

Publishable Executive Summary

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

Periodic Activity Report – Period 1, April 2006 to March 2007

The SABRE Integrated Project started 1 April 2006, and we report here the activity of the first 12 months of a 48-month 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:

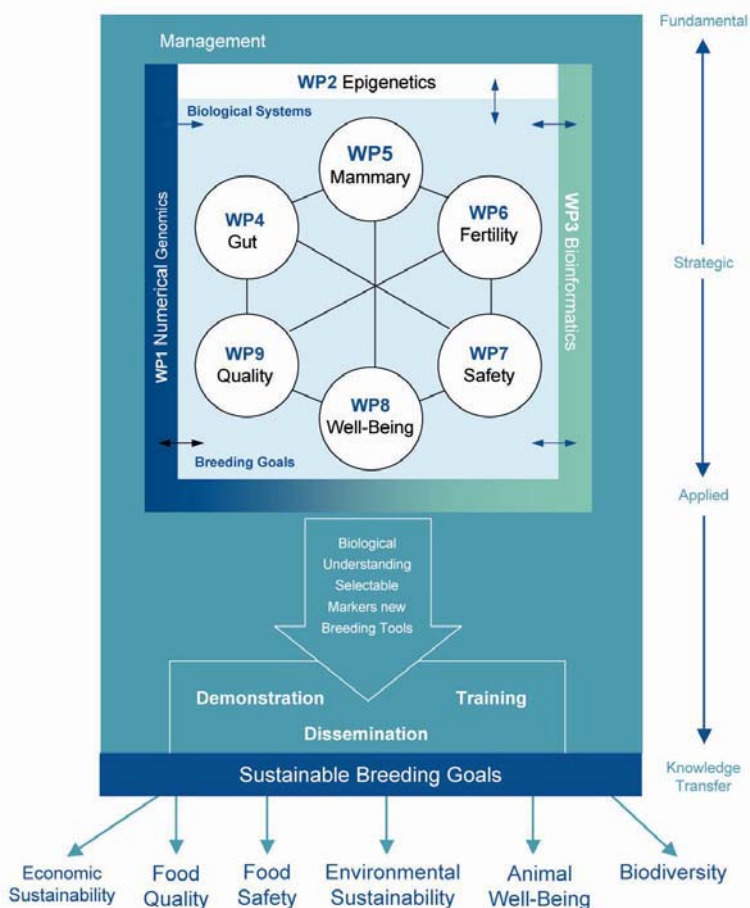
- To provide fundamental knowledge on the genomics and epigenetics relating to livestock
- To provide understanding of biological systems central to sustainability
- To identify genes and markers allowing focused breeding for sustainability goals
- To demonstrate the effectiveness of genomics for sustainable 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 pigmeat. 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.

As expected, much of the first year has been the setting up of experimental resources etc. and the establishment of the necessary tools.

Highlights of progress from year one of the project include:

- A comprehensive report on the needs for software tools and statistical methodologies for the exploitation of livestock genomes (WP1)
- Initial results demonstrating breed differences in expression of metabolic and developmental genes in pigs (WP2)
- First publicly available sequence assembly of porcine chromosomes 7 and 14 representing about 60% of these chromosomes (WP3)
- A large number of experimental resources related to gut health and functionality in pigs and chickens has been generated, together with lists of 'known' candidate genes for both species (WP4)
- Good progress with the collection of biological materials for work on mammary function and fertility (WP5 and WP6)
- For the first time a convenient quantitative method has been established to measure cuticle deposition on eggs (WP7)
- Initial microarray studies comparing uterus, magnum and white isthmus indicate 84 genes unique to the shell gland (WP7)
- Initial microarray analysis shows 241 genes to be significantly regulated by genotype and/or treatment in adrenal glands of Large White and Meishan pigs as a function of their sensitivity to ACTH (WP8)
- 2900 animal samples necessary to perform a genome scan functional genomics studies related to boar taint have been collected. A panel of 7,000 SNPs has been established for the genome scan and an Illumina Infinium Assay based upon the panel is under production (WP9)
- The bull panels needed for the demonstration of genome-wide selection have been identified and this activity has been broadened to make use of a whole-genome 25k bovine SNP panel (instead of the smaller number of SNPs on two chromosomes originally planned) (WP10)

Major Period 1 Outcomes

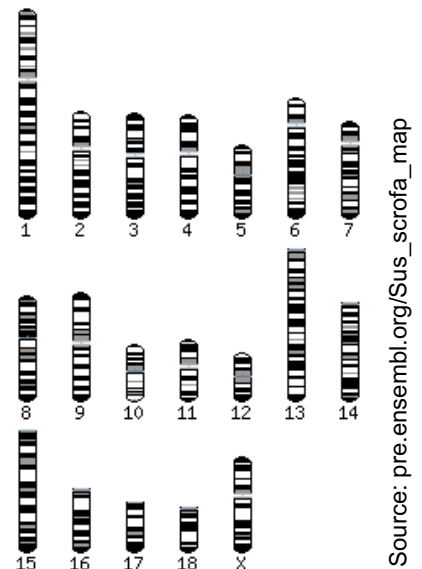
An important element of SABRE' first year is the development of porcine genomic resources for use in later stages of the project. Two of the highlights listed above are worth description in more detail.

Porcine Genome Sequence

SABRE is investing €1.6m in the sequencing of two porcine chromosomes relevant to Work Package 9 on genetics of boar taint. The Wellcome Trust Sanger Institute thus far has sequenced 1029 BAC clones from porcine chromosomes 7 and 14 representing almost 60% of these two chromosomes. All 1.455 million sequence reads (about 150Mb of sequence) have been deposited in the Ensembl trace repository where they are accessible to the public. The first chromosome assemblies and gene predictions of these two chromosomes are also publicly available through the *Sus scrofa* pre-Ensembl web site at

http://pre.ensembl.org/Sus_scrofa/index.html. The full sequencing of these chromosomes is scheduled to be completed by the end of September 2007.

Sequencing of these porcine chromosomes within SABRE is part of a larger international collaboration aimed at sequencing the complete genome of the pig coordinated by the International Swine Genome Sequencing Consortium. Further information about the consortium can be obtained from the following web site: <http://piggenome.org/>. The funding of two chromosomes by the EC was instrumental in attracting about \$10m in additional funding (largely from the USDA) to the Sanger Institute.

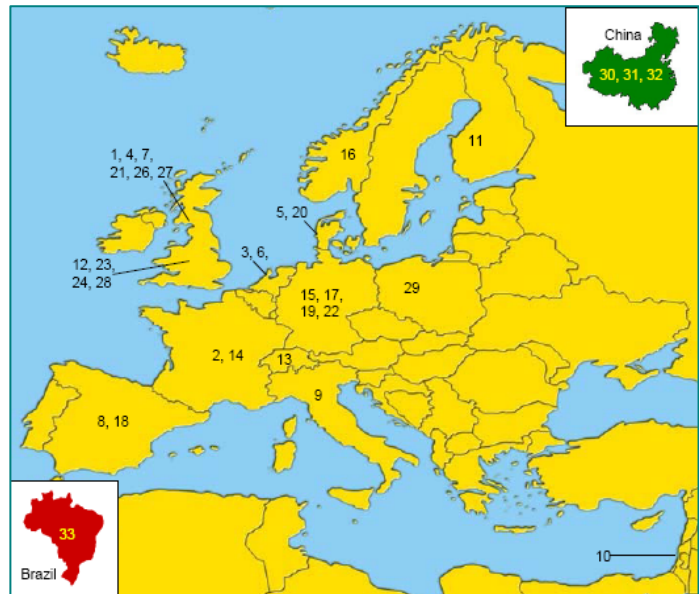


7K Porcine SNP Panel

A panel of ~7000 high quality porcine SNPs (single nucleotide polymorphisms) will facilitate genetic mapping in pigs. The panel is primarily to be used in the genetic research community, but is also available to industry. Presently, the SNPs are for genotyping using the Illumina Infinium genotyping assay and the first assays are under production by Illumina Inc. The panel is a result of scientific input from several SABRE partners including DIAS (now the University of Aarhus, Faculty of Agricultural Sciences), Roslin Institute, Norwegian University of Life Sciences and the Sanger Institute. Funding from a variety of sources including Danish Meat Association, Norwegian Research Council, the EU and others have made the development of the panel possible.

SABRE Participants:

1. Genesis Faraday Partnership
2. Institut National de la Recherche Agronomique
3. ID-Lelystad
4. Roslin Institute
5. Danish Institute of Agricultural Sciences
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. The Royal Veterinary and Agricultural University
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



Co-ordinator: Chris Warkup

Genesis Faraday Partnership
 Roslin BioCentre, Roslin, EH25 9PS, UK
 t: +44 (0)131 527 4358
 f: +44 (0)131 527 4335
info@sabre-eu.eu
www.sabre-eu.eu