Genomic selection breeding programs

M. Lillehammer, Nofima
A.K. Sonesson, Nofima
T.H.E. Meuwissen, Norwegian University of Life Sciences
Breeding programs must be designed to:

1. Facilitate effective use of the breeding values.
2. Create the data needed to perform the breeding value estimation.

• A change in breeding value estimation methods thereby change the optimal design of the breeding program.
Genomic selection

• Facilitates:
  – Selection for traits not measured on candidates
  – More accurate selection at a younger age

• Adds another cost component
Simulation studies - assumptions

- Stochastic individually genome based simulations
- ABLUP or GBLUP
- Moderate marker density
- 10-20 years of selection
- Polygenic and normally distributed traits

- Accuracy is an output of the simulation, depends on breeding scheme
Example 1 – dairy cattle

Challenge: Select males for traits measured on females
The conventional solution - progeny testing

1. Selection of young bulls to be progeny tested

2. Obtain daughters of young bulls and wait for them to get milk records

3. Select elite sires based on progeny performance
Genomic solution

Acc > 0.95

Waiting bull

Acc = ?

Elite sire

Calf

Young bull
Accuracy of selection

Accuracy GEBV - $h^2=0.15$

Lillehammer et al., 2011, J. dairy sci.
Genetic gain

GS_12

Conv
Genetic gain

- Conv
- GS_12
- GS_30
Genetic gain

- Conv
- GS_12
- GS_30
- GS - presel
Genomic pre-selection

- Calf
- Young bull
- Waiting bull
- Elite sire
Take home message:

• Remember to incorporate in the breeding program how the reference population should be updated
Example 2: maternal pig breed

Challenge: multiple traits with different information content
Breeding goal maternal pig breed

• Two main categories of traits
  – Measured on candidates: growth-related traits
  – Measured on sibs: maternal traits (and slaughter traits)

• In a conventional breeding program, most of the genetic gain will come from the first trait category
Selection for two traits: genetic gain

- CAND - trait
- SIB - trait
- Conventional
Selection for two traits: genetic gain
Selection for two traits: genetic gain
Selection for two traits: genetic gain

- Conventional
- Genomic
- +more candidates

CAND - trait
SIB - trait

Legend:
Selection for two traits: genetic gain

- CAND - trait
- SIB - trait
- Genomic + halfsibs of parents
Effect of economic weight

![Graph showing the effect of economic weight on genetic gain in SIB-trait. The x-axis represents the relative economic weight of the SIB-trait, ranging from 0% to 60%. The y-axis represents the genetic gain in the SIB-trait, ranging from -0.40 to 0.40. The graph includes two lines: one blue and one orange, both showing a positive correlation between the relative economic weight and genetic gain.]
Take home message:

• All traits to be improved by genomic selection needs:
  – A considerable economic weight
  – Available data to update the reference population
Example 3: Salmon

Challenge: Several traits measured on sibs of candidates. Different sibs for different traits.
Assuming nucleus males to get offspring with records

Genetic gain ($\sigma_{ap}$) for SIB-trait vs. Relative economic weight of SIB-trait

- $P0$
- $P4500$
- $P9000$
Assuming nucleus animals **NOT** to get offspring with records
How to reduce the costs of genotyping test-fish?

• «progeny test» of already genotyped nucleus animals (could be after selection)

• Pooled genotyping of test fish

• Low density genotyping
  – With imputation
  – Combined with pedigree information
Within family genomic selection

BLUP
Family breeding value

Genomic
Within family deviation

Total breeding value
Take home message

• Evaluate the impact before running expensive genotyping
Conclusions

• The strategy to keep the reference population updated is an important part of the genomic selection breeding program

• Available options:
  – Genotyping of animals with phenotype
  – Obtain phenotypes from (offspring of) genotyped animals
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