Genomic Selection

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Introduction

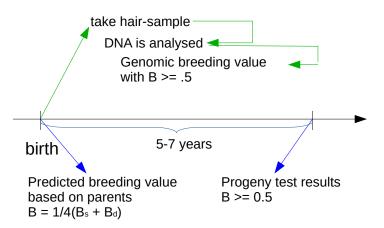
- ▶ Proposed in 2001
- ▶ Widely adopted in 2007/2008
- Costs of breeding program reduced due to shorter generation intervals
- In cattle: young sire selection versus selection based on sire proofs
- ► In pigs: early selection among full sibbs
- Inbreeding must be considered

Terminology

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

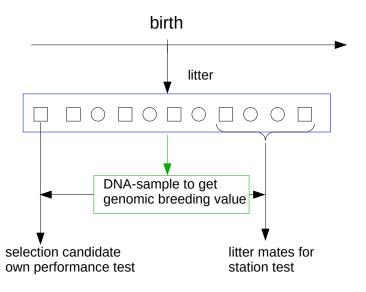
Benefits in Cattle

With genomic information



Without genomic information

Benefits in Pigs

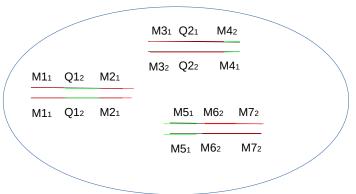


Genetic Model

- 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)

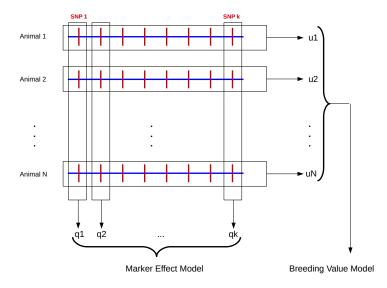
MEM

- marker effects (a-values) are fitted using
 - ightharpoonup a simple linear model ightarrow 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

