

FIRST ANNOUNCEMENT:SABRE INDUSTRIAL WORKSHOPS

Lelystad: 2 & 3 September 2010

Ljubljana: 13 & 14 September 2010

The EC-funded FP6 research project SABRE "Cutting Edge Genomics for Sustainable Breeding" (www.sabre-eu.eu) is due to conclude on the 30th of Sep 2010. To disseminate SABRE Project outcomes and related themes to breeding companies and related organisations a two-day workshop will be held on two occasions:

1. The first workshop will be held in Lelystad on Thursday 2 & Friday 3 September 2010.
2. The second one will be held in Ljubljana on Monday 13 & Tuesday 14 September 2010.

This is not intended to be a large-scale conference, but a focussed workshop with a small number of attendees.

Content

The core of the workshop provides three principle sessions on genomic tools and methods. These sessions will provide a comprehensive review, using SABRE developed tools where relevant as a key component but will not necessarily be limited to solely SABRE outcomes.

Draft Programme Overview

Workshop Day 1

10:00 – 12:00	Registration & networking
12:00 – 13.15	Pre-workshop lunch
13.15 – 13:25	Introduction
13:25– 15:45	Session 1 – Genome Wide Selection (Theo Meuwissen & John Woolliams)
15:45 – 16:15	Break
16:15 – 18:15	Session 2 – MixBLUP (Roel Veerkamp & Han Mulder)
18:15 – 18:30	Break
18:30 – 19:30	Case studies
20:00 – 22:00	Dinner and networking

Workshop Day 2

09:00 – 10:30	Session 3 – Analysis of QTL's, eQTL's and Microarrays (Peter Sorensen & DJ de Koning)
10:30 – 10:45	Break
10:45 – 12:15	Case Studies + Workshop conclusion
12:15 – 12:45	General Discussion

The organisers reserve the right to change the programme

Costs: Attendance at the workshop is free of charge, but pre-registration is required.

Registration and Further information: For expression of interest or for further information, please contact Conference@sabre-eu.eu

Detailed Draft Workshop Programme

Session 1 – Genome Wide Selection

Session coordinators: Theo Meuwissen (presenter Lelystad) and John Woolliams (presenter Ljubljana).

- Basics of genome wide selection.
- Theoretical issues – linkage disequilibrium theory and estimation– training panels size and frequency issues – resource populations etc
- Resources for genotyping- sequenced genomes / chips/ SNP sets size etc - future scope.
- Options for use - whole genome scan - no prior genomic info / SNP haplotypes / candidate genes
- Methods of EBV estimation – regression / BLUP/ Bayesian. No of markers, populations size issues in designing a breeding programme.
- Prediction across families, inbred lines and breeds.
- Implementation in practice - issues - training - predicted benefits – limitations
- Feedback and discussion

Session 2 – MIXBlup

Session coordinators: Roel Veerkamp (presenter Lelystad) and Han Mulder (presenter Ljubljana).

- Background to current software
- Design of the programme
- Scope and limitation especially in practical breeding with commercial populations
- Demonstrations

Please note: Delegates will not be provided with free software.

Session 3 – Analysis of QTL's, eQTL's and Microarrays

Session coordinators: DJ de Koning (presenter Lelystad) and Peter Sorensen (presenter Ljubljana).

Whereas sessions 1 and 2 were commercially oriented, session 3 is a little more academic. It is intended to provide a background to bring industry delegates up to date on the power and potential of these methods:

- New tools / scope / developments / understanding traits
- What have QTL analyses taught us and what are the limitations
- Interpreting data - r grid QTL + demos of new software
- eQTL's creating new 'sub phenotype' traits
- Linking QTL's / expression data to SNPs
- Post transcriptional effects.

Case studies:

The SABRE project involved over 200 scientists in 14 countries. It is divided into 10 research packages. These Work Packages addressed key areas of emerging genomic and epigenetic science, generating new knowledge so it can be applied in practical breeding improvement strategies throughout Europe.

- The mammary gland, the digestive system and fertility are the focus of the basic research.
- Applied research has been aimed at enhancing eggshell quality for food safety; improving animal behaviour linked to welfare; and eliminating boar taint in pork.
- A number of demonstration projects to show case the use of genomic technologies in commercial populations have been organised in collaboration with industrial partners

During the workshop, a number of these subjects will be presented as CASE Studies, showing the outcomes of using new techniques and software. This will illustrate across species how specific traits can be investigated and solutions to improve populations can be implemented.

Technology Transfer Clinics:

In addition to the scientists who are presenting the SABRE results, Knowledge Transfer Managers of the Biosciences KTN will be present during the workshops. They will be available for specific sessions with attendees to guide end-users in the steps to be taken to apply the SABRE outcomes and technologies.