

Genomic Selection

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Introduction

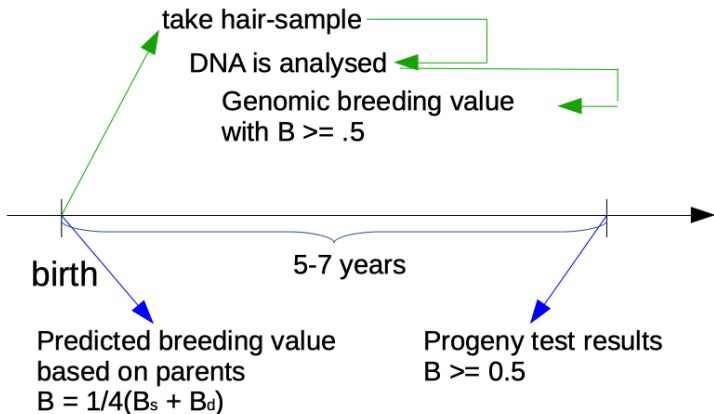
- ▶ Proposed in 2001
- ▶ Widely adopted in 2007/2008
- ▶ Costs of breeding program reduced due to shorter generation intervals
- ▶ In cattle: young sire selection versus selection based on sire proofs
- ▶ In pigs: early selection among full sibbs
- ▶ Inbreeding must be considered

Terminology

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

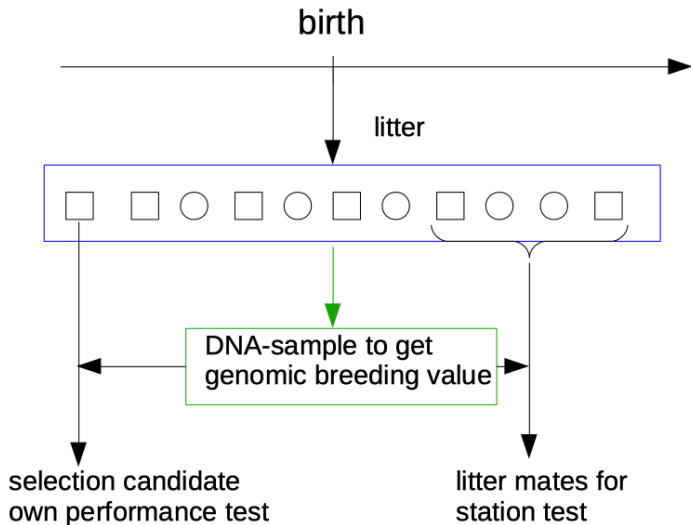
Benefits in Cattle

With genomic information



Without genomic information

Benefits in Pigs

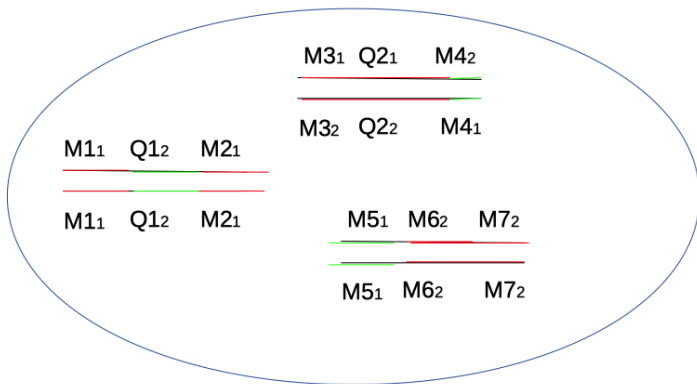


Genetic Model

- ▶ 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)



— Non-Coding region

— Coding region

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 \rightarrow marker effects are fixed
 - ▶ a linear mixed effects model \rightarrow 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)

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