

Program

Session 3:

- 9:10 Assessment and optimization tools in genomic breeding programs
Senior Researcher Christian Sørensen, QGG, AU
- 9:30 Genomic selection and the design of breeding schemes
Professor Theo Meuwissen, University of Life Sciences, Norway
- 10:10 *Coffee break*
- 10:40 On the doorsteps of a new era in plant breeding
Senior Scientist Christian Sig Jensen, DLF Trifolium, Denmark
- 11:05 Making a world-class pig-breeding program even better with genomic selection
Chief Geneticist Mark Henryon, Danish Pig Research Center
- 11:30 Medium to long-term effects of selection in finite locus models with non-additive effects
EGS-ABG PhD Student Hadi Esfandyari, Wageningen University/QGG, AU
- 11:45 General assembly meeting
- 12:30 Lunch
- 13:30 PhD defense: Genomic predictions using combined populations and SNP marker panels
PhD Candidate Rasmus Froberg Brøndum, QGG, AU

GenSAP

Species

Universities

Industries

SFA1

Genetic
architecture of
complex traits

SFA2

Genomic
prediction
models

SFA3

Assesment and
optimisation tools



Scientific Focus Area 3: Assessment and optimisation tools

Christian Sørensen

14.06.2013

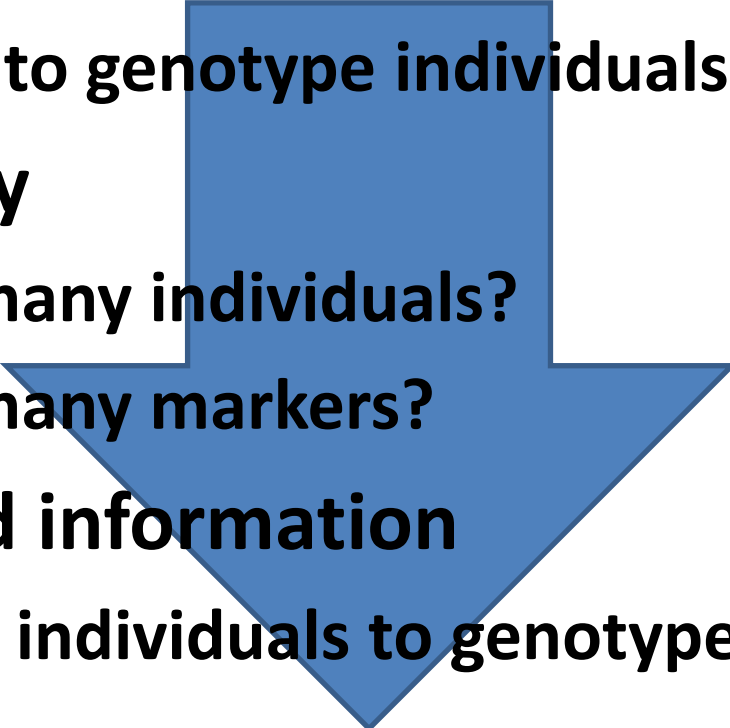
Genetic improvement programs

Challenges from genomic information



- **Breeding objective**
- **Trait recording**
- **Genetic evaluation** ← **Genomic prediction**
- **Selection and mating** ← **Optimisation**

Optimise use of genomic information

- **Timing**
 - When to genotype individuals?
 - **Quantity**
 - How many individuals?
 - How many markers?
 - **Selected information**
 - Which individuals to genotype?
- 

Can it be implemented in the ongoing program, or does it require re-structuring?

Assessment

- **Modelling genetic improvement programs**
 - Realistic genetic architecture
 - Realistic sequence of decisions
 - Realistic breeding structure
- **Evaluate consequences of alternative strategies**
 - Genetic improvement
 - Genetic variability
 - Inbreeding

Optimisation comes from picking the best alternative

Specific challenges addressed in GenSAP SFA3

Extended tool box

- Existing software works well for sexually reproducing, diploid species
- Needs to be extended to
 - Asexual reproduction
 - Polyploidy
 - Non-additive genetics
 - Multiple populations
 - Genotype-by-Environment interactions

Non-additive genetic variation

- **How can this be exploited in animal and plant breeding**
 - **Effect of more accurate additive predictions**
 - **Exploiting non-additive effects in breeding**
- **Long-term effects of selection**

Selection across multiple environments

- **Value of genomic and phenotypic information across environments**
 - For selection directly
 - For merging reference populations
- **In the presence of Genotype-by-Environment interactions**

Use of genomic information for handling inbreeding

- **Define and assess properties of a genomic inbreeding estimator**
- **Include genomic information in dynamic selection tools designed for controlling inbreeding**

Proof-of-Concept

- **Providing first evidence that including genomic information will speed up genetic improvement**
 - Mink
 - Potatoe
 - Wheat
 - Barley
 - Ryegrass

Genomic selection and the design of breeding schemes

Prof. Theo Meuwissen, University of Life Sciences, Norway

On the doorsteps of a new era in plant breeding

Senior Scientist Christian Sig Jensen, DLF Trifolium

Making a world-class pig-breeding program even better with genomic selection

Chief Geneticist Mark Henryon, Danish Pig Research Center

Medium to long-term effects of selection in finite locus models with non-additive effects

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