



EUROPEAN
COMMISSION

Community Research

Genomics research in livestock



What does it offer?

Foreword	3
Genomics for better livestock	4
Workshop highlights	5
End-user perspectives	6-7
What does livestock genomics offer?	8-9
The European approach	10
Project summaries	11-12
Identifying strengths to shape the future	13-15
Genomics for disease control	16-21
<ul style="list-style-type: none"> • Mastitis resistance in cattle (Mastitis Resistance, QLK5-2002-01186) • Genomics, chickens, and immunity (Chicken-IMAGE, QLK5-1999-01591) • Improving the quality and safety of sheep products (Genesheepsafety, QLK5-2000-00656) 	
Genomics for biodiversity	22-25
<ul style="list-style-type: none"> • Biodiversity's role in rural development (Econogene, QLK5-2001-02461) • Measuring biodiversity in pigs (PigBioDiv2, QLK5-2002-01059) 	
Genomics for meat and milk quality	26-31
<ul style="list-style-type: none"> • Beef quality: genetics vs. environment (Gemqual, QLK5-2000-00147) • Mapping for milk quality (BovMAS, QLK5-2001-02379) • Genes, pig welfare, and pork quality (QualityPorkGENES, QLK5-2001-01888) • Pork quality and muscle development (Pordictor, QLK5-2000-01363) • Seafood and consumer protection (DNAIQ, QLK1-2000-30476) 	



Foreword

The human genome project was a milestone in genomics research. Funding for genomics research in the human field has seen major increases worldwide over several years, and the European Communities' Framework Programmes for Research are no exception. Complete genome sequencing of individual species is developing apace, and the European Commission has made significant contributions to the sequencing of the yeast *Saccharomyces* (1996) and the plant *Arabidopsis* (2000).

Yet livestock genomics, in which we include all species kept on farms or fished for human use, does not have the same attraction to the funding agencies as its human counterpart or even as that of smaller animals models like the mouse, the nematode or the Zebra fish. While understandable from the overarching importance of human health and well-being, it is important to recognise the opportunities genomics research in livestock can offer, not only for animal health, but also for human health, food safety, biodiversity and industrial competitiveness, to name but a few.

While recognising these advantages, it is also apparent that the field is developing at an exceptionally fast rate, which hinders or practical response to new developments. It is significant, therefore, that within the Sixth Framework Programme for Research, the European Commission is supporting a major project in functional genomics of livestock in order to structure the European research effort and help Europe benefit from the technology.

We cannot, however, be complacent. In response to this rapidly changing field, the Directorate-General for Research recently organised a meeting to review the state of play of ten research projects in livestock genomics funded under the Fifth Framework Programme, and to encourage a discussion on the demands of industry and the potential of the research community. We recognise also that the rest of society includes important stakeholders in the technology, and ethical, legal and social issues of the use of such biotechnology are addressed by Strategic Support Actions in the Sixth Framework Programme.

This publication reports on the meeting held in Brussels on 10 September 2003 and, as well as offering an overview of the research projects themselves, also describes the priorities the participants saw as of immediate and fundamental importance to Europe. It comes at a crucial time and, I believe, creates a significant base for the further development of livestock genomics in Europe.

Etienne Magnien

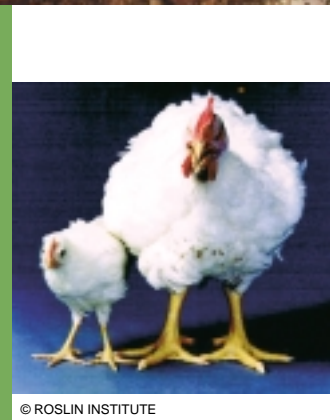
*Acting Director of Biotechnology,
Agriculture and Food Research*

Genomics for better livestock

Europe's world-leading livestock-breeding industry is eager to make the most of the genomic revolution. The European Commission, which already supports research in farm animal genomics, is intent on making Europe "the most competitive, dynamic, knowledge-based economy in the world", and wants to match the diversity of scientific opportunities more closely with the needs of end-users. To obtain a more comprehensive picture of both, the Commission's Directorate-General for Research hosted a workshop entitled 'Genomics in livestock - what does it offer?'. More than 40 experts attended from academia, industry, and governmental institutions (coming from 12 Member States and four Accession Countries), in addition to representatives of five of the Commission's Directorates-General. Their presentations, discussions, and conclusions are outlined in the following pages.



© ROSLIN INSTITUTE



© ROSLIN INSTITUTE



Workshop highlights

The workshop focused on topics such as why we need livestock genomics, how research should be organised and the role the EU should play in this field. The main highlights of the discussion were:

Twin targets

Farm animal genomics can:

- provide the knowledge needed to improve breeding strategies and animal husbandry;
- supply tools enabling breeders to move faster towards breeding goals;
- contribute to better control of livestock diseases (for example, zoonoses, i.e. diseases transmitted from animals to humans);
- lead to the development of better food quality measurements and improved traceability;
- help monitor and maintain livestock biodiversity;
- be a comparative science with human genomics and thus contribute to progress in human health and medicine.

Consequently, this research has the potential to serve a dual purpose: to maintain the competitiveness of the EU livestock-breeding industry and to improve the public good in the form, for example, of improved food safety, biodiversity, animal welfare and support to developing countries. Sometimes these two goals go hand in hand, but there may also be tensions between them. Perhaps genomic research might best be integrated into a view of 'sustainable agriculture', as the 'sustainability' concept likewise includes both economic and broader societal aspects. This may be achieved by maintaining a platform where all stakeholders in this research can contribute to shaping its objectives.

Synergies and bottlenecks

In order to take full advantage of the genomics revolution, it is important to create synergies across Europe. Ways of achieving this include: (1) creating a European centre of excellence in the field, linking national centres and support programmes; (2) promoting Europe-wide sharing of tools and data by developing a flexible system in which heterogeneous databases can be effectively integrated and interrogated; and (3) involving industry at an early stage.

Whenever commercial interests are implicated and this is the case both for industry and, increasingly, for scientists-unresolved intellectual property (IP) issues can be a serious obstacle to collaboration and to the sharing of resources. Participants stressed the need to create a framework at the EU level in which IP is protected while allowing scientists maximum access to genomics tools. Alternatively, EU-funded research in the field could be precompetitive, thus bypassing the IP issue.

Taking the initiative

The European Union got off to a good start with initiatives such as PiGMaP, the first-ever project aiming to map a farm-animal genome. However, the effort to sequence the cattle and chicken genomes is being led by the US, and European scientists are becoming increasingly dependent on US technology for livestock genomics tools. As EU support is aimed at strengthening Union research potential, and improving the competitiveness of European industry, participants called for stronger EU support for farm-animal genomics.

End-user perspectives

The Farm Animal Industrial Platform (FAIP) is a forum of European breeding and reproduction organisations. FAIP has led two EU projects focusing on the link between farm animal production and society, and has published opinions on the future of new technologies within the sector. Dr Jan Merks, Member of the FAIP Steering Committee, provides a view from industry.

Traditional breeding involves setting a breeding goal, scoring animals on the basis of the likelihood they will pass on desirable traits, mating sires and dams with high scores, and repeating the process over as many generations as it takes to meet the original goal. Success is measured in terms of producing quality food at a competitive price, under conditions acceptable to farmers, consumers, and society at large.

In the past, Europe has played a key role in improving the major livestock species worldwide. Today, the EU has a world-leading livestock-breeding and reproduction industry. Yet to remain competitive in the global market, this industry must reap the benefits of advanced life-sciences research and information technology. It is not interested today in animal cloning or genetic modification because, as yet, there are no practical/economic applications of these technologies in the field and because many European citizens do not appear to demand them. However, breeders see great potential in combining traditional breeding practices with genomics.

Genomics can provide the tools needed to refine breeding goals and to achieve them more rapidly. This branch of genetics can also contribute to a more sustainable agriculture, to better food safety, quality, and traceability, to improvements in farm-animal health and welfare, and to maintaining genetic resources. Examples of applications outside the breeding sector include veterinary vaccines and therapeutics, on-line quality measurements, and methods for tracing food contaminants.



Marker-assisted selection

Breeders are initially interested in the potential of the genomics application known as 'marker-assisted selection' (MAS). This involves identifying and selecting genetic markers that are linked to trait-genes (i.e. located close to a gene encoding for a particular trait, and passed on from parents to progeny along with that gene). The ideal marker is the trait-gene itself. MAS is based, therefore, on an animal's actual genetic make-up, rather than on its estimated genetic make-up. This may prove particularly useful in introducing and selecting for a trait that is hard or expensive to measure or that cannot be observed until late in life or after slaughter (disease-resistance traits, meat-quality traits, etc.). In addition, genomics can help to refine breeding goals by shedding light on the genes, physiological pathways, and mechanisms that contribute to generating complex traits.

Recognising traits

Quantitative traits, such as fatness or milk production, show continuous variation in an animal population. A practical aim of farm-animal genomics is to identify marker-delimited genome regions that control such traits, so that the corresponding markers can be used in marker-assisted selection. These regions are called quantitative trait loci or QTL.

To date, many QTL and a few individual genes affecting quantitative traits have been identified in farm animals. Yet the effects of QTL are sometimes inconsistent, particularly when breeds or lines are crossed. Inconsistencies may stem from heterozygosity within farm-animal families, the manner in which traits are defined, the need for better



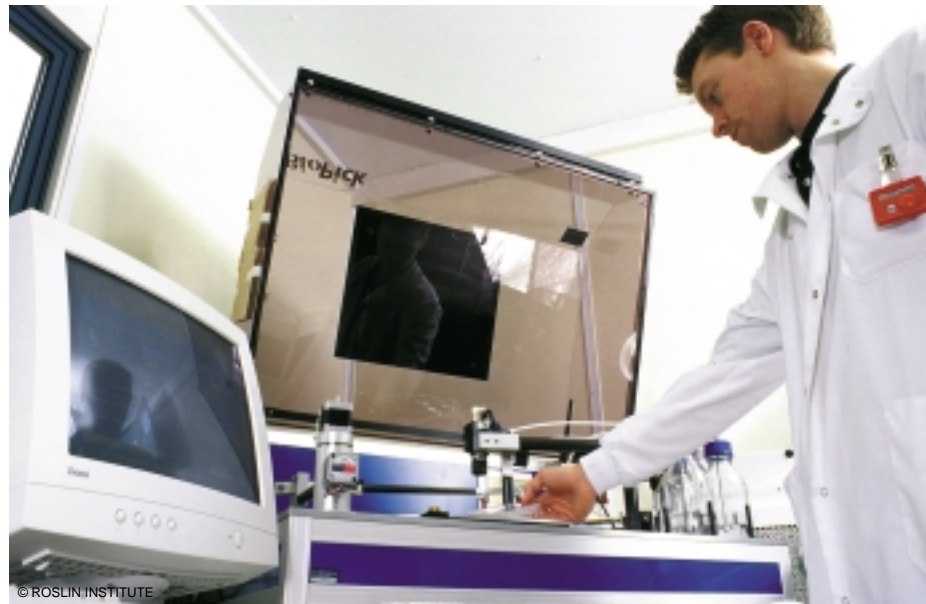
statistical software to analyse the traits, the interplay of different genes, processes affecting gene expression (the sequence of events leading from gene to protein), or the interaction of genetic and environmental factors. More research is needed in these areas.

As the QTLs identified in linkage studies tend to be quite large areas of the chromosome, further goals involve identifying trait genes within QTL and, eventually, understanding their effects. Here, both functional studies and comparative genomics can make a considerable contribution, because a protein playing a key role in one species often has counterparts in other species, encoded by similar genes. Hence, knowledge of a protein's function and the location and sequence of its gene in one species can enable scientists to make educated guesses about the identity of a trait-gene in another species. Comparative genomics can also help identify regulatory elements and possible functional genes that can be used in animal breeding.

End-user priorities

Breeders are calling for research and technology improvement in areas such as comparative sequencing of livestock genomes, marker and functional gene identification and typing, gene expression profiling, bioinformatics and, most importantly, quantitative tools to enable the implementation of genomics in farm-animal breeding programmes.

Since food safety is a major consumer concern, EU-sponsored genomic research might concentrate on areas such as host-pathogen interactions in zoonoses (diseases transmitted from animals to man) and on a few promising diseases, but needs to be carried through to its practical implementation. Only by developing concrete, economically viable uses for genomics is it possible to move from pro-



misg science to realistic business applications. Industry needs to participate in projects from the beginning in order to fine-tune research directions and potential applications. For real co-operation and to prevent competition at the research level, more open intellectual property rights (i.e. right of first refusal) are needed at the European, rather than the individual organisation, level.

Contacts at FAIP:

Dr Jan Merks, Jan.Merks@ipg.nl

Ms Anne-Marie Neeteson, Neeteson@iaf.nl

What does livestock genomics offer?

Farm-animal genomics has revealed QTL, trait genes, and even a 'quantitative trait nucleotide'. Professor Alan Archibald of the Roslin Institute (UK) offered insights into this research.

Livestock genomics aims to discover the genes and processes that control quantitative traits such as growth, fatness, milk yield, meat quality and disease resistance. The results of these studies will lead to improvements in food safety and quality, the efficiency of food production, disease resistance in livestock, animal welfare and also animal models of human disease.

Tool kit

State-of-the-art tools include:

- **polymorphic genetic markers** (identifiable DNA sequences of which several variants exist within a population), for example:
 - microsatellites (comprising a variable number of repeats of the same sequence);
 - single nucleotide polymorphisms (SNPs – characterised by the variation of a single 'DNA letter' within a population);
- **radiation hybrid mapping panels:** DNA is fragmented by ionising radiation and fragment subsets are 'rescued' in hybrid cells formed by fusing the irradiated cells with cells from another species;
- **mapping pedigrees** (families of animals in which markers have been typed);
- **large genome fragments cloned in bacteria**

(bacterial artificial chromosomes, BACs) or yeast (yeast artificial chromosomes, YACs);

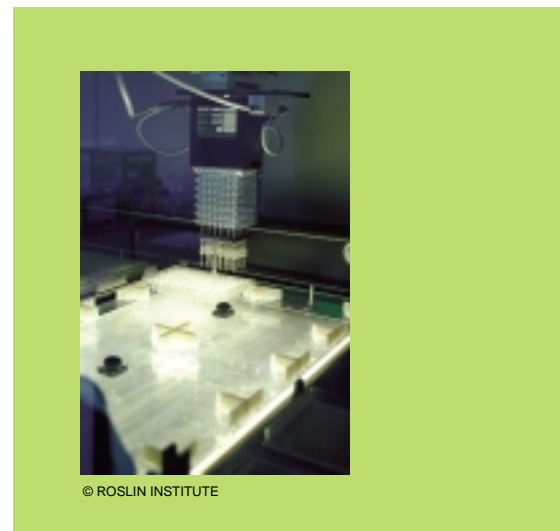
- **cDNA libraries**, i.e. sets of cloned cDNAs (see box);
- **microarrays** (see box), used to study the expression of between hundreds and thousands of genes at a time.

Information generation

Animal genomics generates abundant information in the form of:

- **maps**, particularly linkage maps (showing 'distances' between markers on the basis of genetic linkage), and radiation hybrid maps (showing distances between markers on the basis of their association in radiation hybrids);
- **expressed sequence tags (ESTs)**, i.e. partial sequences of cDNA clones, used for rapid identification of expressed genes by sequence analysis;
- **whole genome sequences:** a draft sequence of the chicken genome is near completion. Preparation of a draft sequence for cattle was due to begin in November 2003. For pigs, 10-15% of the data required for a draft sequence has been generated, but funding remains a challenge;
- **databases** for storing details of maps, sequences and genes.

However, a system for integrating and interrogating heterogeneous independent databases, possibly in a GRID environment, would greatly improve their benefit.





Gene expression and cDNA

A gene is *expressed* when the product it encodes (a protein) is formed. This involves *transcription* of the gene to messenger ribonucleic acid (mRNA), *exit* of a processed mRNA from the cell nucleus, and *translation* of the RNA 'message' into protein. Because gene transcription is a crucial step which is subject to complex regulation, 'gene expression' is often equated with this step.

Complementary DNA (cDNA) is obtained by reverse-transcribing mRNA to DNA. A cDNA thus represents the coding sequence of a gene that has been transcribed. By building a cDNA library representative of all the mRNAs produced in a given situation, and by identifying the cDNAs in the library, scientists can determine which genes are expressed a process called expression profiling.

Strategy

Farm-animal genomes contain an estimated 30 000 to 40 000 genes – as complex as the human genome. To identify quantitative trait genes, the first step is to create a map of 'polymorphic markers' spaced over the entire genome, and then to correlate the inheritance of markers with trait variability. If a trait and a marker variant are inherited together at very high frequency, the corresponding genes are likely to be close together on the same chromosome. A QTL is thus a marker-delimited stretch of DNA that co-segregates with variation in the trait of interest.

Initially, a QTL may contain as many as 200-400 genes. To zoom in on a trait gene, it is necessary to increase the density of markers in the region of interest and either the number of generations over which trait and marker are tracked or the size of the population studied. Finally, candidate trait genes' are proposed, and either confirmed or rejected,

with the help of comparative genomics and functional studies. A recent first was the discovery – within a QTL having a major effect on muscle mass and fat deposition in the pig – of a point mutation responsible for the effect. The candidate gene (coding for insulin-like growth factor 2) was identified by comparing the QTL with the corresponding region in a human chromosome, and the mutation was located by between-breed sequence comparisons.

Contact:

Prof Alan Archibald
Roslin Institute, Edinburgh (UK)
alan.archibald@bbsrc.ac.be

Microarrays

Microarrays are used for expression profiling. They exploit the following facts: (1) DNA contains only four different nucleotides, differentiated by the identity of the base that contributes to their chemical structure – adenine, guanine, cytosine, or thymine; (2) DNA normally exists as two complementary strands, and (3) It is possible to dissociate and re-associate these complementary strands.

DNA fragments characteristic of chosen genes are immobilised on a support and used to 'fish' for complementary sequences in cDNAs representing the genes expressed in the tissue or cells of interest. By labelling the DNA with fluorescent dyes, successful pairing can be detected by fluorescence. In order to compare expression profiles under different conditions (e.g., in tissues from sick and healthy animals), the corresponding cDNAs can be labelled with differently fluorescing dyes.

The European approach

The European Commission (EC) has supported livestock genomics projects since the Second Framework Programme for Research and Technological Development (FP2, 1987-1991). EC sponsorship was a major initiating force behind the first international farm animal genomics project (PiGMaP), in the development of linkage and physical mapping of farm-animal genomes, and in QTL mapping. The Commission also supported the first farm-animal database project, GEMINI.

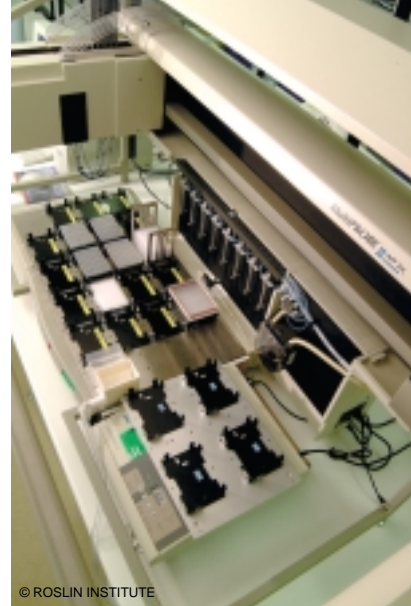
Outside EC-funded programmes, European laboratories have played a part in other noteworthy achievements:

- Mapping the first QTL in farm animals;
- Developing the first genome-wide radiation hybrid map for a farm animal (pig);
- Achieving the first positional cloning of a trait gene (the 'acid meat' RN gene); and
- Identifying the first 'qualitative trait nucleotide' in the pig IGF2 gene (see 'What does livestock genomics offer?', page 8).

Losing ground

Having highlighted these European successes the meeting added a note of concern. Today, US laboratories have taken the lead in both cattle and chicken genomics, and US-based companies have developed genomic resources to which there is no open access. This is not good news for European science or for the EU's livestock industry.

What can be done at the European Union level to remedy this situation? Farm-animal genomics has played a relatively minor part in EU Framework Programmes and the EC is not funding any ongoing farm-animal sequencing. Yet, whole-genome sequencing is "big science", exceeding anything a single national agency can handle. EU participation in major genome sequencing projects may be the key to giving Europe a say, later on, about how genomic data and resources are used.



Back on the map

From within FP6 a Network of Excellence (NoE) has emerged called EADGENE – European Animal Disease Genomics Network of Excellence for Animal Health and Food Safety. Dr Marie-Hélène Pinard-van der Laan (Institut National de la Recherche Agronomique, France) described the network's aims and structure. Focusing on host-pathogen interactions, the NoE will conduct research supporting the development of better vaccines, therapeutics, and diagnostics for animals, of disease-resistant breeds, and of animal models of human disease. Consequently, the work will contribute to better animal welfare while benefiting breeders and farmers, consumers, the agro-food industry, and society at large.

EADGENE currently comprises 14 partners in ten countries, and additional partners may join. At the core of the NoE is a 'virtual laboratory' that will give all participants access to the biological resources, analytical tools, and technical/bioinformatics facilities they need. The work will combine population genetics with structural and functional genomics and will integrate research on different hosts and different diseases. The network will include activities aiming to assimilate knowledge, consolidate partner organisations and promote staff mobility.

The NoE will also emphasise putting results into practice, notably through technology transfer to industry. The network will communicate with industry via a 'club of interest' and interfacing with other scientists, networks and other sections of society is also planned. This is European Research Area (ERA)-building in action and, in the words of one workshop participant: "Networks like EADGENE could put European animal genomics back on the map."



Project summaries

During the workshop, coordinators of both completed or ongoing FP5-funded livestock genomics projects presented the aims and achievements of their research. The key features of the projects are outlined here, but for further details, see pages 16-31.

Sheep breeding for health, quality, and safety

Sheep farming for milk or meat is an essential economic activity in many areas of Europe. New breeding goals for sheep reflect the EU sheep sector's need to reduce production costs while increasing product quality and safety. The **Genesheepsafety** project aims to provide tools that will help breeders achieve these goals. Partners are attempting to identify quantitative trait loci (QTL), and ultimately, genes that contribute to traits such as milkability and mastitis resistance, out-of-season breeding, high levels of health-promoting molecules in milk, and resistance to parasitic worms and fly larvae.

Immunity in chickens

As a result of the disastrous consequences of uncontrolled infections in chicken flocks, it is useful to develop disease-resistant chicken breeds. To support this approach, the **Chicken-IMAGE** project has identified immunologically relevant chicken genes and studied their expression. The work has yielded tools, DNA resources, and a database, and has led to the identification of genes whose expression is either stimulated or inhibited in specific model infections or which are differentially expressed in resistant and sensitive chicken lines.

Mastitis-resistant cows

Mastitis is the most common and costly disease identified in dairy cows. The **Mastitis Resistance** project aims to develop tools for marker-assisted selection of mastitis resistance. This research will lead to identifying and refining mastitis-related QTL. It will also yield statistical methods (for both QTL fine-mapping and marker-assisted introgression between breeds), knowledge on the pathogen

specificity of identified QTL and on genes likely to influence sensitivity/resistance to mastitis, and a knowledge-based strategy for using mastitis resistance QTL in breeding programmes.

Biodiversity and rural development

Biodiversity management is another area where genomics can make a major contribution. This is important because genetic diversity is what makes it possible to improve existing breeds and derive new ones. The **Econogene** project focuses on the biodiversity of sheep and goats in Europe. Its originality lies in combining genomics, socio-economics, and geostatistics to construct maps linking biodiversity, conservation priorities with rural development perspectives. The work will lead to the identification of areas where sustainable conservation of valuable populations is most likely to succeed.

Pigs in Europe and China

In an example of important scientific collaboration between the EU and China, the **PigBioDiv2** project is expanding the European Pig Diversity Database (resulting from two previous projects) by adding data for 50 Chinese pig breeds. A further important goal is to link genetic diversity studies with the discovery of QTL and genes giving rise to breed-distinguishing traits. To achieve this, the PigBioDiv2 partners are refining the concepts and improving the methods and tools used to generate, interpret and exploit diversity data.

Beef quality: breed effects

Both genetic and environmental factors contribute to meat quality. The **Gemqual** project aims to sharply focus on this genetic component by studying quality trait variations in different cattle breeds reared and slaughtered under standardised conditions. Trait variations will be related to the variability of single nucleotide polymorphisms (SNPs) in candidate genes chosen for their likely involvement in both muscle development and composition.

Mapping for milk quality

The **BovMAS** project is providing a powerful platform for the future identification of genes involved in milk production and composition. The results will help EU milk producers maintain productivity while improving the nutritional quality of milk and paying increasing attention to animal welfare and the environment. The work could also lead to achieving genetic progress in minor European breeds equal to that of the major breeds, and may support the introduction (by classical breeding) of favourable gene variants from European breeds into low-production breeds in the developing world.

Higher-value pork products

To enable the selection of pigs that can better meet specific requirements for producing high-value products, the **Qualityporkgenes** project is aiming to identify, by means of gene expression studies, DNA markers for meat-quality traits such as fat cover and shape, marbling, etc. The link with pig welfare is also being addressed. Tools developed in the project may provide the basis for the development of novel quality detection systems.

Pork quality: prenatal effects

Because pork quality depends largely on genes expressed before birth in developing muscle, the **Pordictor** project is comparing gene expression patterns in various breeds at different stages of prenatal development. The work has yielded a shortlist of 50 promising genes showing breed- or stage-specific expression. Project partners will

study the variability of these genes with a view to identifying gene variants that contribute to either desirable or undesirable features in pork meat.

Protecting consumers and maritime resources

The **DNAIQ** project is developing DNA-based tools for identifying and quantifying fish and other seafood species in food products. Three ready-to-use test systems are undergoing validation testing in international end-user trials. Such systems will be precious tools in the hands of authorities charged with the protection of consumers and the prevention of fraud. They may also contribute to preventing overfishing of the seas and co-fishing of endangered species.





Identifying strengths to shape the future

The meeting culminated in a discussion on how to maximise the benefits of livestock genomics research for Europe.

Competition and consumers

Livestock genomics is a key to competitiveness for EU industry. For EU livestock breeders, this science is crucial to maintaining their competitive edge in a global market because it is yielding tools that will both accelerate breed improvement and give breeders a better grip on a wide range of traits that are not readily tackled by traditional breeding and selection. More generally, genomics has the potential to help the livestock sector as a whole, as well as the agro-food industry, notably by reducing losses resulting from common diseases among farm animals while making EU food products both safer and more attractive to consumers.

Food safety ranks high among consumer demands. Livestock genomics has a great contribution to make, particularly through more effective control of zoonoses, better understanding of host-pathogen interactions, and improved traceability. This science is also yielding tools for improving other quality features of meat and dairy products, from taste and texture to nutritional value and health-promoting effects.

There are various ways that the findings of livestock genomics can translate into public goods: improved animal health and welfare, data and tools for monitoring biodiversity and conservation, models of human disease, and systems for drug and vaccine development to name a few. Genomics can also be the key to a more productive and sustainable agriculture in the developing countries.

Harmony and tensions

In food safety and quality, consumers and industry share common interests. Yet there can be tensions between the twin targets of industrial competitiveness and the public good. For instance, emphasis on increasing productivity and reducing production costs is seen as having adverse effects on animal welfare and product quality.



There are other tensions, too. For example, genomics can be a two-edged sword as regards biodiversity, having the potential to reduce the gene pool through marker-assisted selection (particularly if breeding programmes are not carefully managed) while also able to improve the monitoring and conservation of genetic resources (see pages 22-24). In the light of such tensions, policy-makers and research sponsors must strive to strike a good balance when designing research programmes and selecting projects for funding.

Sustainability: a unifying concept

Livestock genomics might best be oriented towards sustainable, as opposed to primarily intensive, agriculture. Sustainability is indeed a unifying concept because, to be sustainable, an agricultural system must produce sufficient food at an affordable price, enable farmers to earn their living, promote competitiveness of the agri-food sector, avoid destruction of the environment and depletion of natural resources (including livestock gene pools), be attuned to consumer demands, and adopt technologies and practices that are acceptable to society.

The Thematic Network Sefabar (Sustainable European Farm Animal Breeding and Reproduction) has pointed out that there is no single recipe for making European farm animals globally competitive on a sustainable basis. Yet the different aspects of sustainability can be translated into concrete breeding goals, which in turn can serve to elaborate scenarios on which to base both strategic decisions and a constructive dialogue with stakeholders. This approach may be helpful in setting targets for livestock genomics research.

Europe's investment

Although Europe boasts some noteworthy firsts in livestock genomics, many participants stressed that the US has now taken the lead, particularly in the development of tools crucial both to the future of the discipline and to the competitiveness of EU industry. Countries such as Australia have begun to invest heavily in this field and the EU must likewise increase its investment if it wants a stake in future developments.

Despite contributing significantly to the sequencing of the genomes of the model organisms *Saccharomyces cerevisiae* (a yeast) and *Arabidopsis thaliana* (a plant), the EC has a limited track record in supporting whole-genome sequencing.

With funding from US agencies, the sequence of the chicken genome will soon be complete. Funding for the cattle genome sequencing is coming essentially from a consortium including NIH/NHGRI in the USA, Genome Canada, the Governor of Texas, and New Zealand, with possibly a minor contribution from one or more EU Member States. A Danish-Chinese consortium has tackled sequencing of the pig genome, and there is some US commitment to this endeavour. Several workshop participants called upon the EC to lever up pig genome sequencing. Not only would this benefit EU industry, they stressed, but it would also put Europe into the livestock genomics debate, rather than keep it sidelined. Yet the window of opportunity is small. Other industrially relevant species, such as duck, bee, fish, and seafood, would also benefit from the sequencing effort.

Synergy with industry

EU livestock breeders need methods combining genomics with traditional breeding so as to integrate molecular knowledge into breeding programmes. It is therefore important to involve breeders early on in livestock genomics research, and the same applies to other industrial stakeholders. In addition to closer collaboration between academia and industry, representatives of industry called for an improved exchange of ideas, open-source intellectual property, and support for SMEs.

One suggestion was to establish, with EC support, a technology platform that would receive input from a wide range of stakeholders. Its activities could include monitoring the experience of the new plant genomics ERAnet and Technology Platform on Plant Biotechnology, so as to benefit from any insights, experiences, and developments relevant to the livestock sector.

ERA-building

Genomics is 'big science' requiring large-scale collaboration. National livestock genomics initiatives have been launched in several Member States, and they are keen to link up internationally with other endeavours. Examples include the Dutch Bioinformatics project, the French genomics initiative AGENAE (focusing on cattle, trout, pig, and chicken), the German National Network for Genome Research, and the UK Centre for Functional Genomics in Farm Animals (ARK-Genomics). Clearly there is fertile ground here for building the ERA.

Access to data and tools

European livestock genomics is yielding a wealth of data and tools of great potential value both to industry and to research teams outside the projects that actually generate them. This raises the question of access.

While complete livestock genome sequences should probably be stored at the European Bioinformatics Institute in Hinxton (UK), together with the human and mouse sequences, individual data sets need to be treated differently. The vision with these is more like the type of solution developed within the EC-funded DataGrid project¹.

¹ <http://eu-datagrid.web.cern.ch/eu-datagrid/>



Led by the European Organisation for Nuclear Research (CERN), DataGrid aims “to build the next generation computing infrastructure providing intensive computation and analysis of shared large-scale databases (...) across widely distributed scientific communities”. Not surprisingly, genomics is one of the scientific fields singled out for this endeavour.

Access to genomics tools (e.g. cloned sequences) raises other issues, such as logistics, cost, and intellectual property rights. Some projects or centres have already developed a framework for making materials accessible to the wider scientific community. ARK-Genomics, for instance, operating on a cost-recovery basis, provides open access to over a million cDNA clones without any IP constraints.

Intellectual property

IP issues constitute a bottleneck at several levels. For livestock breeders, they are linked to the very nature of their trade: R&D involving animals takes a longer time than similar work with plants, and requires expensive facilities. In addition, farm animals are usually bred on the farm and not purchased each year like plant seed, and there is no equivalent in livestock breeding of “plant breeders’ rights”.

Within research projects, IP issues arise whenever there are commercial interests, and this applies to both industrial and academic partners. Such issues can restrict both collaboration and the sharing of tools and data. At the workshop, some participants called for EU-level, rather than partner-level solutions. It was suggested that over-burdensome IP issues might be avoided by keeping EU-funded research essentially precompetitive, leaving it to the industry to generate IP on the basis of this research. Emphasis on producing generic tools rather than on responding to specific developments might also be more compatible with the time frame of accessing public funding. In any case, there may be opportunities to help define solutions through research in FP6.

Beyond genes

Repeatedly, participants insisted that identifying genes and sequencing them is simply not enough. It is important to know which tissues express a given gene, the function of its product, how both gene expression and product function are regulated, and how gene, product, and processes involving them integrate into an animal's physiology, contribute to its features, and determine its responses to pathogens and environmental factors. In short, gene annotation and down-stream research such as functional/physiological studies are all crucial to the proper development of the field.

Conclusions and targets

The meeting provided an overview of the development of livestock genomics, concluding that:

- **Europe and the European Commission EU should invest more heavily in livestock genomics.**
- **Priorities include** *disease resistance in animals (especially zoonoses), sustainable production, product quality, enhanced animal welfare, and preserving biodiversity. There is also a need to develop controls for genetically modified animals from non-EU countries.*

Key targets include:

Developing the science, with the emphasis on, in particular:

- *gene annotation and functional studies;*
- *developing tools such as livestock-specific arrays, high-sensitivity DNA amplification technologies, bioinformatics tools and new software, preferably with free access;*
- *livestock genome sequencing; and*
- *comparative genomics.*

- . **Involving industry at an early stage**
- . **Addressing intellectual property issues**

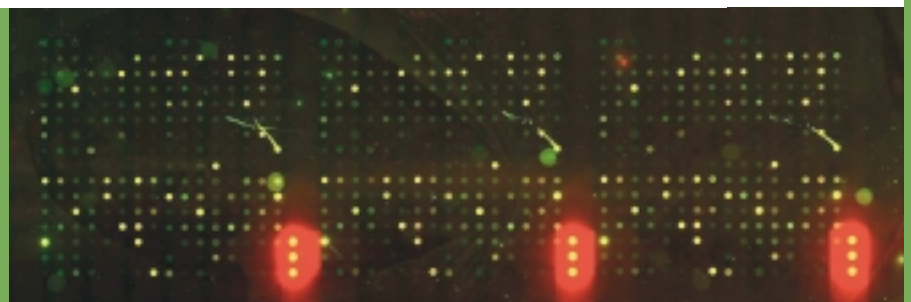
- **Risk-taking is necessary.** *A significant level of failure is the price to pay for making real advances in successful projects.*

Genomics for disease control

To ensure food safety, protect the health of farmers, minimise economic losses, and promote farm-animal welfare, it is important to keep farm animals healthy. Nevertheless, there is pressure to limit the use of antibiotics and other veterinary medicines so as to reduce the risk of residues in meat and dairy products and the emergence of drug-resistant pathogens. One way to reach both of these objectives would be to develop disease-resistant livestock breeds, which was a prime goal of three projects carried out under FP5.



© RBST 2003





Mastitis resistance in cattle

17

The most common and costly disease in dairy cows, accounting for the greatest use of antibiotics in these animals, is mastitis. Despite improved methods of prevention and treatment, the incidence of mastitis has not declined.

Mastitis resistance has been neglected in breeding programmes because it is hard to select for improvement of this trait by conventional means. One reason for this is the low heritability of mastitis resistance – i.e. the contribution of genetic variability to trait variability is minor. In addition, detailed veterinary records of mastitis are only kept in a few countries. As marker-assisted selection (MAS) offers breeders new opportunities for tackling such traits, partners in six European countries have launched the project entitled 'New breeding tools for improving mastitis resistance in European dairy cattle' (Mastitis Resistance).

The project is focusing on Nordic cattle populations for which extensive health and fertility trait records exist. Genome scans having shown that (roughly defined) mastitis-resistance QTL segregate in these populations, the goal is to confirm and fine-map these QTL – and possibly to identify new ones – so as to focus on the genes that underlie the variation

in mastitis resistance in dairy cattle. This involves combining different genome scans into a multi-population, multiple-trait analysis, improving statistical methods, identifying sets of markers associated with specific QTL variants, and dissecting the genetic basis of mastitis resistance.

From tools to strategy

Having recorded traits in, and collected DNA samples from, 88 half-sib families (families of animals sharing one parent), the project partners have selected seven promising chromosome regions for further analysis. For the fine-mapping of QTLs, they will use the radiation hybrid panel and maps constructed in an earlier EC-sponsored project (Comrad). As the work progresses, it should yield both tools and knowledge, in particular:

- **QTL variants** associated with clinical mastitis and/or somatic cell counts, mapped with sufficient precision to allow their use in MAS within a breed and marker-assisted introgression (MAI) between breeds;
- **new statistical methods** for fine-mapping QTL;
- **a statistical tool** for MAI of favourable QTL variants into new breeds;
- **knowledge on which to base further studies:** a list of candidate genes based on their positions (with partial knowledge of sequence variation), knowledge of association/non-association of candidate genes with mastitis resistance, and knowledge of differences in pathogen specificity among identified QTL variants; and
- **a strategy** for the use of identified QTL in breeding programmes, based notably on knowledge gained about how QTL associated with mastitis resistance affect other traits, and vice versa.

Contact:

Dr Johanna Vilkki
MTT Agrifood Research, Finland
johanna.vilkki@mtt.fi



© ROSLIN INSTITUTE

Genomics, chickens and immunity

The poultry sector is an important one in the EU economy, and chicken is the most widely accepted meat source worldwide. Intensive production has brought the price of chicken down, but it has led to the emergence and rapid spread of highly virulent pathogens causing massive losses on poultry farms while organically farmed hens are exposed to a wide range of pathogens.

Uncontrolled infection in chicken flocks can have disastrous economic consequences. As one solution may be to breed chickens that are more resistant to disease, the project Chicken-Image (Chicken Immunity and resistance to disease based upon analysis of gene expression) aims at identifying immunologically relevant chicken genes and to study their expression.

Resources and database

The work hinges on the construction of microarrays for gene-expression profiling. Microarrays have been made using DNA from two main sources. On the one hand, teams have exploited resemblances between the chicken and human genomes, i.e. the fact that genes present on a human chromosome are often found, in the same order and with similar

coding sequences, on a chicken chromosome. In the human genome, well-known clusters of immunologically relevant genes exist, with counterparts in the chicken genome. Teams have analysed the structure of five such clusters in the chicken, and have cloned and sequenced the genes they contain for use in microarrays.

On the other hand, partners have constructed normalised cDNA libraries from immunologically active chicken tissues. ESTs characterising the cloned cDNAs are listed in a database along with their lengths, sequences, clusters to which they belong, and similarity to known genes.

Gene expression profiles

To study the expression of immunologically relevant chicken genes, project partners are studying three model infections, caused by the infectious bursal disease virus (IBDV), the Marek's disease virus (MDV), and the parasite *Eimeria maxima*. These infections were chosen as they are widespread and can prove devastating in chicken flocks, and because they represent very different pathologies. Messenger RNAs were extracted before and after infection from tissues of birds belonging to sensitive and resistant lines. In addition, teams received spleen samples from two genetic lines of commercial birds, vaccinated or not against Marek's disease. The mRNAs were labelled with dye and used to measure the expression of the genes represented on the microarrays.

These experiments have yielded promising findings, such as genes whose expression level changes after IBDV infection, and genes differentially expressed, after infection, in sensitive and resistant bird lines.

Contact:

Dr Rima Zoorob
Centre National de la Recherche Scientifique,
France
Rima.Zoorob@vjf.cnrs.fr



© ROSLIN INSTITUTE



Improving the quality and safety of sheep products

19



Sheep production, whether for milk or meat, is located mainly in the less-favoured rural regions of Europe, and has great economic importance for populations in these areas. To be competitive and to offer products that are attractive to consumers, the EU sheep sector needs breeding programmes focusing on new traits that contribute to reducing production costs and increasing product quality and safety (aptitude for mechanical milking, resistance to diseases such as mastitis, parasitic nematode or nasal fly infections, traits reducing the risk of food contamination and zoonoses, meat- or milk-quality traits, etc.).

Overcoming limitations

Many traits for which today's breeders would like to select are difficult to measure, but genetic maps based on molecular genetic markers are provid-

ing new tools for trait selection. To exploit these tools, several regional projects have been launched, aiming to explore the sheep genome and to identify quantitative trait loci (QTL). Yet these projects tend to neglect traits related to product quality and safety, either because they are too small or because they do not combine all the necessary expertise. To overcome these limitations, several regional programmes have joined forces in a project called 'Genesheepsafety - using genetics to improve the safety and quality of sheep products'. It involves six partners in four countries: France, Spain, Italy, and the United Kingdom.

Tackling traits

The Genesheepsafety project involves maintaining and sharing five 'resource populations' of sheep, marker-typing the populations, measuring traits, identifying QTL, and examining the expression and effects of candidate genes. The project partners are focusing on production traits and on the following Genesheepsafety traits:

Conjugated linoleic acid (CLA) in sheep milk. This is a product quality trait as it seems that dietary CLA may confer to human consumers some protection against diseases such as cancer and atherosclerosis. Here the aim is to correlate CLA levels in milk samples with genetic-marker variability, so as to identify QTL involved in CLA synthesis. In parallel, one team will study variations in the expression of candidate genes believed to encode key enzymes in milk fat and CLA synthesis.

Resistance to mastitis and milkability. Mastitis is a bacterial infection of the udder. It is the second cause for culling dairy ewes and has a direct adverse effect on the quality and safety of milk products. Mastitis in ewes is often subclinical – i.e. the animals do not appear to be sick. Therefore, the measured traits for QTL detection are somatic cell counts for mastitis and a score based on udder morphology for milkability (aptitude for machine milking). Because some udder features linked to milkability are likely to have negative effects on mastitis resistance, researchers will study the relationship between both these traits in high- and low-scoring lines of the same breed.

Resistance to parasitic worms (nematodes) and fly larvae (nosebots). These common parasites have adverse effects on both productivity and animal health/welfare. In addition, the increased incidence of resistance to anthelmintics (anti-worm drugs) in nematodes in sheep makes seeking an integrated approach, including a genetic strategy, of prime importance. Moreover, some of the drugs used to eliminate these parasites raise concerns about contamination of products and the environment. Project partners are seeking resistance QTL on the basis of antibody concentrations (worms, fly larvae) and faecal egg counts (worms). A candidate gene approach is also being carried out for major histocompatibility complex (MHC) and nematode resistance.

Out-of-season breeding. The existence of seasonal anoestrus in ewes imposes major constraints on production. To solve this problem, sheep farmers use hormone treatments to control their ewes' reproductive activity. This raises issues such as consumer concerns about hormones or the possible transmission of pathogens through hormone preparations. The existence of breed differences in out-of-season breeding offers the opportunity to identify QTL for spring fertility.

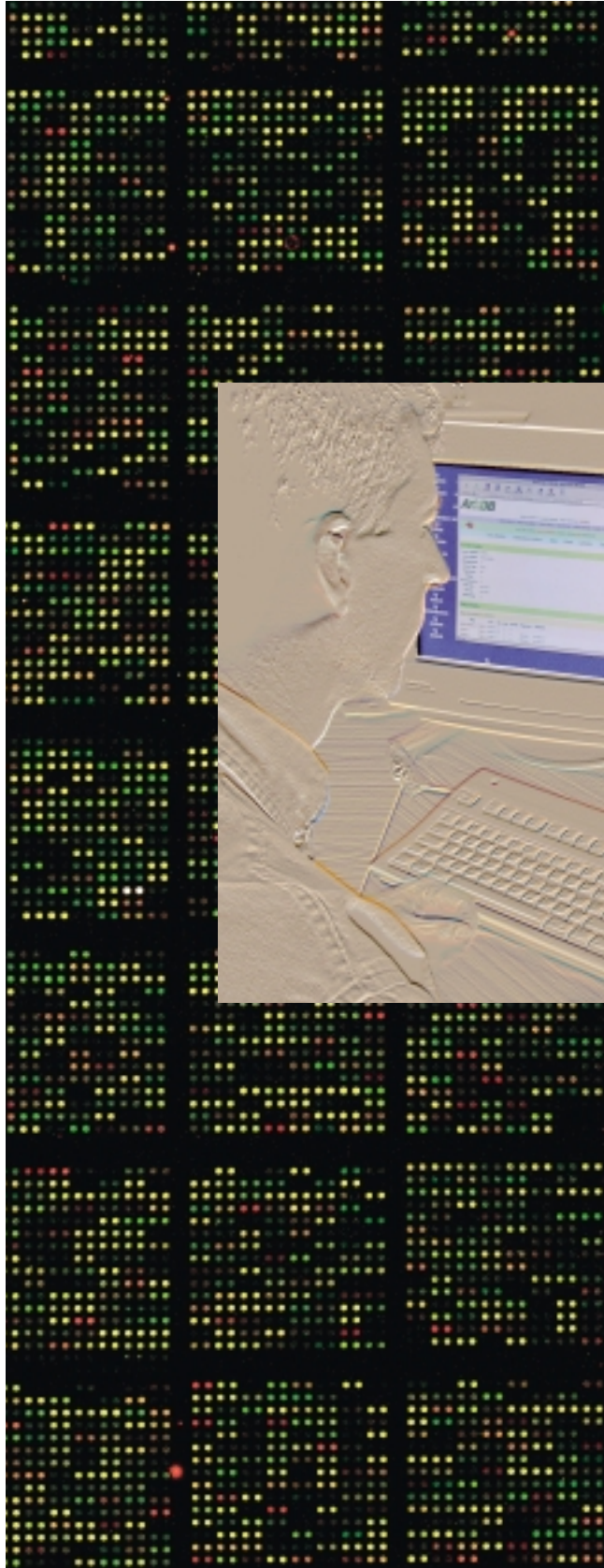
Results

So far, genome scans performed by Genesheep-safety partners on resource populations have led to detection of QTL for several traits of interest: milk yield, milk composition (notably CLA), resistance to nosebots, and resistance to nematodes.

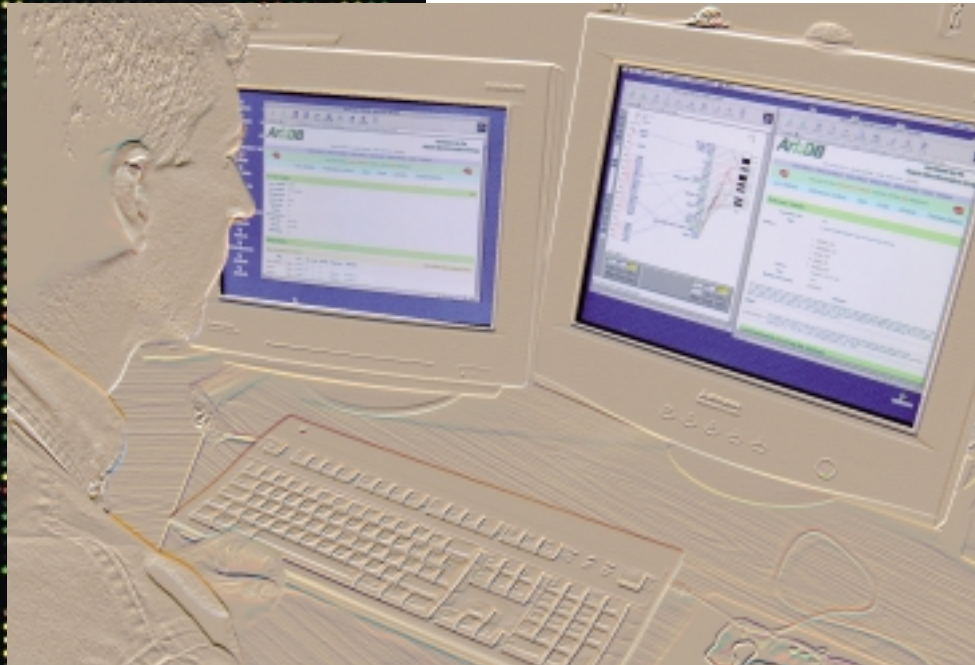
In one CLA-related QTL, a likely candidate gene has been found which codes for an enzyme believed to catalyse a step in CLA synthesis. The partners will study the expression of this and other candidate genes in animals representing high and low extremes of CLA in ewe milk. Another question addressed is whether chromosomal regions associated with given traits of interest are the same in cattle and sheep.

Contact:

Dr Francis Barillet
Institut National de la Recherche Agronomique
(Toulouse, France)
barillet@germinal.toulouse.inra.fr



© ROSLIN INSTITUTE



Genomics for biodiversity

We cannot predict today which gene variants will be needed to meet tomorrow's breeding challenges, so it is crucial to maintain a reservoir of genetic diversity in livestock. Yet, on a global scale, an estimated 1 000 livestock breeds are at risk of extinction. The very process of trait selection tends to reduce within breed variation, and marker-assisted selection, if applied without caution, could accelerate the loss.

Sustainable management of genetic resources, expressed in balanced breeding programmes and well-targeted conservation strategies, is the key to preserving livestock biodiversity. It requires good tools and sound knowledge. Here, genomics has an essential role to play as it can:

- provide tools for monitoring and minimising the loss of within-breed and within-species diversity;
- make it possible to exploit the entire gene pool as a source of favourable gene variants that have either been lost from or have never been present in the few cosmopolitan highly selected breeds adapted to intensive production;
- enable better management and selection of local populations (often too small for the successful application of traditional breeding programmes),
- contribute to enhancing the economic value of typical products derived from original breeds, through better traceability and characterisation.



© RBST 2003



Biodiversity's role in rural development

Global climate change, environmental challenges, the emergence of new livestock diseases, changing consumer demands and agricultural policies... factors such as these make it necessary to adapt breeding goals over time. It is therefore crucial to maintain genetic diversity, the foundation for all breed improvements. For this we need to know where biodiversity is threatened. We need a basis for predicting how policy measures, breeding strategies and the use of new technologies will affect the gene pool. In addition, efforts to maintain biodiversity must integrate harmoniously into the socio-economic context.

The project 'Sustainable conservation of animal genetic resources in rural areas: integrating molecular genetics, socio-economics, and geostatistical approaches' (Econogene) is a multi-disciplinary approach to achieving sustainable conservation of sheep and goat genetic resources. The consortium includes 11 partners, 11 subcontractors, and four additional contributors in 16 countries. The idea is to link a map of conservation priorities with a map of rural development perspectives and so identify areas where sustainable conservation of valuable populations could succeed.

Maps and more

To identify conservation priorities, teams have collected biological samples from over 3 000 animals representing 56 sheep breeds and 44 goat breeds, together with the GPS (Global Positioning System) coordinates of the farms concerned. They have developed molecular tools optimised for the analysis of both maternally and paternally inherited genetic material (mitochondrial and Y chromosome DNA respectively), polymorphic markers, and those expressed sequences likely to affect disease resistance, product quality, and yield. Novel tools include, in particular, DNA arrays and a new technology for SNP discovery and typing.

In parallel, partners are collecting and analysing breed demography, animal husbandry, and production data from over 500 farms in the EU. This work supports the construction of models for estimating the economic value of biodiversity in different regions. Six case studies are also planned, and teams are developing new statistical methods to link the biodiversity map with the socio-economic data. Associated with the project are a website and a database, and the consortium has established links with other sheep and goat projects concerning biodiversity.

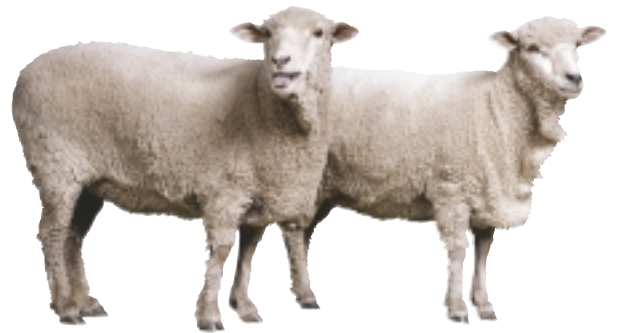
Econogene will serve as a reference for future sheep and goat biodiversity projects. Its findings will support decision-making for both genetic management and rural development, in harmony with common agricultural policy (CAP) objectives.

Contact:

Paolo Ajmone-Marsan
Catholic University of the Sacred Heart, Piacenza,
Italy
paolo.ajmone@unicatt.it

Eradicating scrapie

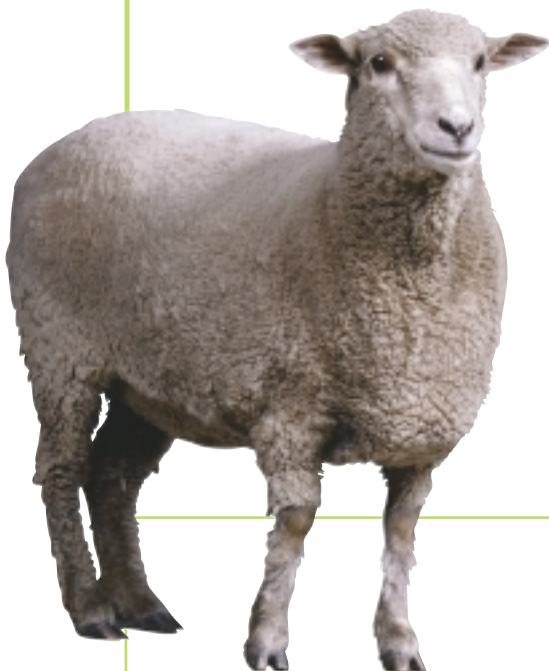
Scrapie is a transmissible brain disease found in sheep and goats (similar to bovine spongiform encephalopathy (BSE), or mad cow disease). There is no evidence of scrapie being transmitted to humans, but it is fatal in sheep and goats. In addition, there is uncertainty as to whether BSE might be present in these animals, and there is no validated routine diagnostic method for distinguishing BSE from scrapie in sheep and goat populations.



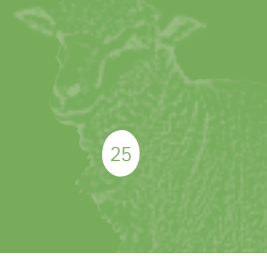
Some animals are resistant to scrapie, and the gene variant responsible for scrapie resistance is known. What is more, experiments suggest that the same gene variant confers protection against BSE infection.

For these reasons, and on the basis of an opinion produced by the EC Scientific Steering Committee, Commission Decision 2003/100/EC requires each EU Member State to introduce a breeding programme for the selection of scrapie resistance. Participation in a national programme will be compulsory from 1 April 2005, although, to limit the potential loss of local breeds, there will be some derogations.

Workshop participants discussed the likely impact of scrapie-resistance breeding programmes on sheep and goat biodiversity. Some expressed the fear that selection for a single gene variant will reduce the gene pools of these species. They noted that the diversity-reducing effects of breeding programmes are usually limited by the fact that breeding goals take more than one trait into account. Other participants felt that if scrapie eradication is managed so as to take the situation of each breed into account, diversity loss can be minimised.



Monitoring of the 'scrapie gene' and its variants is included in the Econogene project.



Measuring biodiversity in pigs

To measure biodiversity, it is not enough simply to record trait differences, because both genetic and environmental factors contribute to an animal's appearance and performance. The study of genetic marker variability makes it possible to measure genetic diversity directly. Three successive EC-sponsored projects have tackled this task in the domestic pig. The first two (PiGMap and PigBioDiv1) used anonymous markers (markers not related to a particular function) to characterise genetic diversity in 70 European pig lines and breeds. They yielded two valuable resources: a DNA bank of European breeds and a European Pig Diversity Database (<http://www.projects.roslin.ac.uk/pigbiodiv/>).

Now the project PigBioDiv2 (Characterisation of genetic variation in the pig breeds of China and Europe to facilitate the maintenance and exploitation of biodiversity) will extend this approach to 50 breeds of Chinese pigs.

Distant relations

In both Europe and China, most commercial lines are derived from a small number of breeds. However, many traditional/rare breeds do still exist, representing considerable biodiversity. In addition, Chinese breeds show some particularly interesting features.

The PigBioDiv2 partners will extend the Pig Diversity Database by typing in the Chinese breeds the same markers that were used in PigBioDiv1. The markers present on (maternally inherited) mitochondrial DNA and the (paternally inherited) Y chromosome will also be studied, and care will

be taken to ensure the compatibility of new and existing data. This will make it possible to compare European and Chinese breeds and to estimate genetic distances between them. In addition, PigBioDiv2 will interface with other projects focusing on wild pig species.

One important aim of the project is to link diversity studies with the discovery of QTL and genes that give rise to breed-distinguishing traits. This research goes beyond fact finding – it requires refining the concepts and improving the methods and tools used to generate, interpret, and exploit diversity data. This means answering questions such as: how are diversity estimates based on anonymous markers related to the diversity of genes that contribute to a breed's distinguishing features?

One approach is to study the variability of genes known to influence traits, such as coat colour, litter size, appetite, and growth, etc. Another is to develop tools for identifying such genes without conducting a mapping experiment. The idea is to locate 'footprints of selection', where variability decreases with proximity to a trait gene that has undergone selection over many generations.

In addition to its scientific and economic interest, PigBioDiv2 is an example of fruitful scientific collaboration between the EU and China.

Contacts:

Dr Sarah Blott

Sygen International plc (Cambridge Laboratory)
scb42@cam.ac.uk

or

Prof Li Ning

China Agricultural University (Beijing)
ninglbau@public3.bta.net.cn



Genomics for meat and milk quality

Selective breeding has been very successful at increasing productivity – through selection for high milk yields or growth rates, for instance – but there has been limited selection of those traits related to product quality. Genomics offers the opportunity to identify markers associated with quality features (meat tenderness or juiciness, milk composition, etc.) for use in marker-assisted selection. It is also providing tools for tracing animal ingredients in foods. Five FP5 projects are bringing genomics to bear on the challenge of improving animal product quality.



© ROSLIN INSTITUTE



© MTT archive/Yrjö Tuunanen



Beef quality: genetics vs. environment

There is mounting evidence of breed (i.e. genetic) differences in beef quality, but it is hard to discern the genetic component because much of the variation in quality comes from environmental differences such as production systems, age at slaughter, or the way animals are handled prior to their slaughter. The Gemqual project (Assessment of genetic variation in meat quality and the evaluation of the role of candidate genes in beef characteristics, with a view to breeding for improved product quality) aims to identify gene variants that contribute to product quality, as a basis for producing higher-quality beef in a commercially viable way.

Breeds and candidates

The project counts ten partners in five countries, combining expertise in molecular biology and genetics, meat science, breeding, and production. The idea is to take different breeds of cattle and to raise and slaughter them under standardised conditions, so as to minimise environmental effects on beef quality. By measuring the quality of meat from these animals, it should be possible to establish breed-related quality differences. Quality is assessed on the basis of both objective physico-chemical measurements (shear force, fat) and more subjective sensory analyses.

Teams are also looking for SNPs in candidate genes chosen for their likely involvement in muscle development and composition and will then search for correlations between SNP variability and recorded differences in quality.



Results and prospects

Work up to April 2003 on 218 candidate genes has led to the identification of 372 SNPs and the hunt for gene variants able to influence beef quality has begun. Examples of candidate genes include the leptin gene (the so-called 'obese gene', variants of which appear associated with increased feed intake), and the myostatin gene (which is partially responsible for double muscling in Belgian Blue cattle).

Data from the nearly complete Bovine Genome Sequencing Project will feed this research. Many ESTs are available, and the project teams are developing microarrays for expression profiling.

Contact:

John Williams
Roslin Institute, UK
john.williams@bbsrc.ac.uk

Mapping for milk quality

Genomics offers the opportunity to optimise milk for qualities such as nutritional value or health-promoting effects. A step in this direction involves the BovMAS project (Quantitative trait loci affecting milk production: mapping and utilisation for marker-assisted selection in dairy and dual-purpose cattle), which aims to produce a moderate-resolution, high-power map of QTL affecting traits related to milk production, milk composition (percent protein and fat), somatic cell count, calving difficulties and fertility.

The five project partners (located in Germany, Austria, Italy, and Israel) are focusing on five resource populations: three dairy breeds, one dual-purpose breed, and a backcross of dairy to dual-purpose breed. With over 150 000 'daughters' belonging to 47 half-sib families, the BovMAS mapping population may become the most powerful of its kind worldwide.

Logistics and strategy

Milk is used as the source of DNA for marker typing. For sample collection, the teams have developed methodologies requiring minimal extra effort for existing milk recording systems. The BovMAS genome scans cover 158 to 210 markers, depending on the resource population studied.

To limit the number of marker-typing analyses, the partners have adopted a DNA-pooling strategy based on the assumption that marker variants closely linked to favourable gene variants should be over-represented in high-performance cows (and, conversely, marker variants linked to unfavourable gene variants should be over-represented in low-per-

formance cows). Each cow is scored according to performance criteria for each trait, and four DNA pools are constituted for the progeny of each (individually genotyped) sire: two corresponding to the highest-scoring daughters (the top 10%) and two to the lowest-scoring daughters (the lowest 10%). Marker-variant frequencies are then determined in these pools. This strategy enables BovMAS to access approximately half the power of a conventional study at only 2% of the cost. Its application can make genome-wide QTL mapping accessible to moderately sized breeding organisations.

QTL and more

So far, genome scans have highlighted some 40 genome regions affecting milk production traits. Two QTL, showing strong effects in a few bulls, provide the first candidates for the next step, high-resolution mapping.

Intent on applying their findings to MAS, the partners are developing a simulation study and application protocol. For this they have adapted a comprehensive software from an Australian pig enterprise to the dairy cattle scenario.

BovMAS should lead to a quantum leap in the efficiency of dairy cattle genetic improvement programmes, paving the way for similar progress with other livestock breeds.

Contact:

Prof Alessandro Bagnato
University of Milan, Italy
alessandro.bagnato@inimi.it





Genes, pig welfare, and pork quality

For the EU pork industry, one key to remaining competitive is the ability to develop higher-value products. In particular, this means producing meat of consistently high quality, a feature determined by traits such as fat cover and shape, marbling, muscle pH, rate of proteolysis, and colour. The importance of such traits differs according to the market or product.

Pork quality depends on how pigs are fed and reared, on the conditions that prevail during transport and slaughter, on carcass and meat-processing procedures, and also on genetics. Although the notorious 'halothane gene', for instance, favours muscle development and meat leanness, it also makes carrier pigs highly susceptible to porcine stress syndrome, which is responsible for high pig mortality during transport to the abattoir and lairage, and results in meat which is pale, soft and watery. This highlights the link between genetics, meat quality, and animal welfare.

Identification parade

The project Qualityporkgenes (New gene tools to improve pig welfare and the quality of pork) aims to identify the genes responsible for variations in pork meat quality, including the relationship with stress and animal welfare. Project results should contribute to the development of tools for both breed improvement and quality assurance.

One task has been to create a unique database of muscle and meat phenotypes (observable/measurable features). For this, partners have recorded in excess of 300 individual traits including more

than 100 carcass and meat-quality traits in samples taken from 500 pigs representing five genetically diverse commercial breeds. Recorded data range from carcass composition to mechanical meat characteristics, metabolic, biochemical and neuroendocrine data, and the results of sensory analyses. Samples from loin and ham muscle were taken from each animal for detailed molecular analyses.

Another objective is to produce cDNA libraries and microarrays to analyse gene expression in muscle at slaughter, so as to relate meat-quality features to the expression of specific genes. This is currently in progress – work with preliminary arrays has already yielded interesting results, such as differences in gene expression between loin and ham muscle. To further understand relationships between gene expression and meat quality, partners are developing proteomics tools to study the proteins present in meat displaying different quality features.

A third objective is to use microarrays and proteomics tools developed in the project to identify markers that explain variation in meat quality (metabolic, biochemical, or neuroendocrine markers, candidate genes or other DNA markers). These may provide a basis for the development of novel quality detection systems.

Contact:

Dr Graham Plastow
PIC International Group, UK
Graham.Plastow@sygeninternational.com

Pork quality and muscle development

In the past, pig breeding has focused on increasing the production of lean meat. Although this has been successful it has, arguably, had an adverse effect on pork quality. In addition, meat quality and carcass traits can only be measured after slaughter, and the public's perception of high-quality pork is not uniform and is subject to change. To facilitate the task of breeding for quality, the PorDictor project (New predictors for pork quality derived from gene expression profiles of skeletal muscle during prenatal development) aims to identify candidate genes that might control meat quality traits, to confirm their effect on meat quality, and to develop DNA tests which are suitable for use in breeding programmes.

Muscle power

Meat is muscle tissue. Meat quality and quantity are related to the number, distribution, relative proportions, and properties of different types of muscle fibres, and these features are largely determined before birth, by prenatally expressed genes. To identify gene variants associated with meat quality traits, the PorDictor partners are studying gene expression in skeletal muscle at different stages of prenatal development. The strategy is to identify candidate genes showing breed- or stage-specific expression and then to screen the most promising among these genes for polymorphism linked to quality trait variability in commercial pig populations.

Stage by stage

The PorDictor partners are focusing on two pig breeds, Duroc and Pietrain, the former being clearly superior to the latter as regards meat taste, juiciness, toughness, and colour. Having

defined seven key stages of muscle development in pigs, teams have collected fetuses from both breeds at each stage, obtained skeletal muscle samples from these fetuses, and extracted mRNA from the muscle samples for use in expression profiling. In parallel, they have characterised muscle features in the fetuses and in their full sibs so as to determine estimated breeding values and correlate them with expression patterns.

Teams have used various techniques to detect genes with breed- or stage-specific expression patterns (microarrays based on genes known to be involved in muscle formation or derived from prenatal muscle tissue, differential display, and subtractive hybridisation). The work has yielded about 300 functional candidate genes for meat quality, showing breed- and/or stage-specific expression. A shortlist of the 50 most promising genes has been established and their differential expression confirmed. Future steps will be to map these genes, to determine whether their expression is associated with specific meat-quality features and to detect SNPs within them with a view to performing genetic linkage and association studies.

Contact:

Dr Klaus Wimmers
University of Bonn
kwim@itz.uni-bonn.de



Seafood and consumer protection

Consumer protection notably means ensuring that a product's label and price reflect its nature and quality. In the case of seafood products, this goes hand in hand with avoiding over-fishing of the seas and the co-fishing of endangered species. Enforcement of food regulations requires sensitive, reliable, practical methods for identifying food ingredients and their actual concentrations.

Traditional methods for determining identities and amounts of seafood species in a product rely on detection of chemical compounds or species-specific proteins. Problems with protein tests include the ease with which some proteins are denatured by processing, such as smoking, cooking and canning, and the fact that different organs or tissues produce different proteins. Genomics offers a new solution here: the detection and quantification of specific DNA sequences. This is promising because DNA is comparatively heat stable and each cell of an organism contains a copy of its genome.

The project DNAIQ (Fish and seafood identification and quantification) aims to develop DNA-based identification and quantification methods for use in quality control and fraud prevention in the fish and seafood sector.

PCR and DNA arrays

One task has involved collecting raw fish/seafood and processed products from trawlers, supermarkets, and food companies. In parallel, teams are developing detection systems for monitoring and quantification. In particular, these systems exploit the 'Polymerase Chain Reaction' (PCR) by which a DNA sequence present in very few copies – even when processing has degraded the DNA to small fragments

– can be amplified for better detection. Real-time PCR, a more recent development, has made PCR applicable to measuring the abundance of a sequence in a sample. Emerging applications are put to the test in validation studies, first among partners and then in collaboration with end-users.

Another analytical tool which has been developed within the project comprises DNA arrays containing probes that are able to 'recognise' sequences of interest.

In-depth analysis

To date, the teams have been able to identify over 60 different species and have developed highly sensitive quantitative assays for detecting either species-specific sequences or a general fish-specific DNA sequence. Three ready-to-use test systems now await validation in international trials, which will be conducted by over 35 end-users in nine European countries. Work on systems for other species is currently in progress.

So far, DNAIQ has focused mainly on raw seafood samples, but studies are planned on samples which have already undergone a wide range of processing procedures. Other plans include contributing to standardisation of the genomic approach in seafood analysis, setting up the basis for the analysis of genetically modified fish, and making fish sequence data from the project and from public sources available in a European database.

Contact:

Olaf Degen

GeneScan Analytics GMBH, R&D, Berlin/Teltow, Germany

olafgenescan@web.de or o.degen@genscan.com

This publication records the proceedings and discussion of a meeting in Brussels on 10 September 2003. It forms one of a series published by the Directorate-General for Research reflecting on agricultural research from the Fifth Framework Programme.

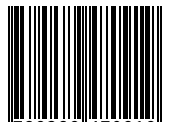
Further information on the projects under the Framework Programmes for research is available on the web at http://europa.eu.int/comm/research/agriculture/index_en.html



Publications Office

Publications.eu.int

ISBN 92-894-7091-7



9 789289 470919