



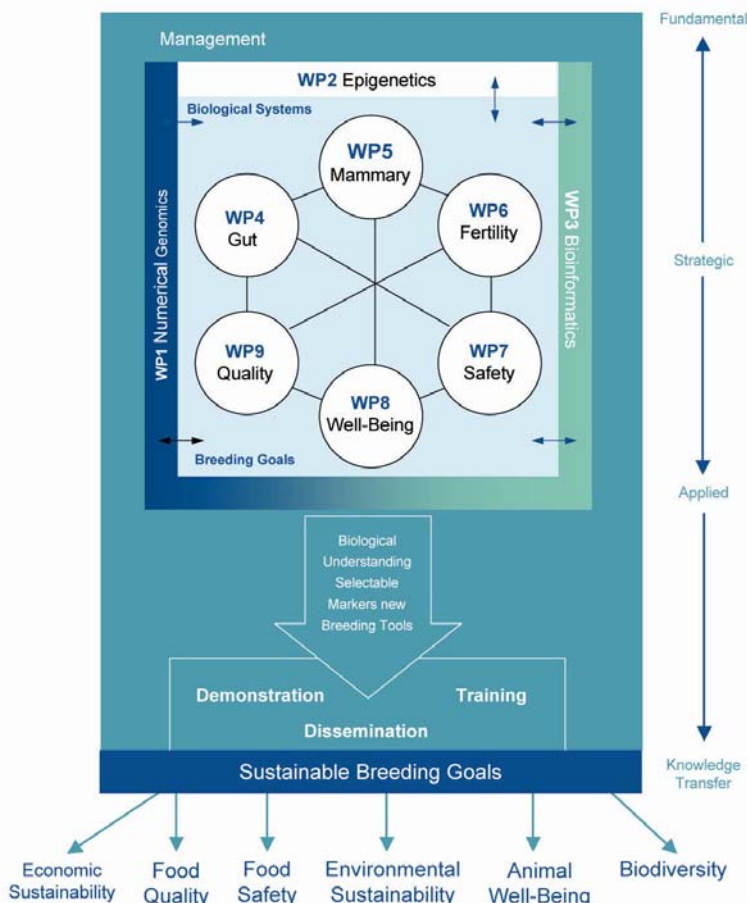
Publishable Executive Summary 2006 - 2009

Cutting Edge Genomics for Sustainable Animal Breeding - SABRE (Food-CT-2006-016250)

The SABRE Integrated Project started 1 April 2006, and we report here the activities up to 31 March 2009 of this 4-year project.

The SABRE Consortium comprises thirty three leading animal breeding research groups and businesses in an Integrated Project - "SABRE – Cutting Edge Genomics for Sustainable Animal Breeding". SABRE utilises the latest techniques in genetic science to develop more economically and environmentally sustainable production systems for cattle, pigs and chickens. The 'headline' objectives of the project are:

- To provide fundamental knowledge on the genomics and epigenetics relating to livestock
- To provide understanding of biological systems central to sustainability
- To identify genes and markers allowing focused breeding for sustainability goals
- To demonstrate the effectiveness of genomics for sustainable breeding
- To disseminate existing knowledge and new results to the user community
- To develop skills and training to best capitalise on new genomics knowledge



SABRE is designed to provide a range of new breeding strategies to improve animal health and welfare; reduce chemical and energy inputs; minimise livestock waste and pollution; and, maximise food safety and quality.

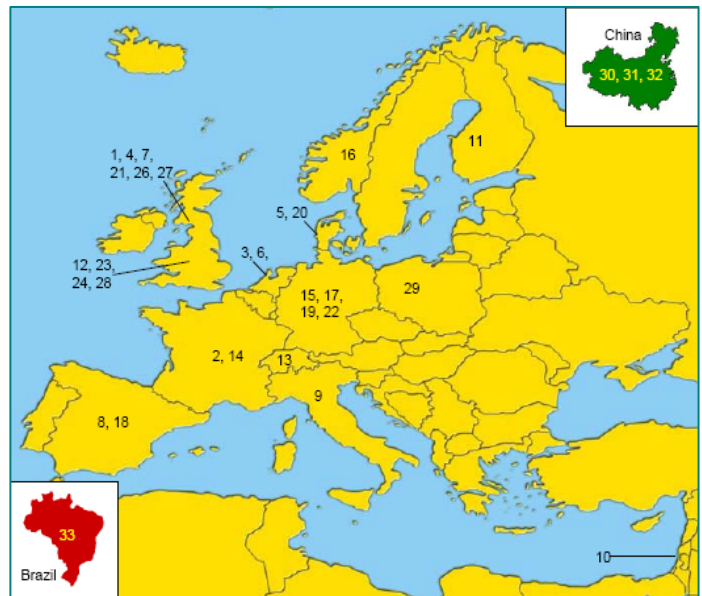
The work programme, involving almost 200 scientists in 14 countries, is divided into 12 research, development and communication work packages (see diagram). These will harness key areas of emerging genomic and epigenetic science to generate new knowledge and apply it in practical breeding improvement strategies throughout Europe.

The mammary gland, the digestive system and fertility are the focus of separate basic research packages, with more applied research aimed at enhancing eggshell quality for food safety; improving animal behaviour linked to welfare; and eliminating boar

taint in pig meat. Three Work Packages address underpinning science, these are; numerical genomics, epigenetics and genomics with bioinformatics. Finally, we have activity on demonstration of genome-wide selection in dairy cattle, and coordinated activity on training/mobility and dissemination of project outcomes.

SABRE Participants:

1. Genesis Faraday Partnership
2. Institut National de la Recherche Agronomique
3. ASG-Lelystad
4. The Roslin Institute and R(D)SVS, University of Edinburgh
5. University of Aarhus
6. Wageningen University
7. Argentix Ltd
8. Cordoba University
9. Parco Tecnologico Padano
10. Agricultural Research Organisation, The Volcani Center
11. MTT Agrifood Research Finland
12. Genus plc
13. University of Berne
14. CNRS-UPR
15. Research Institute for the Biology of Farm Animals, FBN-Dummerstorf
16. Norwegian University of Life Sciences
17. University of Bonn
18. Institut De Recerca I Tecnologia Agroalimentaries
19. Lohmann Tierzucht GmbH
20. University of Copenhagen
21. University of Glasgow
22. University of Munich
23. Cogent Breeding Ltd
24. Wellcome Trust Sanger Institute
25. Institute for Pig Genetics b.v.
26. BioBest Laboratories Ltd
27. Scottish Agricultural College
28. Institute for Animal Health
29. University of Medical Sciences Poznan
30. Jiang Xi Agricultural University
31. Zhejiang University
32. China Agricultural University
33. Universidade Federal De Vicosa



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With many of the larger studies well underway, substantial progress can be reported in a number of important areas of cattle, pig and poultry breeding improvement. Highlights of progress to the end of Year 3 include:

Numerical Genomics:

- Successful development and testing of new breeding software combining traditional and marker-assisted genetic evaluation technologies:
- A variety of software tools have been developed which implement integration of mapping and expression results. These include software routines that are available in R and which enable eQTL analysis.
- “GridQTL” (web-based QTL analysis software) is now running on the National Grid Service and accessible via <http://www.gridqtl.org.uk>) In addition to linkage analyses in a range of populations, combined linkage and linkage disequilibrium (LD/LA) analysis are available as a beta test version.

- A computational framework for high-throughput statistical analyses of gene expression data and genotypic data and phenotypic data has been developed and made available (<http://gbi.agrsci.dk/~pso/GaRT>)

Genomics and Bioinformatics:

- Within the first two years of the project an assembly and annotation have become available for pig chromosomes 7 and 14 (SSC7, SSC14) that cover more than 99% of these two chromosomes (http://pre.ensembl.org/Sus_scrofa/index.html). The sequence of these two chromosomes is a rich resource that enables the identification of additional genetic markers (such as microsatellites and SNPs (single nucleotide polymorphisms)) that can be directly used in genetic studies.
- This information was combined with SNPs from sources outside the project and resulted in over 500,000 SNPs being available for the design of the Illumina Pig SNP60 iSelect Beadchip chip. The chip contains approximately 60,000 SNPs and which became available to the research community and the breeding industry in December 2008, thereby replacing the 7.5k Pig SNP Panels, which had been developed by members of the SABRE Consortium in 2007.
- In close collaboration with the EU-funded Network of Excellence “EADGENE” and a similar initiative in the USA at ISU, an animal trait ontology (ATO) has been developed for “fertility” and a web based ‘wikisaurus’ has been implemented to aid in the further development of ATOs for additional traits.

Epigenetics

- Healthy adult cattle clones of apparent similar phenotypes show high between-animal variability in global DNA methylation compared to monozygotic twins, but hypermethylation was only observed in one of two breeds
- Global methylation analysis was performed on both normal live cloned animals and aborted fetuses of the same genotype (Holstein breed) in muscle and liver tissues to determine the contribution of epigenetics to phenotypic trait variation in domestic species. Results provided evidence of a high variability in the methylation status between clones in both tissues.
- First results point to a diet-dependent regulation of the imprinted IGF2 pathway in pigs
- The results of studies in pigs promote the importance of epigenetic modulation of gene expression and phenotypes and novel knowledge provide will support the development of tools to implement epigenetic aspects into the breeding process.

Animal Health and Fertility

- SABRE Consortium members have biologically validated that a small genomic region on Bovine Chromosome 9 (BTA9) is associated with resistance to clinical mastitis in the Danish Holstein breed The results provide strong evidence that genetic polymorphisms in this region on BTA9 can increase resistance to clinical mastitis in Danish Holstein cattle. This may eventually improve mastitis prevention and treatment strategies in the dairy industry.
- Two QTL for twinning rate and fertility are being pursued in the Israeli Holstein population
- A large number of experimental resources related to gut health and functionality in pigs and chickens has been generated. In relation to E. coli F4ac-susceptibility in

pigs the candidate region has been narrowed down to less than 3 Mb around the mucin 4 gene in the q41-region on pig chromosome 13.

Egg shell quality

- A novel measurement for assessing the quality of the cuticle on table eggs offers considerable promise for use as an additional measurement for inclusion in genetic selection programs aimed at improving egg safety and quality. Heritability (h^2) has been estimated as 0.27 of cuticle 0.67 crystal size. This brings us nearer to the measurement of egg quality by its component parts. This in turn improves our understanding of eggshell quality and safety and the precision of how it is defined and ultimately improved through selection, thereby reducing the risk from diseases like Salmonella.
- Analysis of a cross generated from two pedigree lines used in the production of brown egg laying hens has identified QTL for shell quality traits on chicken chromosomes 2, 3, 6 and 14. Since these are the lines are those currently used in the production of commercial products, the brown egg laying bird, these QTL are potentially useful to select hens for improved egg shell quality. Further analysis of the results will define whether these markers will be suitable for use in a selection programme.

Animal Welfare

- For the prevention of “boar taint” (an off-smell and off taste in pork derived from a percentage of entire male pigs, the majority of male pigs in Europe are surgical castrated - a practice which is increasingly criticised on animal welfare grounds.
- Within SABRE, studies have been conducted to detect selectable genetic markers linked to genes that are responsible for predisposition to boar taint
- Over 4800 samples from pigs have been analysed for Androstenone and Skatole. The abovementioned 7.5k SNP panel has been analysed on 1000 Danish Landrace sib pair males matched for high and low skatole.
- The CYP2E1 gene has been identified as the major factor affecting skatole levels in Danish Landrace. This gene is known to be involved in the breakdown of skatole in the liver and among others has been shown to be differentially expressed in the expression analyses and validated by RT_PCR
- A putative causal mutation for an androstenone QTL on SSC7 has been identified in a transcription factor and significant differences in allele frequencies of high and low androstenone animals from Norwegian Landrace and French Large White were detected.

SABRE Coordinator Chris Warkup stated in the SABRE Press Release in January 2009 as follows: *“The fact that we are seeing such solid gains this early in the process is a testament to the good science and hard work being undertaken by our project partners across Europe and beyond. It bodes extremely well for the full value SABRE will deliver throughout its project life and beyond. The results so far underline the vital contribution research into understanding the genetic basis of difficult-to-measure livestock traits can make in the development of practical tools to help breeders improve the economic and environmental sustainability of commercial animal production in the years to come.”*