Strategic Research Center

GenSAP

Genomic Selection in Animals and Plants

5th Annual Meeting
15-16 November
2017

LEGOLAND Hotel & Conference Center
Billund, Denmark

Practical information

About the meeting:

Welcome to the 5th annual GenSAP workshop.

This year as well, we are very pleased to have many of our international partners represented in the program, and hope that we will have many fruitful discussions about research and plans ahead.

Date:	15-16 November, 2017
Venue:	LEGOLAND Hotel & Conference Center, Aastvej 10, 7190 Billund, Denmark (link to map)
Registration:	Please register for the meeting before 15 October using this link.
Accommodation:	After your registration for the meeting, **please make sure to book your room via this link and no later than 15 October**. The LEGOLAND Hotel offers two restaurants, a large morning buffet, a fireplace lounge and bar, a fitness centre and free access to Billund Bath & Wellness.
Transport:	For those travelling from abroad; Billund Airport is the second largest airport in Denmark. The easiest way to get to Billund is by booking your plane ticket to and from Billund. The LEGOLAND Hotel is a mere 5 minute drive from the airport. If you need any help in travel arrangements, please feel free to contact us.
	For those travelling from Foulum; transport back and forth from Foulum to Billund can be booked when you register. A more detailed plan of pick-up and drop-off will follow later.
Price:	GenSAP pays for the meeting. All expenses in relation to travel and accommodation are covered by the participants through the individual partner grants.
Questions?	Please contact Johanna Höglund (johanna.hoglund@mbg.au.dk)

09.00   Check-in and registration

10.00   **Welcome, general introduction & status and introduction to the sessions**
             Professor Mogens Sandø Lund, QGG-AU

Session 1: Use of full sequence data

10.20   **Introduction to the session by the chair**
             Senior scientist Goutam Sahana, QGG- AU

10.30   *Next generation sequence data in gene mapping and genomic prediction: opportunities and challenges*.
             Senior research scientist Didier Boichard, INRA, France

11.00   *Detection of large chromosomal deletions in cattle and their phenotypic consequences.*
             PhD Student Md Mesbah Uddin, QGG-AU

11.15   *Using model organisms to study complex diseases across species.*
             PhD Student Palle Duun Rohde, QGG-AU

11.30   *Allelic imbalance in sequence-based genotyping data.*
             Professor Torben Asp, MBG-AU

11.45   Speed talks (3 minutes talk accompanied by a poster)
             - *Validation of SNPs from a Nordic WGS based GWAS using independent French populations.*
               PhD Student Andrew Marete, QGG-AU
             - *Imputation to whole sequence variants in pigs.*
               PhD Student Thu Hong Le, QGG-AU
             - *Role of rare variants in genomic prediction.*
               PhD Student Qianqian Zhang, QGG-AU
             - *Using expression data to detect small QTL in dairy cattle.*
               Postdoc Irene van den Berg, University of Melbourne, Australia

12.00   *Lunch*

Session 2: Predictions across breeds and populations

13.00   **Introduction to the session by the chair**
Professor Mogens Sandø Lund, QGG-AU

13.10   *Predictions across breeds and populations.*
Professor Mike Goddard, University of Melbourne, Australia

13.35   *Genomic prediction combining Nordic and US Jersey in models integrating QTL markers.*
PhD Student Aoxing Liu, QGG-AU

13.50   Speed talks (3 minutes talk accompanied by a poster)
- *Predicting the effect of reference population on factors influencing the accuracy of across and multi breed genomic prediction.* Postdoc Irene van der Berg, University of Melbourne, Australia
- *Genomic prediction in admixed populations.*
PhD Student Sayed Mahdi Hosseini, Ferdowsi University of Mashhad, Iran
- *Combining multi-population data for GWAS on milk fatty acids traits.*
PhD Student Grum Gebreyesus, QGG-AU

Session 3: Plants and new animal species

14.00   **Introduction to the session by the chair**
Senior scientist Luc Janss, QGG-AU

14.10   *Genomic selection in wheat and barley.*
Professor Ahmed Jahoor, Nordic Seed

14.30   *Genomic selection in tetraploid potato.*
Postdoc Elsa Sverrisdóttir, University of Aalborg (AAU)

14.45   Speed talks (3 minutes talk accompanied by a poster)
- *Genomic prediction in tetraploid ryegrass.*
Postdoc Xiangyo Guo (Luc Janss), QGG-AU
- *Simulation of genomic selection in cereal breeding program.*
Postdoc Biructawit Bekele Tessema, QGG-AU
- *Genomic analysis using GBS in mink.*
Postdoc Trine Willumsen, QGG-AU
- *Genomic selection in barley for seed quality traits.*
PhD student Theresa Ankamah-Yeboah, University of Copenhagen (KU)

15.00   Poster session/coffee break

Session 4:   Non-additive genetic effects

16.00 **Introduction to the session by the chair**
Senior scientist Peter Sørensen, QGG-AU

16.10 *Estimation of non-additive variance components and SNP effects in five dairy cattle breeds.*
PhD Student Andrew Marete, QGG-AU

16.25 *GxE in ryegrass.*
Postdoc Christiana Paina, MBG-AU

16.40 Speed talks (3 minutes talk accompanied by a poster)
- *Environmental variation partitioned into separate heritable components.*
Palle Duun Rohde, PhD, QGG-AU
- *The Times They Are a-Changin: Bayesian estimation of direct and correlated response to genetic selection on linear or ratio expressions of feed efficiency in pigs.*
Mahmoud Shirali, QGG-AU
- *A GxE model for cereals*.
Postdoc Fabio Cericola and professor Just Jensen, QGG-AU
- *Genomic model with correlation between additive and dominance effects.*
Postdoc Tao Xiang, QGG-AU

16.55 Meeting closure – day 1
Professor Mogens Sandø Lund

17.00 Posters session: Poster contributions by GenSAP PhD students and postdocs/researchers

19:00 **Workshop dinner**

Program – Day 2

Session 5: Analysis of large datasets

08:30   **Introduction to the session by the chair**
Senior scientist Ole Christensen, QGG-AU

08.40   *Robust alternatives to best linear unbiased prediction of complex traits.*
Professor Daniel Gianola, University of Wisconsin-Madison, USA

09.05   *Efficient multi-trait SNP models for prediction of genomic breeding values.*
Senior Scientist Luc Janss, QGG-AU

09.25   Speed talks (3 minutes talk accompanied by a poster)
- *Accounting for genetic architectures of traits in multi-trait genomic prediction using GBLUP.*
Postdoc Emre Karaman, QGG-AU
- *Multi-trait genomic prediction in small-scale recorded traits using correlation at genomic segments with large-scale recorded traits*
PhD Student Grum Gebreyesus, QGG-AU
- *APY in software DMU.*
Postdoc Viktor Milkevych, QGG-AU
- *An overview of REML estimation of variance components: flaws and solutions.*
Postdoc Beatriz Castro Dias Cuyabano, QGG-AU
- *Integrating metabolomics and genomics.*
Assistant Professor Pernille Merete Sarup, QGG-AU

09.40   Poster session/Coffee break

Session 6: Estimation and control of inbreeding using Genomics

10.15   **Introduction to the session by the chair**
Professor Theo Meuwissen, NMBU, Norway

10.25   *Estimation of inbreeding in the genomics era.*
PhD Student Qianqian Zhang, QGG-AU

10.45   *Optimum contribution selection using weighted SNP information to control rates of inbreeding and increase genetic gain.*
Senior Scientist Mark Henryon, SEGES

11.15   *Implementing genomic selection in CGIAR breeding in perspective.*
Professor Søren Rasmussen, University of Copenhagen (KU)

11.30   Speed talk (3 minutes talk accompanied by a poster)
- *Alternative genomic relationship matrices and measures to control inbreeding in genomic optimum contribution selection.*
PhD Student Gebreyohans Gebregiwergis, NMBU, Norway
- *Break-even genetic correlation related to GxE using genomic selection*
PhD student Lu Cao, QGG-AU

11.40   General assembly

12:30   Lunch

13.30   Board meeting incl. comments from the advisory board (agenda will follow)