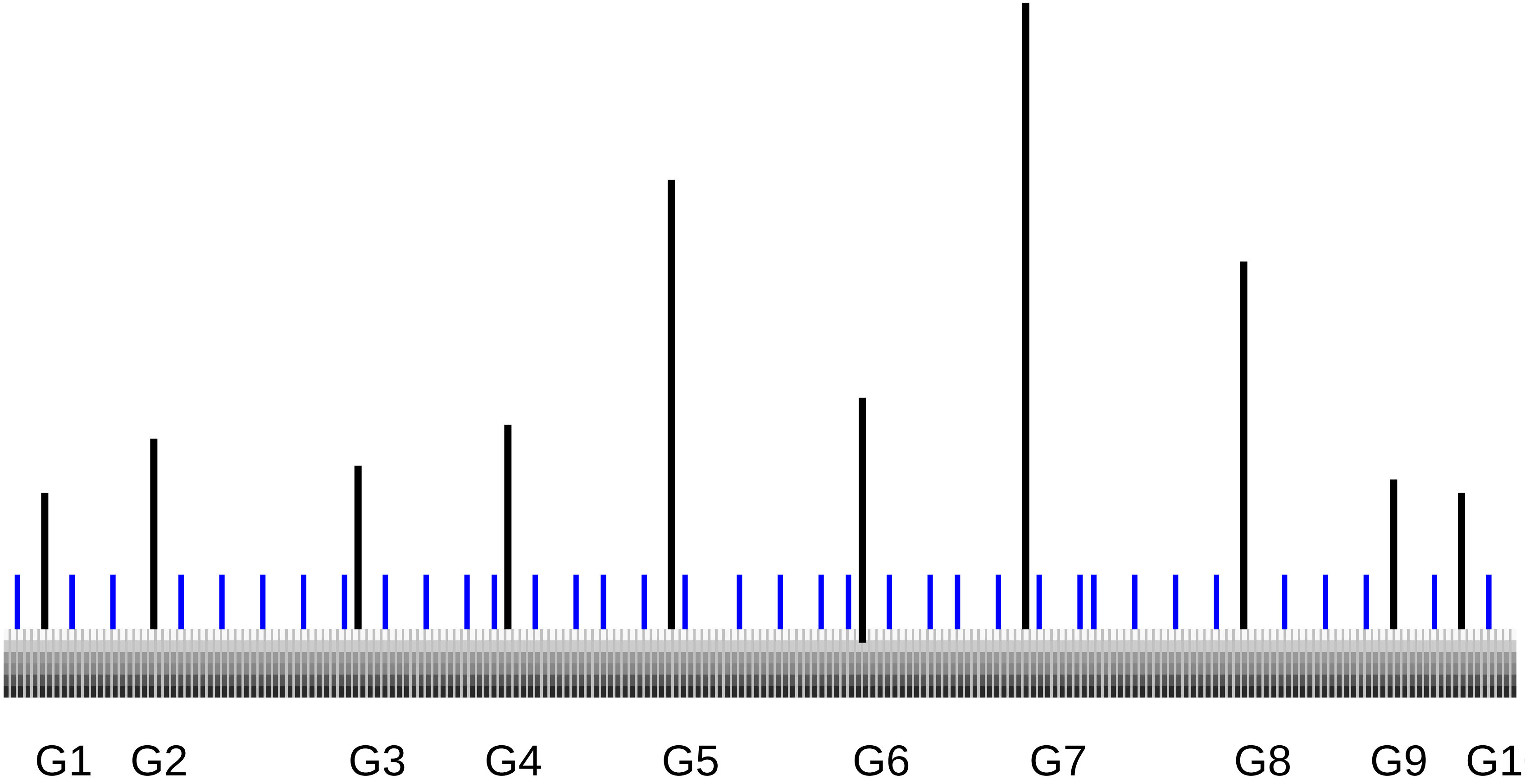


Phenotype = environment + genes

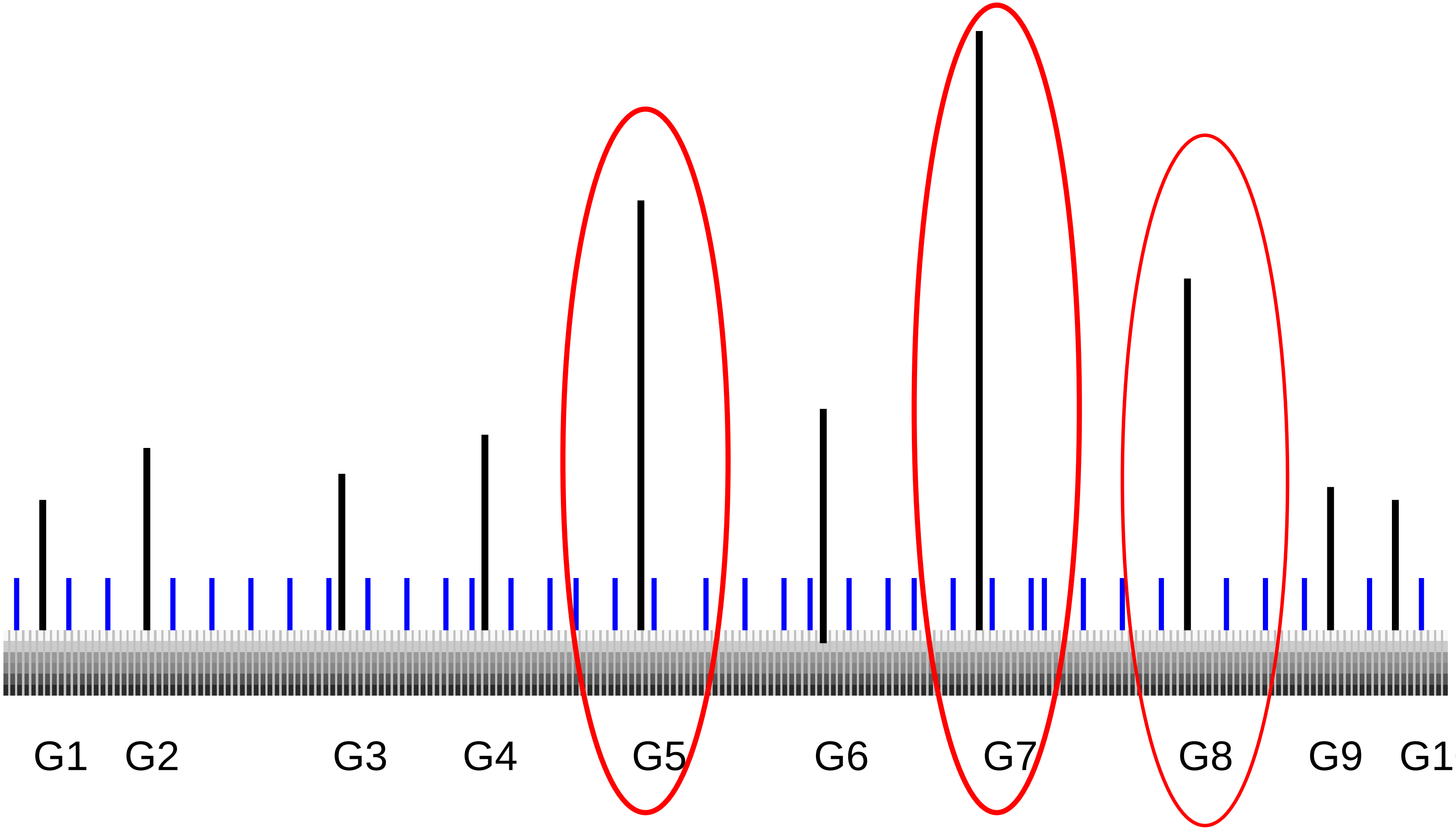
Many genes affect a trait



Genetic markers



Genes with large effect

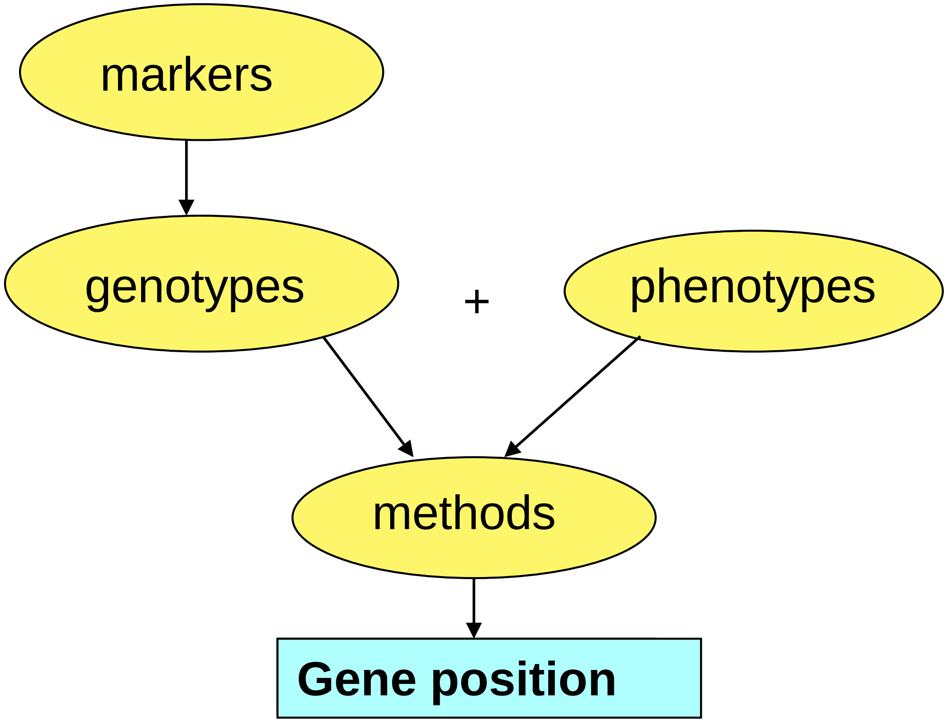


Why Gene mapping?

- To find the gene that affects the trait → selection
- Genetic architecture of different traits
- Gene interactions, genetic pathways
- Additional information to improve predictions of EBV

QTL/gene mapping

- Objective is to find gene areas and ultimately genes that affect traits of interest


markers

genotypes

+

phenotypes

methods

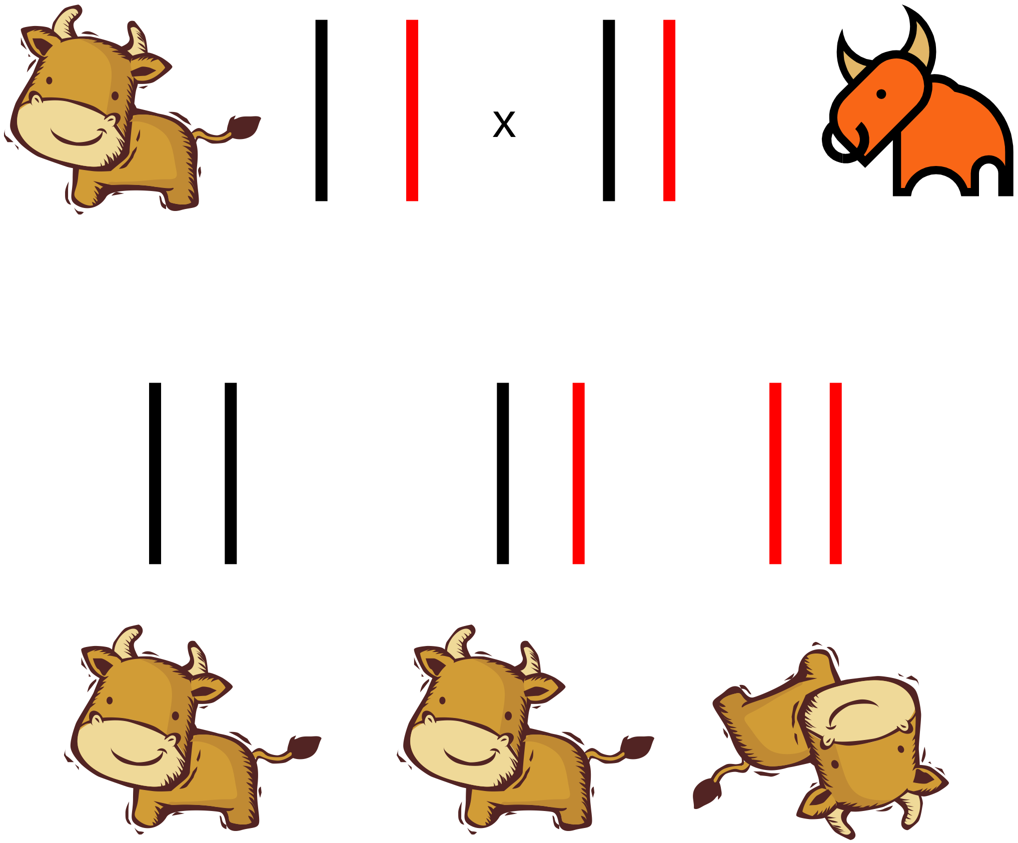
Gene position

Mapping by Aarhus university and MTT

- Holstein
  - 1st stage 2000-2500 bulls, milk, fertility, udder health, calving, conformation
  - Several QTL areas detected for all traits
  - 2nd stage 4500 bulls, 17 indices, component traits of fertility and calving
  - Many additional areas detected
- RDCFIN
  - 1st stage 340 bulls, fertility
  - 2nd stage 1000 -1500 bulls, fertility and udder health
  - Several QTL areas detected
- Jersey
  - 1500 bulls, milk traits
  - Several QTL areas detected

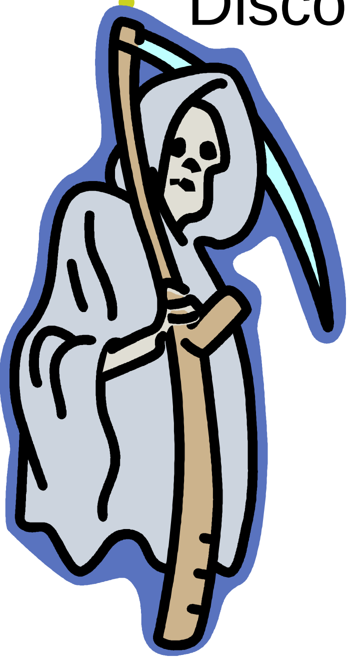
Recessive lethals

- Alleles that cause death of a homozygous individual



Recessive lethals

- Alleles that cause death of a homozygous individual
- Affect an essential gene
- Example CVM in Holstein cattle
- Can spread quickly
- Discovered late approximately at 10% frequency



Detection of recessive lethals

- 1. direct observation of dead calves → mapping of gene

- 2. use marker information directly to look for possible areas in the genome with lethal alleles
  - Construct lethality index to predict an individuals load of recessive lethal alleles
  - Faster identification, works for lethals with early expression

Conclusions

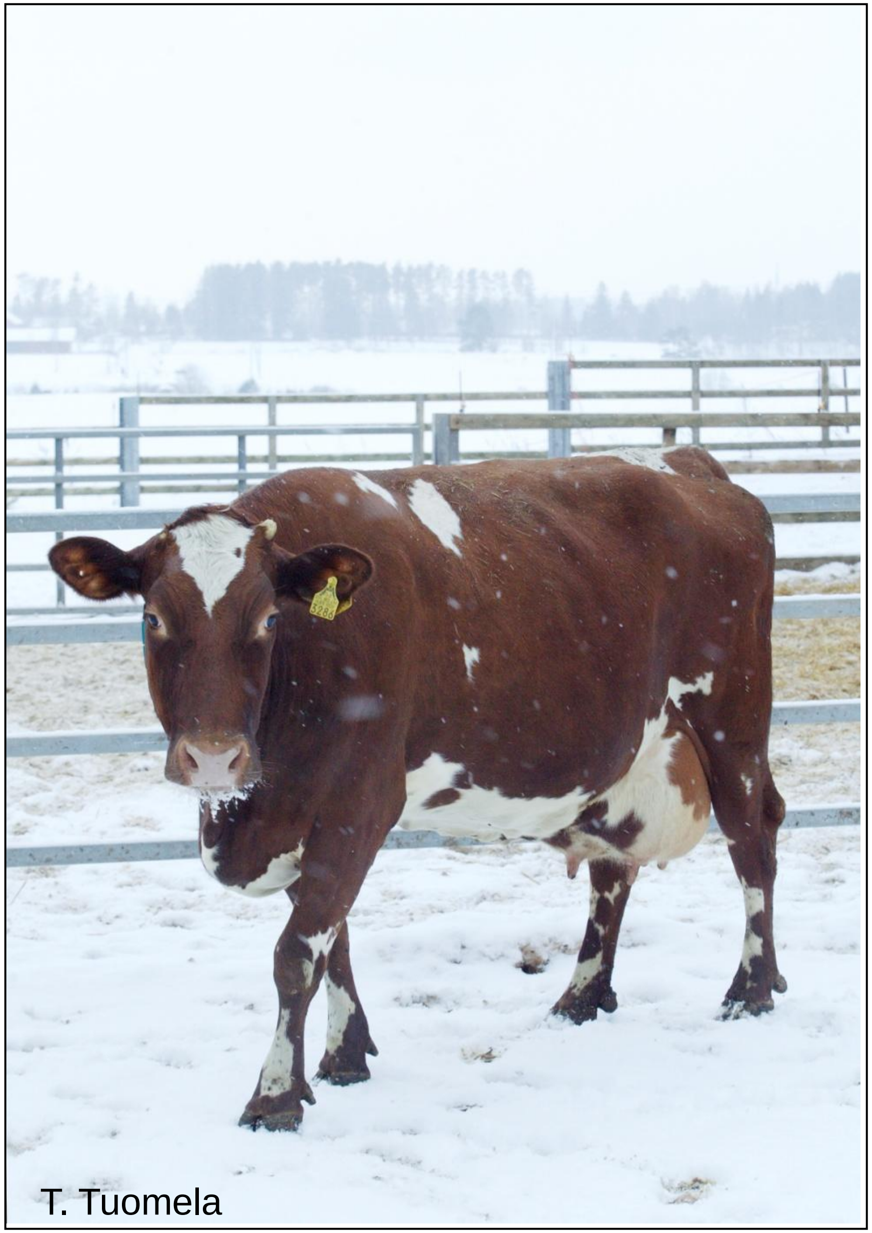
- We have found gene areas with large effect on traits of interest

- Further work needed to find causative mutations

- Gives additional information to improve EBV predictions

- Genome information could be used to predict the total effect of lethal recessive genes

M.Jauhiainen



T. Tuomela