

SABRE

A European Integrated Research Project on
CUTTING EDGE GENOMICS FOR SUSTAINABLE ANIMAL BREEDING



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SABRE is an Integrated Project supported by funding under the 6th Research Framework Programme of the European Union. European Commission, Directorate E03 - Security of food production systems.



Food Quality and Safety

SABRE, Cutting Edge Genomics for Sustainable Animal Breeding, is an Integrated Project supported by a €13.9m grant under the 6th Research Framework Programme of the European Union.

The project involves 33 leading research and industrial organisations working in 14 countries.

SABRE started on April 1st 2006 and will take 200 scientists 4 years to complete.

The project involves the study of Chickens, Dairy Cattle and Pigs.

Total Project Value: €23m

The Key Objectives of the SABRE 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

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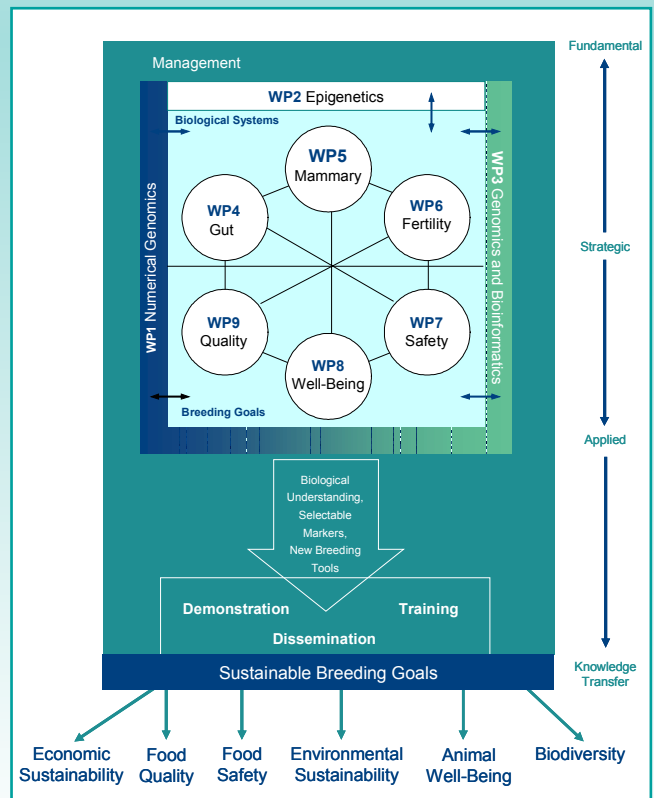
1. Genesis Faraday Partnership (GB)
2. Institut National de la Recherche Agronomique (F)
3. ASG Lelystad (NL)
4. Roslin Institute (GB)
5. Danish Institute of Agricultural Sciences (DK)
6. Wageningen University (NL)
7. Argentix Ltd (GB)
8. Cordoba University (E)
9. Parco Tecnologico Padano (I)
10. Agricultural Research Organization, The Volcani Center (IL)
11. MTT Agrifood Research Finland (FI)
12. Genus plc (GB)
13. University of Berne (CH)
14. CNRS-UPR (F)
15. Research Institute for the Biology of Farm Animals, FBN-Dummerstorf (D)
16. Agricultural University of Norway (N)
17. University of Bonn (D)
18. Institut De Recerca I Tecnologia Agroalimentaries (E)
19. Lohmann Tierzucht (D)
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32. China Agricultural University (CN)
33. Universidade Federal De Viscosa (BR)



The project is divided into 13 Work Packages (WP's):

- WP 1:** Numerical Genomics
- WP 2:** Epigenetics
- WP 3:** Genomics and Bioinformatics
- WP 4:** Gut Health and Functionality
- WP 5:** Mammary Function
- WP 6:** Fertility and Reproduction
- WP 7:** Product Safety
- WP 8:** Animal Well-Being
- WP 9:** Product Quality
- WP 10:** Demonstration
- WP 11:** Training
- WP 12:** Operational Management
- WP 13:** Dissemination

The project also has a substantial commitment to **gender equality** and addressing **ethical issues** in animal breeding.





Many of the 14 million farmers in the 27 countries of the European Union farm cattle, pigs or chickens. Livestock agriculture is important to Europe, not only because it employs many people, but also because it has wide ranging impacts on the food that we eat, our health, the survival of rural communities, the impact we have on the environment and the type of society we want to live in. It also has a substantial economic value of about €132 billion, or 40% by value of agricultural production at farm-gate prices in 2003.

Livestock farming faces a number of challenges if it is to improve its sustainability. In highly competitive times, farmers need to remain profitable whilst producing high quality, safe, nutritious and enjoyable foods at the same time as reducing the negative impacts of livestock farming on the environment (greenhouse gases, ammonia, nitrate pollution of water, odour nuisance) and also respond to societal concerns about the welfare of farmed animals. Improvements achieved through animal breeding are arguably the single best way to improve the sustainability of animal agriculture with the added benefit that the improvements made are cumulative and permanent. Europe has a high proportion of the world's leading animal breeding organisations and so technology transfer to the farmer, the enduser of the animal breeders efforts, is relatively easy because the improvements are packaged in the genes of the breeding stock bought by the commercial farmer.

Animal breeders have made considerable progress in recent decades in improving the economic efficiency of food production (this is one of the reasons the real price of food has fallen), but in recent years animal breeding has become more complex with breeders needing to broaden their breeding objectives. Nowadays breeders want to improve a wide range of traits, such as product quality, welfare related fitness traits and disease resistance. Many of these traits are difficult or expensive to measure and this is where the science of genomics is valuable. Through research such as the SABRE project, scientists are beginning to unravel which genes and which variants of these genes are important to explaining the genetic component of these new selection traits. 'Sustainable Animal BREeding' is the main focus of the SABRE Integrated Research Project.

SABRE will provide the fundamental knowledge of the genomics and epigenetics of animal health, food safety and food quality traits of livestock species, together with the strategies to deliver such technologies for use in selection. This will enable producers to move animal breeding and production towards more sustainable, environmentally and welfare friendly, low-input systems, that deliver safe and high quality foods in line with consumer expectations and European Policy.

Our overall strategy is to combine the power of gene mapping technologies, gene expression studies in target tissues and modern bioinformatics tools with available and expanded genome sequences, to determine the origin of genetic variation in key traits in important livestock species. These new breeding strategies will help industry improve animal health and welfare, adopt lower chemical and energy inputs, reduce livestock waste and pollution, produce safer and better quality foods whilst maintaining biodiversity and economic sustainability. The project will undoubtedly have a lasting positive impact on the EU animal breeding industry, scientific community, farmers and consumers long after its completion in 2010.



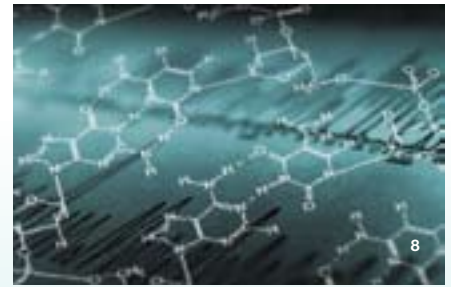
Developing numerical tools to exploit fully the new genomic data being generated in the SABRE project and elsewhere.

The objective of Work Package 1 of the SABRE project is to develop statistical tools and software for use during and after the SABRE project. The project is producing a large volume of data involving a range of different techniques and therefore requires the development of sophisticated statistical modelling and numerical analysis tools in order to capitalise on the enormous opportunities the project has created for greater understanding and exploitation of genetics.

This Work Package is developing methods allowing integration of studies such as analysis of QTL, gene expression* and proteomics*. This will help to optimise inference on underlying genetic causality and to facilitate gene* identification. Once genes linked to markers associated with sustainability issues are identified the information must be combined with information from phenotypic* and other sources in order to allow the breeder to obtain desired genetic improvements without unforeseen side effects. This will allow for greater control of animal genetics for the ultimate benefit of livestock producers, consumers and animals.

Much of the experimental and demonstration work performed in the rest of the SABRE project will require the assistance of scientists involved in this Work Package. They will share the approaches developed and use them for the analysis of data from other Work Packages. The scientific tools and software will be designed to be user-friendly in order to make them more accessible and manageable for a range of users with different requirements. They will be used long after the SABRE project has ended and it is hoped they will make future studies easier and more efficient to conduct.

*Please turn to page 11 for a glossary of terms



Key Facts

Gregor Mendel, the “Father of Genetics”, developed the ‘Laws of Heredity’, published in 1866.

Livestock has increased its production levels by approximately 50% over the last 40 years. Much of this improvement is a consequence of animal breeding.

Work Package 2: Epigenetics



Improving our understanding of how epigenetic changes affect livestock traits and how this information might be used in animal breeding.

Epigenetics is the study of changes in genome function that occur without a change in the sequence of DNA. It considers, among other factors, the way genomic DNA is folded and compacted into the nucleus by the surrounding proteins that forms a dynamic structure called chromatin*. Epigenetics involves the study of how gene expression changes, during the differentiation of one cell type into another as part of embryonic development or in response to environmental factors.

Epigenetic changes are heritable and can thus be transmitted from one generation to the next. Epigenetics can explain why for instance the nutritional conditions of the mother can affect the birth weight of her daughter’s children and why identical twins can develop so differently revealing that one genome* can generate many ‘epigenomes’ as the fertilised egg progresses through development.

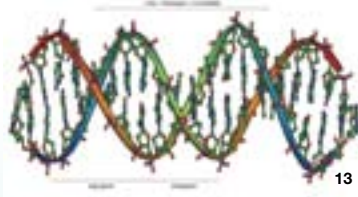
Work Package 2 studies the epigenetics of two species involved in the SABRE project (cattle and pigs). It aims to generate new knowledge of how epigenetics contributes to the variability of traits. It will develop a sensitive readout of the epigenetic status of the genome* for use in the selection process together with molecular genetic testing. The study will look into how a genome “learns by experience” and how genomic and environmental influences can control and manipulate the genome.

The information generated will not only benefit other areas of the SABRE project but will create a more stable basis for future experiments. It will allow for more effective control and management of such effects for the benefit of animal well-being and economic and environmental efficiency.

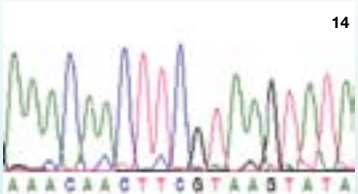
*Please turn to page 11 for a glossary of terms

Key Fact

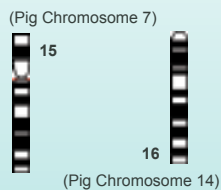
Some large genetic effects in livestock are known to be **imprinted**; i.e. whether the effect of a particular gene variant is expressed or not depends from which parent it is inherited.



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Key Facts

The DNA double helix was first described in 1953 by Francis Crick and James Watson.

The chicken and cattle genomes were sequenced in 2004 and 2005 respectively.

The focal point for exchange of genomic information and development of bioinformatics tools within SABRE.

Livestock genomics* can loosely be defined as the study of livestock DNA, its organisation into structural, regulatory and protein coding components and how variations in DNA sequence and expression interact with each other and environmental factors to describe the heritable component of livestock variation.

Bioinformatics is the science of managing and analysing biological data using advanced computing techniques and informative tools such as computer systems, algorithms and statistical techniques. Bioinformatics provides the infrastructure behind the other Work Packages in this project and creates efficiencies in the study of animal genomics as information can be collated into a searchable format so as duplicate studies are not required and specific areas of the genome can be focused on quickly.

Integration of different studies such as genomics and bioinformatics is important, as the results of one study are often vital to the validity of another study. The SABRE project has therefore a dedicated taskforce in Work Package 3, which is responsible for providing accurate information on the three selected SABRE species (dairy cattle, pigs, chickens) and will provide a strong foundation for all other areas of the SABRE project. This Work Package combines its efforts with Work Package 1 (Numerical Genomics) in order to provide Work Packages 4 to 10 with vital information for their studies.

Work Package 3 has also allocated €1.6 million of its budget to sequencing the genome of two key pig chromosomes (7 and 14) in the search for a solution for Boar Taint in Work Package 9. Investments in this area of the project will make other areas of the project more efficient and easier to conduct.

**Please turn to page 11 for a glossary of terms*

Work Package 4: Gut Health and Functionality

Identifying genetic variation involved in susceptibility to infectious disease and nutrient uptake in the digestive tracts of chickens and pigs.

Disease of the digestive tract can be a major cause of poor efficiency and the gut can also harbour micro-organisms capable of infecting humans. Livestock with healthy digestive tracts are likely to be more efficient, both from an economic and an environmental point of view, than those with unhealthy digestive tracts. There is evidence of genetic variation in gut health and the genetically more healthy animals are likely to be more efficient at nutrient uptake and hence produce lower levels of pollutants.

Work Package 4 is focused on creating healthier gut functionality in animals through better breeding strategies. Gut health is a crucial factor in the reduction of the risk of food borne infections, the reduction of antibiotic and additive levels in animal feed and the reduction of pollutants created by livestock. By the end of the study a list of biological and positional relevant genes associated with gut health and functionality will be published.

Work Package 4 is conducting studies such as gene expression analysis, QTL analysis and fine mapping* (which will be integrated into the studies of other Work Packages such as Work Package 1 and 3) that will provide very detailed information on genetic areas involved in controlling gut health and functionality in two main species: pigs and chickens. This will give a more detailed understanding of the genetics involved in gut health and functionality and this will improve the ability of breeders to select for these traits so closely related to sustainability of livestock production.

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Key Facts

Pig Population (EU-25, 2004): 151.7 million

Chicken Population (EU-25, 2004): 1,166 million



Identifying important genes and genetic pathways involved in the immune response to Mastitis.

In 2005 there were nearly 23 million dairy cattle in the EU, producing over 500 million tonnes of milk. Over 600,000 people are involved in the dairy industry which has a turn over of €117 billion. It is clear from these statistics that the EU dairy sector is very important to the agricultural output of the EU and that any problem which harms milk production can negatively affect many people and animals.

Mastitis is an infectious bacterial disease which causes inflammation of the mammary gland. This causes discomfort to the animal, makes milking difficult and can reduce milk quality. It is estimated that mastitis infections affected 30% of dairy cattle and cost the EU dairy industry about €1.55 billion in 2005. A genomic approach to selective breeding of cattle for mastitis resistance may offer more sophistication than current selective approaches.

Work Package 5 is concerned with mammary function and in particular genetic resistance to mastitis. Mastitis often negatively affects desirable production traits (physical characteristics) such as milk production and milk quality. This Work Package is employing a range of genomic techniques to identify and learn more about the genes involved in mastitis resistance. Genetic analysis will focus on both genes involved in mastitis resistance and genes for desirable production traits in an attempt to identify cattle which have both higher levels of genetic resistance and other desirable traits.

This Work Package will use techniques such as QTL assessment*, fine mapping QTL*, gene identification and SNP identification. Outputs of this Work Package will enable selective breeding* schemes to be refined, thus increasing both animal welfare and profitability.

*Please turn to page 11 for a glossary of terms



Key Facts

Dairy Cattle Population (EU-25, 2005): 23 million

Estimated number of dairy cattle affected by Mastitis (EU-25, 2005): 6.9 million (30% of population)

Est. cost of Mastitis per animal: €150-€300

Work Package 6: Fertility and Reproduction



Key Facts

Annual R&D spending by cattle breeding organisations in Europe: €150 million.

Target period between calving: 365 days.

Actual period between calving: up to 411 days (Dutch dairy cows in 2005).

*Please turn to page 11 for a glossary of terms

Generating basic genomic knowledge of the biology of reproduction and fertility.

Fertility is important for sustainable livestock production. Infertile dairy cattle, for example, are not cost-efficient as they need to regularly deliver a calf in order to maintain high milk yield. There has been a decline in fertility in recent years, probably in part due to side effects of selective breeding for increased milk production. Poor fertility is an important reason for premature culling of cows and new tools to breed for fertility would be a valuable way of improving sustainability.

Work Package 6 studies the reproductive system of livestock species, specifically the genomic regulation of follicle (i.e. female egg) maturation, oestrus related behaviour and hormonal events, and embryo development. Embryonic development, embryo maternal interactions and foetal development determine the outcome of pregnancy and may have long lasting effects during life. Biological variation seems especially the result of changes in patterns of gene expression and with microarrays we now have the tools to simultaneously measure thousands of gene products.

The information that Work Package 6 generates with such new techniques needs to be integrated with other sources of information and this is part of work to be done. Gene expression data are linked to QTL information and a tool (i.e. ontology database) is constructed to facilitate the interpretation of data in a meaningful way. Work Package 6 also involves the identification of segregating QTL* affecting conception rate in dairy cattle and in general it increases knowledge of the genes regulating genetic variation in fertility and reproduction.

This Work Package will contribute to the understanding of the biology of livestock reproduction traits. Ideally, the knowledge generated will result in the design of more successful breeding programs that will improve the sustainability of the industry, including animal welfare.

Reducing instances of infection of bacteria, such as Salmonella, by understanding the genetic basis of variation in egg shell quality to create stronger barriers to contamination.

Inhabitants of the EU produce and consume about 6.5 million tonnes of eggs per year. Over 140,000 cases of Salmonella infection of humans are reported in the EU per annum. Eggs are probably responsible for only a minority of these cases and control measures are reducing the incidence. However, it is important that the risk of humans catching infections by eating infected eggs are minimised by ensuring that hens produce eggs that are strong, healthy and act as a barrier to bacterial transfer.

Eggs feature natural barriers to the entry of bacteria and egg shells are part of this barrier. Some hens produce better shells than others and Work Package 7 attempts to understand the genetic basis of this variation. In addition to reducing health risks, improved egg shell quality also improves the perception of the product and can reduce the amount of waste from cracked or damaged eggs, so improving the sustainability of the egg industry.

The SABRE project will take egg shell analysis a stage further than traditional measurement techniques such as static compression and acoustic techniques by using genomic techniques to highlight the hens which naturally produce strong, healthy eggs.

Work Package 7 will also characterise gene expression in the shell gland, the organ depositing the shell on the egg, in order to help identify gene candidates and pathways* which underlie the genetic locations that determine egg quality. Ultimately the information will be used to supplement egg shell strength testing to select hens that lay better, healthier eggs.



Key Facts

Production and consumption of Eggs EU-25:
6.5 million tonnes of eggs per year

Reported cases of human Salmonellosis in EU, 2004: 192,703

**Please turn to page 11 for a glossary of terms*

Work Package 8: Animal Well-Being



Key Facts

Average poultry and pork consumption (EU-25, 2005): respectively 15.7 and 42.9 kg per capita.

Production of broiler chicken meat and pork (EU-25, 2005): respectively 7.6 & 21 million tonnes.

Estimated number of animals transported between farms in EU per year: 20 million.

**Please turn to page 11 for a glossary of terms*

Applying genomics research to support the development of more welfare friendly animal production.

Meat quality is highly influenced by the muscle pH and its change over time postmortem, which in turn is strongly dependent on pre-slaughter conditions, especially the level of animal stress. More stress-sensitive individuals in a population can become stressed in a range of situations such as; during transportation, before slaughter, when interacting with more aggressive animals and when being handled.

Transportation stress and pre-slaughter stress are areas of animal treatment which are coming under increasing scrutiny. Measures are being put into place to help eliminate unnecessary stress at all stages of the animal's life and genetic research is playing a role in this by highlighting animals for breeding which have temperaments best suited to dealing with potentially stressful situations. This Work Package is primarily aimed at improving the lives of animals, but also has an important role in product quality.

Work Package 8 involves the study of stress responses and how they play a role in the sustainability of animal breeding, animal welfare, growth, and the quality and safety of products. The Work Package aims to determine gene expression responses to stress in pigs and poultry and detect polymorphisms* in candidate genes* associated with stress responses.

Stress responses are variable among individuals and are influenced by genetic factors. Phenotypes of interest include behavioural traits such as emotional reactivity and biological stress responses such as the release of stress hormones by the adrenal gland. By studying the stress responses of pigs and poultry, Work Package 8 will be able to provide breeders with information which will help them to devise better breeding programs.





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Applying functional genomics to describe genes and proteins associated with boar taint in pig meat; aiming to increase meat quality and avoid the need for castration.

Boar taint is a problem which can affect the quality of pig meat. It is an off-flavour and smell in meat caused by the production of certain hormones and other compounds in a small proportion of boars (uncastrated male pigs) of normal slaughter age. Castration of male pigs is a solution to boar taint. Castration halts the production of hormones which are related to the quality problem. This is however a painful procedure that should be avoided if possible. There are added advantages to stopping castration; uncastrated male pigs grow faster and more efficiently than castrated male pigs, so an end to castration will improve the environmental sustainability of pig production.

Boar taint is damaging to the industry because it creates waste and inefficiencies in the industry and it is a practice which can harm public perception of pig meat (when tainted) or pig production (when castration is practiced). Meat affected with boar taint is not suitable for direct human consumption as fresh meat but it can still be used in processed meat products.

Key Facts

Male pigs are called: Boars, **Female pigs are called:** Sows

Population (EU-25) Pigs 2004: 151.7 million

Consumption (2005): the 460 million inhabitants of the EU eat an average of 42.9kg of pig meat annually.

Boar taint can be caused by high levels of: (16-androstene) steroids and skatole.

Work Package 9 is concerned with product quality in the area of pig meat. It is using genetic analysis techniques such as QTL identification*, comparative studies and integrative mapping of SNP* data in order to better understand the genetics involved with production of taints. Work Package 9 aims to help marker assisted selective (MAS*) breeding become a viable alternative to castration in order to improve animal well-being and the quality of pork. Valuable genomic data on relevant chromosomes will be provided by Work Package 3.

**Please turn to page 11 for a glossary of terms*

Work Package 10: Demonstration

Clearly demonstrating how the results from SABRE can benefit consumers, animals, the environment and industry.

The demonstration Work Package is integral to the SABRE project's remit. It involves clearly defined routes of information transfer, as well as tools and knowledge dissemination for commercial use. The ultimate goal of this Work Package is to demonstrate how far the SABRE project and science in general have progressed in their ability to predict function and performance in individuals by using molecular genetic tools.

Work Package 10 will regularly communicate with the end users of the technology produced in order to make it as user friendly and appropriate as possible. By the end of the project Work Package 10 will have demonstrated genome-wide selection in action in two dairy cattle populations, determined frequencies of relevant new alleles in a range of species and breeds, and also provided advice on sustainable breeding strategies to the animal breeding industry. Integration between other Work Packages helps to ensure that the generated tools and knowledge are capitalised upon for the benefit of EU genomic research and other partner institutes. The demonstration Work Package will help to identify and resolve likely technical and organisational problems involved in the practical implementation of tools and software created during the project.

In order to make the breeding strategies as relevant as possible to the breeders Work Package 10 has allocated resources to determine the allele frequencies* for new DNA diagnostics determined within the study, and the association between these alleles and traits in diverse genetic backgrounds (G X G) and production systems (G X E)*.

**Please turn to page 11 for a glossary of terms*



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Key Fact

The first gene marker for animal breeding was industrially applied in 1991: The Halothane test, which identifies stress susceptibility in pigs

SABRE is taking a thorough approach to ensuring that learning and scientific progress is maximised at every stage of human involvement.

The Training Work Package helps scientists develop new skills and disseminate best practice within the consortium to ensure that our research benefits from the latest techniques. A separate Dissemination Work Package involves the dissemination of knowledge generated throughout the project to ensure that all project partners, people involved in the animal breeding industry and interested EU Citizens learn from and can exploit the findings of this 4-year project.

Extra emphasis is being placed on the training of women scientists, young scientists and scientists from new EU member states to combat fragmentation and strengthen EU science for the benefit of all concerned. In both Training and Dissemination we are utilising a portfolio of different approaches ranging from classical broadcast methods, such as publications, through distance learning tools to face-to-face dissemination. One of our goals is to improve the awareness among scientists of industry needs.



Key Facts

SABRE awards 22 subsidised short term placements for scientists from SABRE, new member states and INCO members to attend workshops.

5 short term placements for Early Stage Researchers are awarded to provide training in industry skills.

Operational Management

The SABRE project is managed through four clearly defined levels to ensure efficiency.

Lead Scientists of each of the 33 participating organisations are responsible for completing the Work Package Tasks that make up each of the Work Packages. Work Package Leaders are responsible to the Operational Management Group (OMG) for reporting progress on their respective Work Packages in order to allow the OMG to report and/or make recommendations to the Board. To ensure that the SABRE project and all of its individual Work Packages are managed effectively on a day-to-day basis, SABRE has a full-time Operations Manager, who is also a member of the OMG and reports directly to the SABRE Co-ordinator.

This structure encourages attention to all three aspect of the project envelope: quality, timeliness and cost.

1. Project Board:

The 5 core partners and instigators of the SABRE project: SABRE Co-ordinator and chair of the Board, Genesis Faraday, Institut National de la Recherche Agronomique, ASG Lelystad, the Roslin Institute, Danish Institute of Agricultural Sciences. The Board acts as an overseer and facilitator for all sections of the project.

2. Operational Management Group (OMG):

Members of the Board and Work Package Leaders. The OMG facilitates integration and provides an ideal environment for problems to be resolved.

3. Work Package Leaders:

Experts in relevant field of research, representing the people involved in their Work Package. Work Package Leaders coordinate the progress of individual tasks within their Work Packages to ensure they are completed in a timely and cost efficient manner.

4. Lead Scientists:

The individuals responsible for each participant's contribution to their respective Work Packages. Lead Scientists undertake specialist activities vital to the completion of Work Package tasks.

SABRE Project Commitment to Gender Equality and Ethics

Addressing issues relating to gender equality and ethics.

SABRE is committed to conducting the project in an open and transparent manner and addressing all concerns relating to the project. Standards are being upheld by project management internally ensuring that all partners and people involved in the project follow all EU and national regulations, guidelines and legislation. As part of this, a Gender Representative has been appointed to monitor gender equality and implement initiatives to create a more equal scientific community, and an external independent Animal Behaviour and Welfare Consultant is employed to monitor the research on animals within the project.





Alleles and Allele Frequencies	Alleles are inherited loci (stimuli) for certain traits. A single allele for each locus (e.g. colour of eyes) is inherited from each parent. Allele frequencies involve a study of the relative frequency of a genetic locus in a population and show the genetic diversity of a species.
Candidate Genes	Candidate genes are genes located in a chromosome region suspected of being involved in the expression of a trait such as a disease.
Chromatin	Chromatin is a complex DNA and protein found inside the nuclei of complex cells.
Diverse Genetic Backgrounds (G X G) and (G X E)	The term diverse genetic backgrounds (G X G) refers to the interaction of a Gene with a varying Genetic Background (i.e. the same gene in a broiler chicken that has been intensely selected for meat production may be influenced by other genes also linked to selection for meat production and thus produce meatier animals, whilst the gene may have a different effect in a wild fowl with a different genetic background where such selection has not occurred and these other meat production genes are not present, whilst (G X E) refers to the interaction of a Gene with different environmental backgrounds, i.e. a gene controlling fat production in cattle may result in fat animals if the cattle are well fed and kept on a farm, but not if they are kept in a desert.
DNA and DNA Sequence	DNA stands for Deoxyribonucleic Acid. It is the molecule that encodes genetic information. DNA sequence is the relative order of DNA, whether in a DNA fragment, gene, chromosome or entire genome.
Expression Analysis and Expression Data	Expression analysis is the realisation of genetic information encoded in the genes to produce a function protein or RNA. In its broadest sense it encompasses both transcription and translation only. Expression data is the raw genetic readings expressed before the expression is analysed. The data is produced by technical equipment such a DNA arrays.
Fine Mapping QTL and QTL assessment	Fine mapping QTL and QTL assessment involve identifying genes and genetic trends associated with a specific production trait e.g. high resistance to Mastitis. Once this is carried out further studies can be conducted. Fine mapping involves the assignment of DNA fragments to chromosomes. As the study progresses a clearer picture of the genome is compiled.
Gene	The basic physical unit of heredity consisting of a DNA sequence at a specific location on a chromosome.
Gene Expression	Gene expression involves the realisation of genetic information encoded in the genes to produce a functional protein.
Gene Pathway	A gene pathway is a set of interactions occurring between a group of genes who depend upon each others individual functions in order to make the aggregate function of the network available in the cell.
Genome	The genome refers to all of the genetic material in the chromosomes of a particular organism.
Genomics	Genomics is the study of the genome and the function of genes. Genomics can be used as a diagnostic tool and manipulation can also be conducted as a solution to a particular problem. Bioinformatics is the science of managing and analysing biological data using advanced computing techniques.
Marker Assisted Selection MAS	Marker Assisted Selection (MAS): Selection for specific alleles (which affect an economically important trait) with the use of genetic markers. The actual genes under selection may be unknown.
Nucleotide	A nucleotide is a chemical compound that consists of a heterocyclic base, a sugar, and one or more phosphate groups. There are five different nucleotides: Adenine (A), Cytosine (C), Guanine (G) and Thymine (T) and Uracil (U). They link together to form strands of DNA (A, C, G, T) and RNA (A, C, G, U).
Phenotype	A phenotype is an observed physical characteristic of an organism. These characteristics are determined by the organisms genotype and the environment.
Polymorphisms	Polymorphisms are differences in the sequence of DNA among individuals that may or may not affect the phenotype. A polymorphic locus implies two or more alleles for that locus or gene.
Proteomics	Proteomics is the large scale study of proteins, their structures and functions.
Selective Breeding	Selective breeding involves breeding animals which produce positive traits which complement one another and not breeding animals with genes which react badly with one another to produce negative traits.
SNP	SNP stands for Single Nucleotide* Polymorphism which are DNA sequence variations that occur when a single nucleotide (A, T, C, or G) in the genome sequence is changed.

Image Sources

Microsoft Clip Art 2006, images: 1 Water ripple, 4 Chicks, 5 Dairy Cattle Grazing, 7 Piglets, 6 Chicken, 8 Genomics image, 9 Genomics Graph, 10 Genomics Monitor, 11 Dairy Cows, 22 Pig, 23 Chicken, 24 Pig grazing, 25 Pig and Piglets, 26 Group training, 27 Man typing on laptop, 28 Genomics teacher blackboard, 29 Woman and Men.

Wikipedia 2006, images: 2 Holstein Cow, www.wikipedia.org/wiki/Cow, Keith Weller 2006, Public Domain image, 13 DNA Structure, www.wikipedia.org/wiki/DNA, Michael Ströck 2006, GNU Free documentation license, 14 DNA Sequence, www.wikipedia.org/wiki/DNA_SEQUENCE, Chris Dixon, Public Domain image, 17 Pig and piglet, www.wikipedia.org.uk/wiki/Pig, Scott Bauer, Public Domain image, originally from Agricultural Research Service USA, 18 Hen and Chicks, www.wikipedia.org.uk/wiki/Chicken, Unknown author, GNU Free Documentation license, 19 Udder, www.wikipedia.org/wiki/Udder, Unknown author, GNU Free Documentation license, 20 French Cow and Calf suckling, www.wikipedia.org.uk/wiki/Cow, David Monniaux 2005, GNU Free documentation and Creative Commons Attribution licences.

Roslin Institute 2006, images: 3 Sow with piglets feeding, 12 Wilbur, 15 Pig Chromosome 7, 16 Pig Chromosome 14.

The Avian Biology Laboratory, Glasgow University 2006, image: 21 Eggs light testing.



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