

SABRE's Cutting Edge

CUTTING EDGE GENOMICS FOR SUSTAINABLE ANIMAL BREEDING

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Get Involved

Dear colleagues,

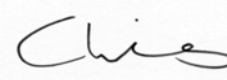
This 5th issue of SABRE's Cutting Edge is on the theme of 'Get Involved'. You will find the reports on our 3rd Conference on "Welfare and Quality Genomics" and two joint SABRE-EADGENE workshops.

Moreover, there are currently several opportunities available for scientists at academic and industrial organisations alike to apply for funding to get more closely involved with the SABRE activities. These range from attendance at future meetings, to applying for short-term placements with SABRE Consortium Members or testing genetic markers in commercial populations. Further details on all of these can be found on the SABRE website.

Kind regards,



Toine Roozen - SABRE Operations Manager



Chris Warkup - SABRE Co-ordinator

3rd SABRE Conference: Welfare and Quality Genomics

Over ninety delegates attended the 3rd SABRE conference on "Welfare and Quality Genomics" in Foulum, Denmark on 10 and 11 September 2008.

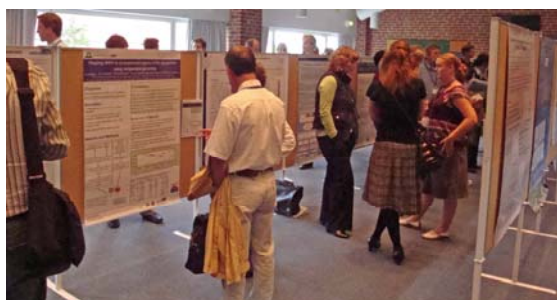
The conference started with keynote speakers giving a comprehensive introduction to the complexity of the genome with examples from research in humans, giving interesting descriptions of the genetic analyses necessary for identification of genetic causes for different phenotypic traits. This was followed by a discussion on the ethical aspects of animal breeding which highlighted the importance of consideration of ethical aspects when incorporating the new technologies into animal breeding.

The session finished with interesting SABRE talks on epigenetics with a comprehensive background review on epigenetics followed by a presentation on results achieved in cattle showing surprisingly large influences of epigenetic variation among cloned animals.

Session 2 started before lunch with an interesting keynote talk on genetics related to behavioural traits which led participants to discuss whether epigenetics has an influence on behavioural traits. This was followed by a number of shorter talks giving excellent examples of incorporating genetics of behaviour into actual breeding and the benefits that can be obtained from incorporating animal interactions into genetic analyses.



In the afternoon a keynote talk on the genetics of robustness emphasised the need to include robustness as a breeding objective in modern dairy farming. Alternative approaches for genetic selection for robustness were discussed. Talks from SABRE's mammary function (WP5) and fertility and reproduction (WP6) work packages reported the results of gene expression studies revealing some of the molecular genetic mechanisms underlying mastitis and reproduction traits in dairy cattle.



The poster session in the afternoon was well attended and the discussions around the posters were plentiful. The exhibited posters represented different aspects of the SABRE project: quantitative genetics analysis methods, genetic and association mapping, epigenetics, gene expression, protein expression, SNP usage, CNV analysis, and presentations of SABRE and related EU-projects.



On the second day, there was an interesting keynote talk on the conditions animals are exposed to in relation to consequences for health, welfare and pathogen pressure. This talk raised a number of issues on the methods used for breeding animals - especially chickens. This was followed by a number of shorter talks giving results obtained during the SABRE project on both aspects of boar taint with different approaches and genetic resistance towards *E. coli* F4ab/ac in pigs. The latter also described usage of the obtained knowledge on the genetic aspects of resistance in breeding systems. The results in chickens concerned description of detected QTLs for eggshell quality, and the problems in finding a reliable method for determination of the trait.

Feedback from the delegates was positive and we would particularly like to thank our hosts at the University of Aarhus, Faculty of Agricultural Sciences (AU-DJF, previously known as DIAS) at their Research Centre Foulum (central Jutland) in Denmark for helping to make this event a success. Presentations from the conference can now be downloaded from the SABRE website at www.sabre-eu.eu > News & Events > 3rd SABRE Conference.



Joint SABRE and EADGENE Workshops

SABRE and the EADGENE Network of Excellence have recently held two joint workshops.

The first was a satellite meeting on **"How to get in touch with two EC funded animal genomics projects"** at the 59th Annual Meeting of the European Association for Animal Production (EAAP), on 23 August 2008 in Vilnius, Lithuania. The workshop programme aimed to increase understanding of the opportunities, resources and facilities that these projects could offer to scientists from Eastern European Countries (EEC). The workshop revealed numerous topics for possible collaboration between SABRE and EADGENE member laboratories and researchers in the EEC countries. Probably the most promising collaborations could be developed in the field of molecular characterisation of endogenous breeds and application of molecular markers to support marker assisted selection. Presentations from this meeting can be accessed via the SABRE website: www.sabre-eu.eu > News & Events > SABRE & EADGENE Workshop at EAAP 2008.

EADGENE and SABRE also joined forces to hold a workshop on **annotation and the post-analyses of microarray data**. The aim was to evaluate and present already existing methods and software, and potentially to propose new methods to deal with the post-analyses of microarray data, using real data sourced from within EADGENE and SABRE. The results were presented during the three day event, held at the Animal Sciences Group in Lelystad, 12-14 November 2008, and attended by over 50 delegates. The presentations are now available on the SABRE website at www.sabre-eu.eu > News and Events > EADGENE and SABRE Post-analyses Workshop. The results will also be written up in a series of papers to be published in BMC Proceedings in 2009.



Delegates at the EADGENE and SABRE Post-analyses Workshop. Photo courtesy of ASG.

Upcoming SABRE Meetings: 16 & 17 Feb, 24-27 Aug 2009

SABRE Partners can now register online for the **4th SABRE Consortium meeting on 16 and 17 February 2009** near **Schiphol Airport**. The 2-day event will include WP meetings, Scientific meetings and Management meetings. The main objective of the meeting will be to work towards SABRE's 3rd Year-end Report and the 4th year Plan. Agenda and registration at www.sabre-eu.eu > News & Events > 4th SABRE Consortium Meeting.

The **4th SABRE Conference** (open to all interested parties) will be held as part of the 60th Annual Meeting of the EAAP at Fira de Barcelona in **Barcelona** from **24-27 August 2009**. Deadline for submission of papers is 1 March 2009. SABRE will provide funding towards EAAP delegate fees for SABRE publications (Rules will apply). Further details will in due course become available on www.sabre-eu.eu > News & Events > 4th SABRE Conference

PGI Course CD ROMS

SABRE WP11 (Training) has 7 copies of the CD ROM-based distance learning course on the "Principles of Genetic Improvement" available for SABRE participants who can demonstrate why they would like a copy and how the course will benefit them. The CD ROM - developed by the University of Edinburgh, Scottish Agricultural College and Roslin Institute to promote knowledge in the field of genetic improvement in animals - contains over 40 hours of lectures in an easily accessible format that allows you to learn at your own pace, is interactive and includes web based support. Further information and an application form can be found at www.sabre-eu.eu > Get Involved > Training

SABRE Placements: Call for Applications

We are pleased to announce the release of new calls for applications to receive SABRE training funds for:

- ♦ **SABRE 'Integrating' Awards** - Ten integrating awards for scientists involved in SABRE to carry out activities which help promote integration within the SABRE project. Such activities may include short-term placements at another SABRE partner, a series of short visits to another SABRE partner, a small working group meeting to tackle a specific problem or a small workshop.
- ♦ **Early Stage Researcher (ESR) Short-term Placements** - Two short-term placements for Early Stage Researchers (ESRs) involved in SABRE to spend time working with another partner within the SABRE project.
- ♦ **New EU Member State and INCO Scientist Short-term Placements** - Four short-term placements for scientists from new EU Member states. Four short-term inward placements for scientists from INCO countries. Preference will be given to applications from female scientists.

For full details of all the calls and information on how to apply and reports on completed placements, please go to www.sabre-eu.eu > Get Involved > Training. Extracts from a selection of those reports can be found below.

Expression profile of genes in the bovine endometrium

Christine Große-Brinkhaus and **Dessie Salilew-Wondim** of the Rheinische Friedrich-Wilhelms-University Bonn were funded to visit the University of Aarhus in Denmark in Summer 2008 as part of SABRE WP6 (Fertility and Reproduction). Below follows Christine's report. Dessie's report can be found on www.sabre-eu.eu.



The main objective of Christine's research was to investigate the expression profile of genes in the bovine endometrium based on a successful pregnancy after embryo transfer in dairy cattle. Endometrium samples were categorised based on the pregnancy success after the transfer and transcriptome analysis of endometrium samples was performed at the Rheinische Friedrich-Wilhelms-University Bonn. She then took the raw data of all gene expression to Denmark and performed the statistical and bioinformatics analysis under the supervision of Peter Sørensen using different packages of the R/Bioconductor analysis software.

Differentially expressed genes were identified using linear modeling and empirical Bayes methods and adjusted for multiple testing to control the false discovery rate. Dr. Sørensen demonstrated the different possibilities for creating research-specific annotation packages using the AnnBuilder and BioMart software and how to increase the number of annotated bovine genes by adding homologous human information. Afterwards it was possible to characterise different functional groups within the differentially expressed genes using statistical methods such as gene set enrichment analysis.

captured by a linked SNP locus, taking different characteristics of CNV and SNP loci into account. The objectives of this study were to investigate the LD between SNP and CNP loci, the ability of a linked SNP to explain genetic variation resulting from a CNP, and the additional benefit of including the CNP, either by its genotype or by a continuous measure mimicking raw hybridisation intensities, next to the SNP in the model. These objectives were investigated both using deterministic and stochastic simulations.

In the stochastic simulations we assumed that the mutation rate is much higher for CNVs than for SNPs, and that the number of alleles may be larger for CNVs than for SNPs. Mendelian inheritance was assumed for both the CNV and SNP loci.

Despite the different characteristics of the CNV and SNP loci, it was found that SNP loci explain more variance caused by a CNV locus compared to variance caused by a SNP located at the same physical distance. Adding raw hybridisation intensities of CNV loci that contribute to genetic variance, did increase the amount of explained variance considerably. In conclusion, genotyping CNV loci in addition to SNP loci may only be beneficial for association studies when CNV loci are expected to contribute to the genetic variance.

Use of Copy Number Variation in association studies

Mario Calus of the Animal Sciences Group in Lelystad, visited Roslin Institute for 5 weeks in Winter 2007 to work with Chris Haley and Dirk-Jan de Koning on the potential use of Copy Number Variation (CNV) in association studies.



A CNV locus comprises a string of DNA, of which different individuals may have different numbers of copies. An important question is how well possible genetic variance that is caused by a CNV locus, can be

Full versions of these and other placement reports are available at: www.sabre-eu.eu >> Get Involved >> Training >> SABRE Placement Reports





Placement Allocations

Funding was recently allocated for the following placements at SABRE member institutes.

EU NMS and INCO placements:

- ♦ J. Kalina (BIOPHARM, CZ) to visit I. Dunn/J. Woolliams (RI): 'Copy number variation in Avidin, an egg antimicrobial gene'.
- ♦ A. Abdoon (National Research Center, Egypt) to visit K. Schellander (University of Bonn): 'Microarray analysis of genes in vivo, in vitro and parthenogenetically developed buffalo and bovine embryos'.
- ♦ N. Ganai (Uni. Kashmir, India) to visit DJ. de Koning (RI): 'Experimental designs and Statistical Methods for QTL detection'.

SABRE to SABRE Placements:

- ♦ N. Duivensteijn (IPG) to visit DJ. de Koning/C. Haley (RI): "Cooperation between SABRE WP9 and WP1 to analyse boar taint data and optimize structure".
- ♦ X. Liu (CAU) to visit H. Sang (RI): "Produce transgenic chicken by lentivirus".

Funds available to genotype commercial populations

As part of the SABRE's 'Demonstration' activities SABRE intends to fund work to demonstrate the application of outcomes of the SABRE project across the EU and Associate States.

Available funding: Funding is available up to a total of €100k by competition. It is not expected that any one application will receive more than €40k. The funding available can be used for genotyping costs only. However, Demonstration funds within Framework 6 projects may cover only 35% of the total costs of the activity. The other 65% must be funded by the applicants. The applicants' costs of participation in this activity may include the collection and processing of DNA, the collection of phenotypes and the analysis of data.

Who can apply? Applications for an allocation of demonstration funds for genotyping may be from any legal entity within the EU-27 with access to relevant DNA and phenotypic data from mainstream commercial breeding populations of dairy cattle, pigs or chickens within the EU or Associate States. Applications are most likely to be from breeding companies, cooperative breeders or breed societies.

What polymorphisms may be tested? Proposals may be to demonstrate/test the utility of any DNA polymorphism where existing research results indicate a good association between the polymorphism and one or more traits related to sustainability of production of the dairy cattle, pigs or poultry. Proposals related to the use of dense genomic information for genomic selection will also be considered.

Proposals that seek to demonstrate outcomes from the SABRE project will have priority in the process to select which proposals will be funded.

Registration of interest. To register your interest and receive more information send an email with your details to demo@sabre-eu.eu.

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Your comments and contributions are welcome.

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New SABRE activities

The SABRE Board has agreed to award funding to a number of additional SABRE activities (following a process known internally as "Reallocation of funds") which are listed below. These additional activities with a total value of €313,500 build on early SABRE results and are expected to enhance the SABRE outcomes/results.

Activity	WP	Partners	Value €
Marker-assisted breeding value estimation for mastitis resistance in Finnish Ayrshire cattle	1, 5	ASG Lelystad & MTT Finland	48,500
Selective genotyping of purebred population for boar taint	9	Institute for Pig Genetics & Roslin Institute	70,000
Application of validated SNPs to egg shell quality QTL	7	MTT Finland & Roslin Institute	70,000
Targeted additional pig genome sequencing	3, 4, 8, 9	Sanger Institute	125,000



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Food Quality and Safety