

# Genomic Selection

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# Introduction

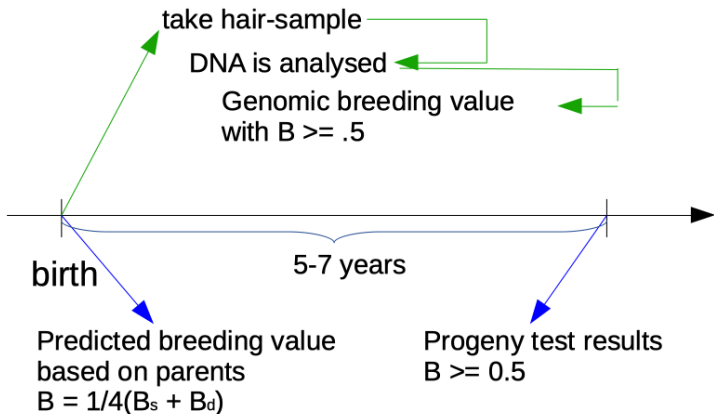
- ▶ Proposed in 2001
- ▶ Widely adopted in 2007/2008
- ▶ Costs of breeding program reduced due to shorter generation intervals
- ▶ In cattle: young sire selection versus selection based on sire proofs
- ▶ In pigs: early selection among full sibbs
- ▶ Inbreeding must be considered

# Terminology

- ▶ **Genomic Selection:** use of genomic Information for selection decisions
- ▶ Genomic Information is used to predict **genomic breeding values**

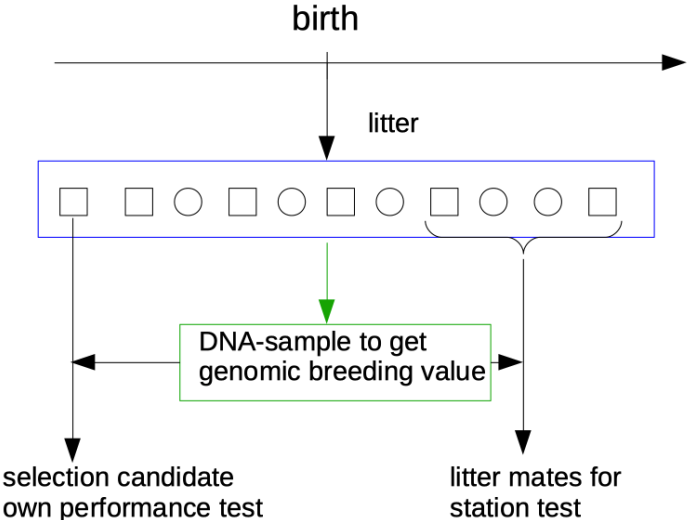
# Benefits in Cattle

## With genomic information



## Without genomic information

# Benefits in Pigs

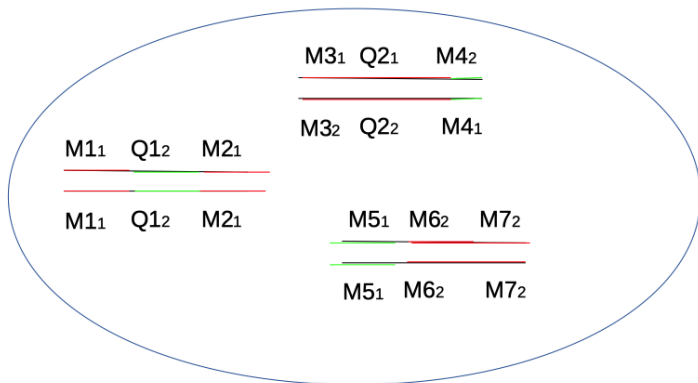


## Genetic Model

- ▶ Recall: BLUP animal model is based on infinitesimal model
- ▶ Prediction of genomic breeding values is based on **polygenic model**
- ▶ In polygenic model: **Single Nucleotide Polymorphisms (SNP)** are used as markers
- ▶ Marker genotypes are expected to be associated with genotypes of **Quantitative Trait Loci (QTL)**

# Polygenic Model

## Distribution of SNP (M) and QTL (Q)



M1<sub>1</sub> Q1<sub>2</sub> M2<sub>1</sub>

M1<sub>1</sub> Q1<sub>2</sub> M2<sub>1</sub>

M3<sub>1</sub> Q2<sub>1</sub> M4<sub>2</sub>

M3<sub>2</sub> Q2<sub>2</sub> M4<sub>1</sub>

M5<sub>1</sub> M6<sub>2</sub> M7<sub>2</sub>

M5<sub>1</sub> M6<sub>2</sub> M7<sub>2</sub>

# Statistical Models

Two types of models are used

1. marker-effect models (MEM)
2. genomic-breeding-value based models (BVM)



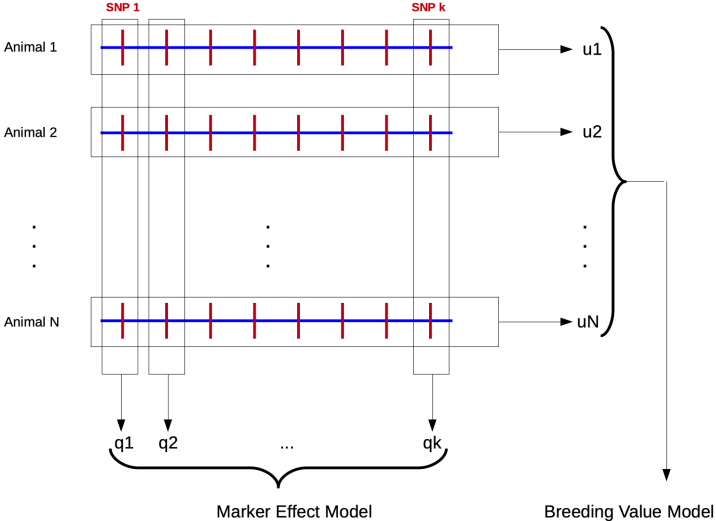
# MEM

- ▶ marker effects ( $a$ -values) are fitted using
  - ▶ a simple linear model → marker effects are fixed
  - ▶ a linear mixed effects model → marker effects are random
- ▶ Problem of finding which markers are associated to QTL
- ▶ With high number of SNP compared to number of genotyped animals: very large systems of equations to solve

# BVM

- ▶ genomic breeding values as random effects
- ▶ similar to animal model
- ▶ genomic relationship matrix ( $G$ ) instead of numerator relationship matrix ( $A$ )

# MEM versus BVM



# Logistic Procedures

- ▶ Two Step:
  - ▶ use reference population to get marker effects using MEM
  - ▶ use marker effects to get to genomic breeding values
- ▶ Single Step
  - ▶ MEM or BVM in a single evaluation
  - ▶ difficulty how to combine animals with and without genotypes

# Two Step Procedure

