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Genomic selection breeding programs

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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



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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







Accuracy of selection

Accuracy GEBV - h2=0.15



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







Genetic gain





Genetic gain









Take home message:

• Remember to incorporate in the breeding program how the reference population should be updated



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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







Conventional

CAND - trait

SIB - trait

Conventional



















Effect of economic weight









Take home message:

- All traits to be improved by genomic selection needs:
 - A considerable economic weight
 - Available data to update the reference population



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Example 3: Salmon

Challenge: Several traits measured on sibs of candidates. Different sibs for different traits.



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Assuming nucleus males to get offspring with records





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





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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