A decade of EU-funded

animal production research

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Contents

Introduction

With the global population projected to reach 9 billion by 2050, a 70% increase in total food request and a double demand for livestock products will occur. Increasing productivity throughout the whole chain is therefore essential if we want to meet a growing demand, whilst minimising its impact on the environment and the world's natural resources.

Improving livestock productivity encompasses many management aspects, such as higher nutrition efficiency, decreasing greenhouse gas emissions and optimising the use of waste. Preserving animal health is key as healthier animals use resources more efficiently, experience higher standards of welfare and produce safer food. Optimised fertility and longevity reduce the ecological footprint of livestock. The preservation of breeds adapted to the local environment helps maintain good productivity even in sub-optimal conditions.

Innovation has a central role in livestock systems. Advanced knowledge in genomics, the development of high throughput tools and the characterisation of new biological traits paves the way to more sustainable breeding schemes. Information and Communication Technology tools allow the continuous monitoring of farm animals and control systems that greatly improve the management of individual animal needs at all times, even when the production scale reaches industrial proportions.

This catalogue brings together the fruits of European efforts during the Seventh Framework Programme for Research and Innovation (FP7). Targeting various features of animal production, it includes over 30 projects with a total budget approaching EUR 100 million. The scope of the work is large, ranging from innovative feeding methods and enhanced management systems to efficient selection schemes relying on new genomic data, and on the discovery of different biomarkers related to robustness.

Thanks to these results, Europe retains a leading position in livestock production which is an important sector within the bio-economy. This publication highlights the impact of our funding on guaranteeing both food security and food quality for all European citizens while reducing the negative impact of livestock on our natural environment as far as possible.

In the coming years, Horizon 2020 will go beyond FP7 in scope and ambition with projects solving specified societal challenges. In many cases, it will mean multidisciplinary, multi-actor actions that bring together different competences across Europe and beyond.

Sharing research results widely will help create new opportunities for innovation and will secure sufficient supplies of safe and high quality food and other bio-based products, accelerating the transition to a sustainable European bioeconomy.

Nutrition

Nutrition

A growing world population demands agricultural systems that increase the volume of food produced, and livestock products in particular, which are seen as a key source of dietary protein. This increase in production must be achieved with limited resources and minimal ecological footprint.

Nutrition is a key component of farmers' toolkits here. But to maximise nutrition efficiency, more knowledge is needed on the impact of diet – both its content and how feed is given. A greater understanding of the interaction between diet and the recipient is also required..

Feed efficiency is a complex parameter, influenced not only by ration composition, but also by specific nutrients, management factors, animal health status, microbiome and genotype – and the interaction between each of these elements.

The projects in this chapter tackle challenges such as optimising rumen function to reduce nitrogen or methane excretion, identifying the regions of the bovine genome associated with feed intake efficiency and understanding microbiomes and gut function – and the way they interact with one another. One project also looks at the problems faced by small and medium-sized enterprises wishing to develop and market novel feedstuffs.

[RedNEx]

Innovative and **practical management** approaches to reduce nitrogen excretion by ruminants

Keywords

Nitrogen utilisation, ruminants, monitoring tools.

Summary

Dairying is an important sector of EU agriculture, but intensification has been accompanied by an increase in nitrogen (N) surplus. This has a negative environmental impact. The EU seeks to stimulate measures that improve the management of nutrients, waste and water as a first step towards management practices beyond 'usual good-farming practice'. The objective of RedNEx is to develop innovative and practical management approaches for dairy cows that reduce N excretion into the environment through the optimisation of rumen function, leading to improved understanding and prediction of dietary N utilisation for milk production and excretion in urine and faeces.

Problem

In the EU, 25 million dairy cows produce more than 130 billion tonnes of milk per year, providing an annual income for the 2.8 million dairy farmers of more than ca. € 40 billion. However, dairying within the EU is becoming more intensive and more specialised. As intensification increases, the application of nitrogen fertilisers and manures usually rise to levels exceeding crop requirements or the ability of the soil to retain them.

Increasing milk yield from 8 700 kg to 20 500 kg per hectare in Dutch farms raised the N surplus from 376 to 650 kg per hectare. Increasing intensification of dairy production thus have potential impacts on groundwater (pollution with nitrates) and surface water (eutrophication), as well as on the atmosphere (de-nitrification and ammonia volatilisation). Therefore measures that improve the management of nutrients, waste and water are needed. RedNEx is contributing to the scientific and technical data required for policy measures that reduce N input and consequently N losses during the production of milk and meat by ruminants, and providing a methodology to translate this data into practice.

Aim

The central focus of the project is to provide the dairy sector with approaches that reduce N input on dairy farms without a substantial reduction in N output via consumable proteins in the form of milk. The specific objectives are to:

- Develop standardised rapid tools to measure fermentation characteristics of feeds;
- Improve feeding strategies to provide low-N rations to high-producing dairy cattle;
- Provide a better understanding of amino acid absorption, metabolism and secretion in milk;
- Stimulate N recycling within the animal while reducing total N inputs;
- Develop biomarkers in urine, plasma or milk to monitor the nutrient status in dairy cows;
- Develop and expand predictive models of N output at cow and herd levels;
- Disseminate knowledge of N management on dairy farms.

Expected results

The main outputs of REDNEX can be summarised as follows:

Rapid analytical techniques (FTIR and NIR spectroscopy) have been developed to estimate degradation characteristics of protein and fibre. In fact, lowering dietary N far below present recommendations decreases the digestibility of organic matter and fibre and consequently energy intake and animal performance. The rumen microbial population does not adapt to protein underfeeding by increasing the efficiency of microbial protein synthesis. Attempts to reduce the protein degradation by influencing the ruminal microbial population were unsuccessful.

Compared to fibre-rich diets, starch-rich diets resulted in a more than an 8% increase in N use efficiency (milk N output / N intake) in dairy cattle. Correcting the amino acid profile of metabolisable protein to obtain an "ideal" amino acid profile increased the efficiency of metabolisable protein. Using this amino acid balance it is possible to lower dietary N content, resulting in reduced N excretion and metabolic protein supply while maintaining animal performance.

A large proportion of ammonia hydrolysed from recycled urea never reaches the rumen pool, and this may be an obstacle to using recycled urea to improve N efficiency of dairy cattle. Advanced mechanistic models of gut wall and liver metabolism were successfully developed and evaluated.

A variety of analytical methods have been used to analyse samples in the search for new biomarkers of the efficiency of N utilisation and N sufficiency. This has highlighted the use of previous biomarkers, such as purine derivative excretion in urine and the secretion of odd-and-branched-chain fatty acids in milk, and has indicated the potential of several new markers, which are undergoing further investigation.

N excretion per cow may vary from 107 to 138 kg per year, in relation to N content in the diet and level of production. Nitrogen excretion per tonne of milk varied from 10 to 18 kg and this variation is significantly linked to urinary N excretion. These results clearly show that it is possible to make significant progress in reducing N output by a dairy herd.

Potential applications

The project will result in two mathematical models. The first will give insight into protein flows within the dairy cow, which will be a helpful tool for nutritionists in formulating low protein diets without disturbing essential pathways and processes in the digestion, absorption and metabolism of amino acids.

The second model, COWNEX, will estimate the effect of herd and feeding management on the excretion of nitrogen at herd level. This can be used as a tool for strategic and operational management, and as an estimator of nitrogen utilisation.

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Project website

www.RedNEx-fp7.eu

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- European Association of Animal Production, IT

[SMEthane]

Technological platform to develop **nutritional additives** to reduce methane emissions from ruminants

Keywords

Ruminants, methane, additives, greenhouse gases.

Summary

SMEthane addressed some of the restrictions that small and medium-sized enterprises (SMEs) face in developing and marketing novel compounds – in particular plant extracts – capable of decreasing methane production from ruminant animals.

Problem

Methane (CH4) is the second most important greenhouse gas, after CO2. At a global scale, livestock farming contributes up to 18% of total greenhouse gas emissions. In Europe, almost all livestock-related CH4 emissions arise from fermentation in the digestive tract of herbivorous animals (70%) and in their waste (30%). In order to improve the greenhouse gas balance of farming, methane production by ruminants must be reduced and in particular the methane produced in the digestive tract.

Various approaches to reducing methane emissions from enteric fermentation have been studied. The use of different biotechnologies to modify the microbial ecosystem in the rumen, and more recently, the development of new food additives (mainly based on plant extracts) to decrease rumen methane production, have been reported. Despite optimistic announcements in the press, plans for their implementation appear premature. This is because trials are performed under conditions far removed from the field, mainly tested *in vitro*, and with a limited number of diets that cannot be applied to the wide range of ruminant production systems in Europe. The variability and contradictory nature of the results reported prevents/restricts the uptake and use of these new compounds in the animal feed market.

Aim

To provide SMEs with scientific and technological knowledge to advance the development of animal nutritional additives that will reduce methane emissions and improve animal productivity.

Results

The results of stability tests showed that the pelleting process may contribute to a loss of between 8% and 74% of the antimethanogenic activity, while storage temperature accounted for a variable loss (from 0% at 4ºC to 80% at 30ºC). Whether the active compound had been protected – especially those with high volatility – also had a great impact on the losses.

The *in vitro* screening showed variable antimethanogenic activity, depending on the active molecule: up to 28% for essential oils, 8% for saponins and 63% for organosulphorous compounds, in a range of 200 to 600 ppm. However, the effect was largely influenced by the basal diet and by the pH. The compounds with more potential were further tested *in vivo* in small ruminants at three levels of inclusion within the diet over seven-day treatment periods.

Overall, most of the compounds confirmed their potential, but the concentration needed to reach the same effect as reported *in vitro* was much higher. When the compounds were tested in cattle over 42 days, the results revealed a lesser effect than in small ruminants in some cases. But in other cases, the reduction of methane observed (up to 32%) did take place after 2-4 weeks of treatment. Analysis of the milk from treated dairy cows showed no transfer of the essential oils used, but organosulphorous compounds were present.

Three workshops were held in the UK, Spain and France, several companies from the European feed sector attending. All materials presented in the three workshops are available at www.smethane.eu

Potential applications

The project has significantly advanced knowledge or technological progress by:

- Describing for the first time the correlation between *in vitro* and *in vivo* data (such an established relationship would greatly facilitate the development of these products).
- Developing a novel *in vivo* screening system that allows rapid testing of compounds of interest in appropriate animal models.

- Providing data on dose response curves to plant extracts *in vitro* but also *in vivo* (vital information for the development of new products).
- Describing the variation seen in response to a mitigation strategy over different production systems and diets. This information is required if we are to fully understand the potential of such an approach to decrease greenhouse gas emissions in Europe; it is also vital information for the SME partner for registration of their products.
- Addressing concerns over the transfer of residues into milk (vital both in terms of public acceptability and registration).

Project website

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- Agolin SA, CH
- Nor-Feed Sud, FR
- Phytosynthese, FR
- DOMCA SA, ES

[Interplay]

Interplay of microbiota and gut function in the developing pig – **Innovative avenues** towards sustainable animal production

Keywords

Sustainability, microbiota, gut function, microbial imprinting, neonatal development.

Summary

INTERPLAY is a multidisciplinary consortium of 12 public and private partners from across and beyond Europe with complementary expertise in gut microbiomics, immunology, physiology, animal genomics and nutrition. The project is using an integrated approach to build a sound understanding of the interaction of early colonisation of the intestine and gut function development in piglets. This knowledge will help identify innovative management strategies that address host genotype as well as nutritional means to provide a framework for sustainable animal production offering high food and consumer safety levels and improved animal health and welfare.

Problem

Low-input farming occurs under non-SPF (specific pathogen free) conditions. The European ban on in-feed antibiotics exposes piglets to a higher microbial pressure. The postnatal priming of piglets with a diverse microbiota may affect the development of the piglets' host-defense and gut function. By reversal, the piglets' developing host-defense may affect the development of gastro-intestinal tract (GIT) microbiota. Moreover, this intricate interplay between gut microbiota and the host during the early phases of life is expected to affect animal health and performance later in life.

The gut microbiome is an immensely diverse ecosystem that has co-evolved with its host. Recent research on microbe-host interactions has provided novel insights into the role of commensal microbes in several physiological processes, ranging from epithelial barrier and immune-system development to various neurological aspects. Nevertheless, we are only just starting to understand the molecular mechanisms governing cross-talk between the host and microbe. Recent conceptual and technological advances have set the stage for the integrated application of a complementary set of high-throughput approaches for comprehensively profiling GIT microbiota composition and functionality, as well as the animal's intestinal function.

Aim

The central INTERPLAY hypotheses are that:
- Spatio-temporal kinetics of early colonisation of the neonatal piglet GIT by commensal and potentially pathogenic microbiota drives the dynamics of microbiota composition and activity, intestinal function and host-microbe interaction after birth and later in life.
- Sows can affect the co-development of intestinal microbiota and gut function either directly through their genotype, or indirectly through their own microbiota, which they transmit to their offspring at or immediately after birth.
- The rearing environment, including postnatal antibiotic treatment, affects the interplay of microbial colonisation and gut function development.
- Improved management strategies can be developed based on innovative pre- and probiotics for sustainable pig production, capitalising on animal health and welfare as well as food and consumer safety.

INTERPLAY follows a number of objective-driven lines of research. Firstly, a dedicated toolbox and knowledge base for profiling microbiota and GIT function serves the key objectives by providing standardised beyond-state-of-the-art technologies. INTERPLAY is investigating the dynamics of microbial colonisation of the GI tract and its intricate interplay with the development of gastric and lower intestinal function.

Building on this research, the project will study the effect of the host genotype, the rearing environment, the presence of microbial as well as dietary antigens, and innovative pre- and probiotics-based dietary interventions, on the co-development of microbiota colonisation and GIT function. These investigations are expected to generate novel hypotheses and leads for sustainable management strategies; ultimately enabling guidelines for the rational design of such strategies – aiming at improved animal health, welfare and food safety.

Expected results

The strategic aims of INTERPLAY's research are to contribute to maintaining Europe's world-leading position in pig production and to implement sustainable management strategies that promote optimal animal health and welfare, alongside food and consumer safety. INTERPLAY will generate the knowledge base needed to support the Common Agricultural Policy sustainable development objectives.

Furthermore, as the pig is recognised more and more as a large model for biomedical research with respect to gastro-intestinal function, investigations carried out using pigs by INTERPLAY are not only of importance to animal production, but also of major interest for human health research.

Project website

http://interplay.wur.nl

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[ECO-FCE]

A whole systems approach to **optimise feed efficiency** and reduce the ecological footprint of monogastrics

Keywords

Pig, poultry, feed, efficiency, environment, gut and genetics.

Summary

A growing and developing world population requires agricultural systems that increase the volume of food produced, including protein sources such as pig and poultry meat. But this increase must be achieved in an environmentally sustainable manner and thus with limited resources. Improving production efficiency is key to increasing food production sustainably. The ECO-FCE consortium aims to increase the efficiency with which pigs and broiler chickens use feed, while also reducing the sector's ecological footprint. This will be achieved through better understanding (and manipulation) of interaction between nutritional factors, gut characteristics and micro flora, and host genetics. Animal welfare and product quality will also be monitored to identify opportunities for improvements.

Problem

EU climate change policy is to reduce greenhouse gas (GHG) emissions by 20%, compared with 1990 levels, and increase energy efficiency by 20%. Furthermore, food security is a major global challenge and the European Food Security Group recognises sustainable agriculture as a key factor in achieving global food security. However, the processes to attain 'food security' (i.e. produce more food) can contradict efforts to minimise climate change (i.e. reduce emissions). Furthermore, food security needs to be assured while resources such as water, land for food cultivation, and phosphorus are decreasing.

Aim

ECO-FCE aims to improve the feed-use efficiency of pigs and poultry, whilst also reducing their ecological footprint. To do this, the team needs to work towards five key scientific objectives. The team will:

- Summarise the current library of publications on monogastric feed-use efficiency, organise it into a knowledge-warehouse, use it to identify gaps in knowledge, and establish the relative importance of feed, gut and genetic factors.
- Study the effects of feeding strategies (the way in which feed is offered) and feed additives on FCE and the ecological footprint of monogastric animals and relate these to gut micro flora and animal genetics. A greater understanding of the effect of pre- and peri-natalnutritional factors in piglets will also be investigated.

Acronym:
ECO-FCE

Project number:
311794

EC contribution:
€5 999 814

Duration: 48 months

Starting date:
01/02/2013

Contract type: large scale collaborative research project

- Identify common gut and genetic factors in pigs and chickens with good and poor feed-use efficiency and enhance understanding of the interrelationship between gut structure, function and microflora, and host animal genetics.
- Investigate how to manipulate the gut of monogastrics to promote good FCE.
- Develop genetic biomarkers to advance identification and breeding of efficient monogastrics. These biomarkers must be:
  - a diagnostic for the contemporary use and partitioning of nutrients,
  - indicative of the animal's reactivity to nutritional and management interventions towards improved FCE, and
  - informative regarding the genetic potential of the animal to breed animals with inheritable beneficial feed conversion properties.

Expected results

By the time the project ends in 2017, the ECO-FCE team hopes to have significantly improved understanding of the level of variation in the functioning of monogastric digestive systems and both evaluated and adopted new systems and feed ingredients for pigs and poultry. These systems should optimise FCE and reduce environmental emissions.

The project should also lead to new tools that aid selection for FCE when breeding pigs and chickens, and a new awareness of how to improve both animal welfare and product quality while also improving FCE and reducing the ecological footprint.

Potential applications

The knowledge gained in ECO-FCE will mainly be applied within the feed and animal breeding industries and thus reach pig and poultry production systems. The global pig and poultry production industries will therefore benefit from the technologies under investigation.

Project website

www.eco-fce.eu

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[RUMINOMICS]

Connecting the animal genome, gastrointestinal microbiomes and nutrition to **improve digestion** efficiency and the environmental impacts of ruminant livestock production

Keywords

Methane, nutrition, feed efficiency, metagenomics, ruminants.

Summary

RUMINOMICS will integrate, at the highest possible level, expertise and technologies to increase the efficiency and decrease the environmental footprint of ruminant production, significantly advancing current knowledge in this sector. The project is exploiting state-of-the-art – omics technologies to understand how ruminant gastrointestinal microbial ecosystems, or microbiomes, are controlled by the host animal and by the diet it consumes and how this impacts on greenhouse gas emissions, efficiency and product quality.

Problem

Ruminants provide a crucial source of nutrients while also delivering hides and fibres for clothing, faeces for fuel, transport, and a means of conserving wealth in poor countries. Unfortunately, ruminants cause 8% to 10% of total greenhouse gas (GHG) emissions through the production of methane and nitrous oxide. The former is a normal end-product of ruminal fermentation. The latter arises indirectly from N-rich excreta in soils and slurries. Both represent losses of energy and potential protein, with significant economic consequences.

Acronym:
RUMINOMICS

Project number:
289319

EC contribution:
€5 974 674

Duration: 48 months

Starting date:
01/01/2012

Contract type:
Large-scale
integrating project

Aim

The main objective is to alleviate these problems by using state-of-the art - omics technologies to define the host genome-ruminal microbiome-emissions axis.

The team will develop models and tools to enable the livestock industry to decrease environmental damage from methane and nitrogen emissions, and to improve the efficiency of feed utilisation. A large-scale genetic association study involving 1 000 dairy cows will relate feed intake, digestion efficiency, milk production/composition and methane emissions to the ruminal microbiome and host genome. This will lead to new indicator traits and tools for use in both traditional and genomic selection.

Cow-reindeer metagenomic studies will establish how host species influence ruminal microbiology and function. Bovine twins studies will define how the rumen microbiome varies in an identical-host genetic background. Nutrition work will assess how dietary oils, nitrogen and carbohydrates affect the ruminal microbiome and product quality. A meta-barcoding 16S rRNA analysis protocol will be developed to investigate ruminal microbiomes more accurately, rapidly and cheaply. Saliva and faeces will be analysed as possible tools for non-invasive assessment of the ruminal microbiome and function. A novel method for on-farm methane analysis will be refined for easy application.

Additional objectives include dissemination and industrial liaison, targeted towards the enlarged EU, and candidate and developing countries.

Expected results

The results will provide information that could be used to breed livestock with low GHG emissions and high feed conversion efficiency. Results will be publicly available through an online data warehouse that will provide tools to build new queries and create novel information.

Potential applications

The new knowledge could be used to develop tools for indirectly determining the GHG gas emissions of ruminant livestock.

Project website

www.ruminomics.eu

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- European Forum of Farm Animal Breeders, NL
- Quality Meat Scotland, UK

Global cooperation to develop **next generation** whole genome SEQuence SELection tools for novel traits

Key words

Feed intake, efficiency, dairy, cattle, sequence, genomic.

Summary

The objective of SEQSEL is to build upon the recently initiated, but as yet informal, relationships between several world-leading research partners in the EU (Ireland, the UK, and The Netherlands) and Oceania (i.e., Australia and New Zealand); this in order to conduct joint research to identify regions of the bovine genome associated with feed intake and efficiency. The study will be undertaken in dairy cattle. To satisfy the greater food demand of the growing world population from a shrinking agricultural land base, there must be greater efficiencies of production in both plants and animal production.

Problem

The world's human population is expected to grow to 9.1 billion by 2050. To satisfy the 70% greater food demand this will entail, from a constant, or likely shrinking, agricultural land base, is a real and significant global challenge. This challenge must be met through greater efficiencies in both plant and animal production, and with minimal environmental consequences.

Dairy products are, and will remain, a significant proportion of the human staple diet as a source of essential amino acids, minerals and vitamins. The definition of feed efficiency in dairy cows is not simple and therefore requires an international initiative involving in-depth discussions to best define the relevant traits and methods of analysis. Because routine access to feed intake data for use in traditional breeding programmes is not feasible, alternative methods, exploiting state-of-the-art technologies such as genome sequences, is favoured. SEQSEL exploits and develops further knowledge and pipelines for the handling and exploitation of genome sequences.

Aim

The objective of SEQSEL is to build upon, solidify, formalise and condense the relationships between several world-leading research partners in the EU and Oceania in order to conduct joint research and participate in knowledge exchange to identify regions of the bovine genome associated with feed intake and efficiency. Consortia have already developed in the EU, through FP7 projects (e.g., www.robustmilk. eu; www.sac.ac.uk/greenhousemilk/), and between Australia and New Zealand.

This project will formally merge both consortia to become a global virtual centre of excellence for genomic selection using deep phenotypes on especially novel traits.

The particular focus of this project is to develop international critical mass, exploiting the skills' sets developed in different research partners in the area of whole genome selection for difficult to measure and novel traits in cattle. The focus is on dairy cattle, primarily because the genomic data are readily accessible. However, the tools developed are relatively easily transferable to beef cattle, as well as other species. Furthermore, feed efficiency in dairy cattle to-date has not received the same attention as in beef, due primarily to a lack of a concerted global effort to address the gaps in knowledge.

Expected results

SEQSEL will organise exchanges of ideas among experts in contrasting, yet complementary disciplines such as database management, phenotyping, statistical modelling and genetics, and genomics. It will build knowledge on the suitability and relevance of collating data from multiple international sources for use in international genetic evaluations. Genomic evaluations for feed intake and efficiency in dairy cows using the largest database ever used will be produced, as will information on putative regions of the bovine genome associated with feed intake and efficiency in dairy cows.

Potential applications

The project will make available an international genomic evaluation for feed intake and efficiency in dairy cows which has not been possible up to now. It will also identify genomic regions associated with feed intake and efficiency in dairy cows to facilitate a greater understanding of the genomic and biological mechanisms governing differences in animal feed intake and efficiency.

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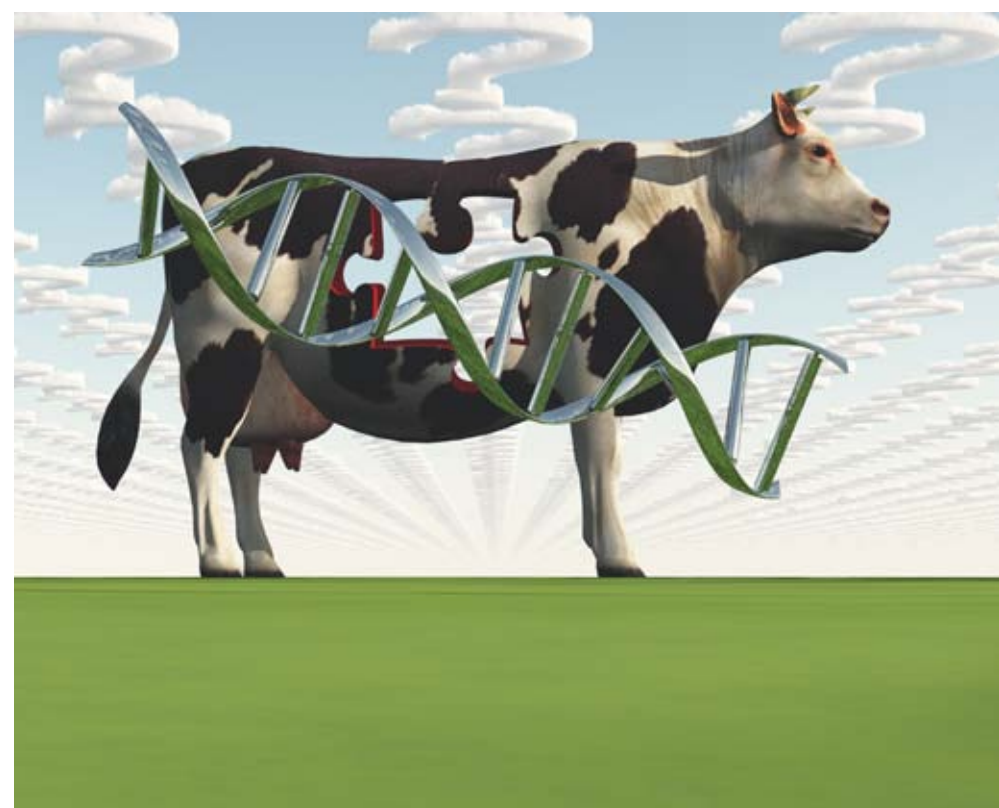
Fertility

Fertility

Efforts to constantly increase milk production in dairy cows have had an unexpected side effect – a progressive decline in the fertility of dairy cows worldwide. With the sustainability of dairy cattle farming systems – and economic viability – relying heavily on reproductive performance, researchers are now seeking to reverse the trend.

The decline in fertility is partly due to a change in management techniques combined with negative genetic correlations between intensive milk production and reproduction. Nutritional and physiological factors, as well as embryonic lethal recessive mutations due to inbreeding, are likely to play a role.

To ensure optimised reproduction, farmers need to know the exact time to inseminate. They must also be able to optimise the intervals between successive calvings in order to maximise the efficiency of dairy production.

The projects in this chapter address various topics, such as defining new factors for oocyte quality, identifying biomarkers and genetic loci linked to fertility, the search for embryonic lethal mutations, developing new management practices, and determining the optimal timing for insemination through a improved detection of oestrus. One project is also seeking to improve the cryopreservation of ram semen.

[SheepRep]

Advanced Studies on Improving Sheep Fertility by Using Artificial Means of Reproduction

Keywords

Sheep, cryopreserved semen, artificial insemination, improved conception rate

Summary

Artificial insemination (AI) is undoubtedly the management technique that has most contributed to the genetic improvement of livestock in modern animal production, while also optimising reproduction efficiency. Cryopreservation is a well-established method for preserving semen used worldwide for performing AI, as it can preserve cell life indefinitely. The main disadvantage is that freezing and thawing induce several forms of cellular lesions, which dramatically reduce semen quality and subsequent fertilising ability.

Sperm motility, viability, membrane integrity and biochemical parameters are all routinely tested to assess the quality of frozen-thawed semen. However, acceptable motility and viability of spermatozoa do not necessarily lead to acceptable conception rates. The SheepRep project is seeking to increase the conception rate in ewes following AI, by using new technologies for frozen-thawed semen.

Problem

Assisted reproduction, especially AI and *in vitro* fertilisation (IVF), has been successful in both human and animal reproduction. The popularity of AI is due to the simplicity of the techniques involved and to the advantages it provides to the producer. Through AI, one genetically superior male can be used to inseminate multiple females to maximise the distribution of desirable genes within the population.

However, for genetics to be quickly and economically introduced into flocks, there is a need to improve AI efficiency.

AI can be performed using fresh or stored ram semen, but fresh ram semen cannot be kept alive and fertile for long. There are two preservation technologies: refrigeration and cryopreservation. Although refrigeration seems to be less harmful, semen refrigeration is not as widespread as cryopreservation, as cells live longer when cryopreservation is used.

Acronym: SheepRep

Project number: 295137

EC contribution: €197 700

Duration: 24 months

Starting date: 01/01/2012

Contract type: Marie Curie action, International research staff exchange scheme (IRSES)

Cryopreservation damages a large number of spermatic cells, thus decreasing the semen's fertility properties and the efficiency of AI. Ram semen in particular appears to be quite sensitive to cryopreservation. Freezing and thawing of spermatozoa induce several forms of cellular lesions that can be reduced by incorporating cryoprotectants although some of them are toxic for the sperm of certain species.

Another problem in sheep is that the fertility of cryopreserved semen seems compromised when using vaginal or cervical inseminations. For a minimum acceptable level of fertility in superovulated ewes (this is approximately 20% compared to using fresh semen), the most effective method currently available is transuterine or oviductal insemination by laparoscopy. While time-efficient and minimally invasive, laparoscopies cannot be performed extensively within flocks.

In conclusion, an optimal method for improving conception rates following AI has not yet been found, although this is of paramount importance from the cost-efficiency point of view.

Aim

The goal is to increase the conception rate in ewes through artificial inseminations, by using frozen-thawed semen. The specific objectives of the project are:
- Increasing fertility of cryopreserved ram semen, by improving freezing technologies and optimising the media;
- Establishing a biochemical profile of the cryopreserved ram semen;
- Optimising the quality of cryopreserved ram semen by using the innovative biotechnology, the Helium-Neon laser;
- Making accurate correlations between obtained *in vitro* parameters and the reproduction indexes.

- The SheepRep team starts with a number of hypotheses, including:
- Enhancing or depriving adenosine triphosphate (ATP) production, especially those which govern the mitochondrial function, affects sperm motility.
- The levels and transport of intracellular Ca^{2+} into the irradiated sperm cells in some species can influence the motility, capacitation and acrosome reaction.

Expected results
- Increased fertility of cryopreserved ram semen through improved freezing technologies and optimised semen extenders;
- A method of *in vitro* analysis, statistically correlated with fertility indexes;
- Higher cell energy load, thanks to He-Ne laser irradiation that improves parameters conducive to fertility;
- A biochemical framework of ram cryopreserved semen, from which a correlation of the biochemical and cytological parameters following freezing-thawing can be performed;
- A dilution-freezing extender that induces minimal damage to the plasmatic membrane, based on the correlations made between the ultra-structural and cytological parameters of the ram spermatic cell;
- Identification of the cryopreserving technology that leads to the best fertility results among ewes following AI, based on the correlations made between the *in vitro* studied parameters and the reproduction indexes obtained following the *in vivo* tests.

Potential applications
The project outputs will be of interest to industrial players interested in new reproduction techniques to increase conception rates within their flocks by using AI and cryopreserved ram semen. The new knowledge will also be shared with education and research institutions, as actual developments and innovations in the field of assisted reproduction.

The findings could also have implications for human assisted reproduction, where *in vitro* fertilisation (IVF) faces similar problems to those encountered within sheep flocks, i.e. a conception rate of less than 20%. Researchers studying IVF may wish to build on the SheepRep project's findings and approaches.

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[BOVINOSE]

Pheromone-based sensor system for **detecting estrus** in dairy cows

Acronym:
BOVINOSE

Project number:
232460

EC contribution:
€1 003 389

Duration: 24 months

Starting date:
01/06/2009

Contract type:
Research for the
benefit of SMEs

Keywords

Sensors, dairy cows, artificial insemination, pheromones, detection of oestrus.

Summary

Artificial insemination (AI) is widely used to control calving intervals – and therefore optimise milk production and maximise offspring in dairy cattle. Currently, the conception rate of AI varies from 30 % to 70%, and a successful insemination depends mainly on the correct timing – 8 to 12 hours after the start of estrus. The problem can therefore be narrowed down to detection of estrus in a cow. The BOVINOSE project investigated a novel type of 'electronic nose' to detect estrus in dairy cows, and thus to determine the optimal timing of artificial insemination. This technology will help European dairy farmers, the vast majority being micro-enterprises run as family businesses.

Problem

Non-optimal calving intervals cause large economic losses to dairy farmers. The calving interval affects dairy farm profitability in three ways: (a) milk production, (b) the number of dry cow days, and (c) replacements. In short, successful reproductive management has a significant impact on a herd's overall performance and the profitability of a dairy farm, second in importance only to mastitis.

Several sources report that the single most important problem limiting high reproductive efficiency in dairy herds is poor detection of oestrus. Failure to detect oestrus, or erroneous diagnosis, has been estimated to cost over $300 million to the dairy industry in the USA. Current detection methods are largely based on visual signs (mounting behaviour) and/or palpation by a veterinary doctor. These are not always reliable, they are labour-intensive, and require skill and experience. Farmers detect around 35%-60% of the heats; this huge variation confirms that heat detection is not always easy and that it depends on an individual farmer's skill. Improving the success rate would undoubtedly increase a dairy farmer's profitability significantly.

Aim

The goal of BOVINOSE was to develop a novel and easy-to-use device that enables a dairy farmer to accurately determine a cow's ovulation timing. To this end, the device should be equipped with sensors, able to detect the specific bovine sex pheromones – simply put, an artificial bull's nose. To achieve this the project has investigated the info-chemicals that make up the sex pheromones in cows and which are only released during oestrus.

Results

First the research used natural and induced samples from faeces, urine and saliva from various dairy farms. Faeces were the most suitable source of sex pheromone, and the acetic and propionic acids were qualified as sufficient indicators of reproductive status of cows, able to define an optimal insemination time. The project then developed a set of sensors for detecting bovine sex pheromones and integrated these into an easy-to-use, yet reliable, system for oestrus determination in cows.

A set of sensors for detecting these sex pheromones was researched, designed and developed, resulting in a functional prototype. This was based on a set of defined user and technical requirements, consisting of a probe, an array of sensors and a dedicated, integrated software system for control and end-user interaction.

Extensive field trials, closely accompanied by veterinary experts, were undertaken on a dairy farm. These trials addressed both the info-chemicals and the fitness-for-use by the anticipated end-user through a technical evaluation. The prototype tested under farm conditions proved able to measure volatiles from faeces samples. It performed equally well in field conditions as in the laboratory.

A dedicated dairy farmers' questionnaire was defined and developed and used in interviewing dairy farmers and veterinary doctors. The outcomes have been used in the BOVINOSE commercialisation strategy as a basis for a successful market introduction. The team concluded that the electronic nose could be used in farming, forestry and agriculture whenever rapid, sensitive and reliable methods of specific odour detection is essential.

Potential applications

The results have applications in the dairy farming market for farmers wishing to pinpoint the timeframe when individual cows should be inseminated.

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Project website

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[Pro-Ovum]

Role of Progesterone **Receptor Membrane** Component-1 in oogenesis and mammalian fertility

Acronym: Pro-Ovum

Project number: 303640

EC contribution: €100 000

Duration: 48 months

Starting date: 01/02/2012

Contract type: Marie-Curie Action: Career Integration Grants: (CIG)

Keywords

Oocyte, meiosis, fertility, dairy cattle.

Summary

Infertility is a major problem affecting domestic mammals and declining fertility is damaging the profitability of dairy farms in Europe and worldwide. Since declining fertility in cattle is largely due to the poor quality of oocytes, research on the factors that affect oocyte quality is essential. Based on our preliminary data, we propose that Progesterone Receptor Membrane Component 1 (PGRMC1) is one of the key factors that regulate mammalian oocyte quality.

Problem

For dairy farms it is estimated that a slight increase in pregnancy rates results in a significant increase in profitability. This could make all the difference to whether a family farm remains in operation or not. There are multiple reasons for the declining fertility of cattle, but 57% of the pregnancy failures can be attributed to alterations in early embryo-development, while an additional 18% are related to fertilisation failure, which are probably due to the poor quality of the oocytes.

These findings suggest that defining the factors and mechanisms that contribute to oocyte and embryo quality is essential for improving female fertility. A basic understanding of which proteins within the oocyte regulate meiosis, oocyte fertilisability and developmental potential would help significantly. Our data, the suggest that the Progesterone Receptor Membrane Component 1 (PGRMC1) could have a crucial role for proper chromosome segregation, ensuring a correct ploïdie of the mature oocyte.

Aim

The Pro-Ovum project is rigorously testing the hypothesis that PGRMC1 plays an essential role in chromosomal alignment and segregation, which occurs during bovine oocyte maturation. In particular, studies are focused on two specific objectives:

- The team is first determining to what extent PGRMC1 plays an essential role in maintaining the ability of bovine oocytes to undergo maturation, fertilisation and early embryonic development *in vitro*. This will be done by genetically manipulating the levels of PGRMC1 within the oocyte.

- The next step is to determine the mechanism of action of PGRMC1. This involves identifying oocyte proteins that interact with PGRMC1. The team is testing the hypothesis that PGRMC1 regulates meiosis through interaction with Aurora kinase B (AURKB), a component of the chromosomal passenger complex that is involved in chromosome alignment and segregation, and that this interaction is mediated by PGRMC1 sumoylation (i.e. conjugation of PGRMC1 with the Small Ubiquitin-related Modifier SUMO 2/3).

Expected results

Pro-Ovum should lead to several discoveries, contributing to advancing the state of the art in the field of reproductive biology through the assessment of factors that regulate mammalian oocyte maturation, fertilisability and developmental potential. This will be a major advantage for Europe since dairy cow fertility is a priority for economic sustainability in modern dairy farming.

Potential applications

The idea that PGRMC1 can regulate meiosis is innovative and the results of this study will enhance understanding of pathophysiological mechanisms of livestock fertility. To take full advantage of the benefits of assisted reproductive technologies, one must understand the basic physiology of the female and male reproductive systems. Pro-Ovum will provide new knowledge and potential molecular markers for improving the success rate of assisted reproduction technologies in domestic animals, and will open a new branch of research and methods in the field of reproductive biology.

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Website

www.redbiolab.unimi.it/RedBioLab/proovum.html

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[DAMONA]

Mutation and recombination in the cattle germline: genomic analysis and impact on fertility

Acronym: DAMONA

Project number: 323030

EC contribution: € 2 258 000

Duration: 60 months

Starting date: 01/03/2013

Contract type: European Research council (ERC)

Keywords
Mutation, recombination, fertility, dairy cattle.

Summary
DAMONA is carrying out genetic analyses of dairy cattle to identify variations in male and female mutation and recombination rates. Mutation and recombination are fundamental biological processes that determine the adaptability of populations in changing environments. The mutation rate that prevails in a population reflects the equilibrium between the need to be adaptable, the burden of the mutation load, the resources invested in reducing the error rate (cost of fidelity), and random drift that determines a lower limit in achievable fidelity.

Problem
Recombination fulfils an essential mechanistic role during meiosis and is exquisitely regulated to ensure proper chromosomal segregation. It affects the rate of creation and loss of haplotypes with cis-configured favourable alleles, imposing second order selection pressure on local and global modifiers of recombination.

It is becoming increasingly apparent that recombination and mutation rate vary between individuals, and that these differences are in part inherited. Both processes are therefore evolvable themselves, and hence amenable to genomic analysis. Identifying the genetic determinants underlying these differences would provide novel insights into the molecular mechanisms regulating mutation and recombination. The mutational load, and in particular the number of lethal equivalents per average individual, remains poorly defined. This is because epidemiological and molecular data yield estimates differ by an order of magnitude. A relationship between recombination and fertility has been reported in Icelandic women, but has not yet been confirmed.

Population structure (small effective population size; large harems), phenotypic data collection (systematic recording of > 50 traits on millions of cows), and large-scale SNP genotyping (for genomic selection), make dairy cattle populations uniquely suited for genetic analyses.

Aim
DAMONA is exploiting these unique resources, in combination with recent advances in next-generation sequencing and genotyping, to:
- quantify and characterise inter-individual variation in male and female mutation and recombination rates;
- map, fine-map and identify causative genes and variants underlying QTL influencing these four phenotypes;
- test the effect of loss-of-function variants in protein-coding genes on >50 phenotypes including fertility;
- study the effect of variation in recombination on fertility.

Potential applications
In addition to providing fundamental new insights into the processes of mutation and recombination, DAMONA will generate deliverables of immediate practical and general utility in dairy cattle breeding programmes. The project will generate diagnostic tests for a number of recessive embryonic lethals. These will be immediately made available to farmers using standard procedures (allowing elimination of at-risk matings).

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[FECUND]

Optimisation of early **reproductive success** in dairy cattle through the definition of new traits and improved reproductive biotechnology

Acronym: FECUND

Project number: 312097

EC contribution: €2.999.393

Duration: 48 months

Starting date: 01/02/2013

Contract type: small scale collaborative research project

Keywords

Fertility, dairy cow, energy balance, genetic merit, – omics technologies, reproduction technologies, biomarkers, new phenotypes.

Summary

Good fertility is essential for sustainable livestock production. However, in parallel with intensive selection for higher milk yields, the reproductive performance of dairy cows has declined in recent decades. This is a major concern for farmers and the dairy industry. FECUND is addressing the problems of reproductive success in the cow using an interdisciplinary approach that integrates *in vivo* and *in vitro* studies, biology, physiology, – omics technologies and bioinformatics.

The Problem

Successful reproduction requires the development of viable gametes, fertilisation, the establishment of pregnancy by implantation of the embryo, gestation of the foetus and eventually the delivery of a viable offspring. Thus, the reproductive process encompasses many molecular and cellular interactions which require that cows are in an appropriate metabolic state and that a complex series of physiological events occur correctly with the appropriate timing. Improvement of reproductive success may be achieved by better animal management and through genetic selection for better fertility. To achieve this, a better understanding of the reproductive process is needed, helped by improved measurement of reproductive traits, better recording and the application of new reproductive techniques, together with increased knowledge of gene function and regulation.

Aim

FECUND is addressing the problems of reproductive success in the cow using a systems biology approach to develop molecular indicators of the ability of the cow to support the early stages of reproduction, when most embryonic loss occurs, to underpin genomic selection for better fertility and to improve advanced reproductive biotechnologies. Research is addressing: studies on early development; new ways of defining, measuring and recording fertility traits; linking phenotypes and metabolic profiles to fertility; identifying biomarkers to quantify new phenotypes in the early stages of reproduction; and identifying genetic loci associated with good reproductive performance in breeding populations.

Expected results

An important outcome will be a better understanding of the physiology of early reproduction with the definition of novel fertility phenotypes and the identification of biomarkers for improved reproduction. The project will increase knowledge of transcriptomics and epigenetics events as well as the metabolic pathways occurring during the early events of reproduction. This will help improve advanced *in vitro* reproductive technologies to take full advantage of genomic selection for accelerating the rate of genetic progress. FECUND will deliver new traits and new markers for use in genetic improvement programmes. This information will help with interpreting the functional significance of physiological variations associated with energy balance and genetic merit and their effects on particular reproductive functions or phases.

The project will organise several dissemination activities related to its results to contribute to a strong European breeding industry and help ensure that it is sustainable. These activities will reach out to the broader European cattle industry, from farmers to experts in reproduction. Dissemination workshops will be coordinated with existing European structures involved in the development of the European breeding industry, in particular EFFAB, the European Forum of Farm Animal Breeders as well as other organisations including ESDAR (European Society of Domestic Animal Reproduction), AETE (European Embryo Transfer Association), and EAAP (European Association of Animal Production).

Potential applications

The FECUND project will have a major impact on improving cattle fertility by revealing the underlying mechanisms of reproductive biology and their application to improved selection and animal management. This will provide the European cattle industry with the cutting edge molecular and physiological tools, and improved reproductive techniques needed to meet the challenge of declining reproductive success in dairy cattle.

In the field of genetics, results will include biomarkers that are more easily applied in the field to collect sufficient data in order to construct accurate estimated breeding values for reproductive potential, which can then be used in selection programmes. New physiological knowledge on the effects of negative energy balance on the underlying mechanisms of oocyte formation, early embryonic development and the responses of the mother during early reproductive events will help improve cow management to maximise fertility.

Diagnostic biomarkers that predict negative energy balances will enable farmers to devise strategies to address energy deficiency, for example by providing high energy diets prior to calving, or by reducing milking frequencies in early lactation for high risk cows. A major impact will be the implementation of advanced reproductive technologies including better culture techniques and protocols to produce high quality oocytes and embryos.

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Project website

under construction

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[PROLIFIC]

Pluridisciplinary study for a RObust and **sustainabLe Improvement** of Fertility In Cows

Keywords

Dairy cow, fertility, modelling, - omics analyses, genomic breeding value.

Summary

Intensive genetic selection in dairy cattle has resulted in a modern cow with very high milk yield but reduced fertility and poor calving performance. The sustainability of dairy cattle farming systems relies in large part on the ability of cows to maintain reproductive performance as they cope with the constraints imposed by environmental conditions and livestock practices. The strategic aim of PROLIFIC is to unlock the potential for proactive herd management by providing the farmer with improved tools for on-farm reproductive monitoring and management.

Problem

The undesirable environmental and welfare impacts of current animal farming systems indicate a need to increase their sustainability. At the same time, food security and biofuel requirements are pushing ruminant production systems towards more marginal environments. Optimising production systems to achieve maximum sustainability under these conditions is a major challenge, especially as a likely consequence of global warming is increasing variability in environmental conditions.

The sustainability of dairy cattle farming systems relies in large part on the ability of cows to maintain reproductive performance as they cope with the constraints imposed by environmental conditions and livestock practices. Reproductive performance is central to farm sustainability as it underpins cow productivity (lactation) and longevity (replacement risk). Genetic selection has been highly successful and has resulted in modern dairy cows with very high milk yields, but there has been a parallel reduction in fertility. This has created a situation where, through decreased reproductive performance, farmers are losing control of a key component of cattle system sustainability.

Aim

The strategic aim of PROLIFIC is to unlock the potential for proactive herd management by providing the farmer with improved tools for on-farm reproductive monitoring and management. To achieve this, the project is seeking new phenotypic and genetic markers for fertility, and is identifying groups of genes and pathways involved in coordinated changes in the reproductive system under different environmental conditions. It will identify the functional mutations associated with fertility (based on progesterone measurements) and estimate genomic breeding values using whole sequence information on individuals. It will also provide integrated, quantitative, models to describe interactions between genotype, nutrition and reproductive physiology.

At the technological level, the project is developing decision support tools to optimise the timing of reproductive management decisions, improve the rate of successful inseminations, and provide reproductive performance benchmarking. These tools will be deployed and demonstrated on-farm. The team is also developing simulation tools that will allow evaluation of economic and environmental impacts of changes in breeding management at the farm level.

At the agricultural level, the project will identify improved breeding strategies to optimise cow fertility and robustness. It will also set out sustainable management approaches that make use of the adaptive responses of dairy cows to low and high input dairy systems, in the context of the economic and environmental changes forecast for the next decades.

Expected results

PROLIFIC will increase understanding of the mechanisms in animals that influence reproduction characteristics. The planned transcriptomic, epigenetic, proteomic and metabolomic analyses will help pinpoint the effectors produced in reproductive tissues that have a positive or negative effect on cow's fertility. The project will develop three tools to:

- Provide the farmer with an evaluation of the 'insemination worth' of a given oestrus. This is expected to allow substantial improvements in on-farm conception rates.
- Allow a farmer to evaluate the consequences on herd reproductive performance of adopting different oestrus detection and insemination windows, as well as different technologies (reliability of detection, and other factors).
- Benchmark based on progesterone. On farms that are using new technologies for progesterone monitoring, the tool will allow reproductive diagnostics based on the differences between the reference and observed progesterone profiles. This will provide a simple means to combine the improved understanding of reproductive biology that the project will generate with state-of-the-art on-farm technologies.

Potential applications

PROLIFIC's research will help breeders identify new fertility markers for genomic selection of the most fertile animals. Furthermore, the new fertility markers will be used to improve the Herd Navigator® cattle management solution that, in the current commercialised version, monitors reproduction based on progesterone only. The project results will help orientate or identify new cattle management approaches; they will help optimise the balance between productivity, fertility and health according to local conditions; and they will contribute to improving quality-of-life and rural sustainability.

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Project website

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Selection for
Health

Selection for health

From mycobacterial diseases and mastitis to endometritis, worm or Coliform infections, livestock are susceptible to a range of diseases that can not only cause immense suffering for the animals involved, but also devastate production and lead to huge losses for farmers.

Genomics offers real hope here. Researchers are continuing to advance understanding of genetic differences between breeds and what makes specific animals less prone to diseases. The goal is to enable breeders, through increased understanding of disease control mechanisms, to select for disease resistance together with high genetic merit.

Increasing knowledge of host-pathogen relationships will also lead to the development of new tools and strategies for the diagnosis, prognosis, treatment and prevention of infectious diseases.

The projects highlighted in this chapter are taking research forward in areas such as the infection process and cellular responses, genetic control, genomics tools and the use of high-density single nucleotide polymorphism in selection programmes. A Network of Excellence also brought together experts in genomics, bioinformatics, animal health and animal models, contributing to the long-term integration of European skills and knowledge.

[MACROSYS]

Macrophage Systems biology applied to **disease control**

Keywords
Bovine, macrophage, bovine tuberculosis, bovine paratuberculosis.

Summary
The focus of the MacroSys project is to better understand the genetics of susceptibility of cattle to mycobacterial infections and the role of the macrophage in controlling diseases caused by these bacteria. The project created new knowledge about the infection process and the cellular response to disease, as well as approaches to disease control.

Problem
Diseases caused by mycobacteria include bovine tuberculosis (TB), which is caused by mycobacterium bovis, a significant zoonotic disease of cattle in many countries worldwide, and Johne's disease (Para-TB), which is caused by mycobacterium *avium subsp. paratuberculosis* (MAP).

Left unchecked, TB, which is a zoonotic disease, can have significant economic and health consequences for cattle and people. Para-TB causes chronic enteritis in a wide range of animal species. The clinical phase of the disease is characterised in dairy cows by a drop in milk production, followed by progressive loss of condition and weight and, eventually, death. Johne's disease has been linked with the occurrence of Crohn's disease in man.

The striking feature of mycobacterial infections is the prolonged survival of the bacteria in the lysosomes of macrophages. These diseases progress slowly and animals may only become clinically ill two to six years after infection. Infected animals develop lesions in the gut and many do not progress further to clinical disease. This long incubation period and high turnover of cattle, particularly in dairy herds, means that even when there is high prevalence of infection, few clinical cases are usually observed.

Aim
The MacroSys project used a combination of functional and classical genomics, together with systems biology approaches, to investigate host-pathogen interactions and the host immune response to mycobacterium infection. These studies have increased knowledge of the macrophage function and the genetic control of the host response to mycobacterial infections.

Results
In vitro infection studies of gene expression have shown differences in macrophage response to different *Mycobacterium bovis* and MAP strains – and between the two pathogens – at the level of gene expression. Changes observed at the RNA level for TB are more important than changes observed with para-TB.

Testing gene function: the role of genes associated with mycobacterial infection identified from the literature review and from gene expression studies performed in the MacroSys project are now being investigated by *in vitro* knock-down of their expression. Reliable methods for targeted gene knock-down were developed using transfected small interfering RNA (siRNA). Five candidate genes were identified and the effects of knocking down the expression of these genes on pathogen uptake and viability are currently analysed.

Genetic studies: analysis of field cases of 500 MAP infected cattle and 500 controls in a 'Genome Wide Association Analyses (GWAS)' identified six single nucleotide polymorphisms (SNPs) significantly associated with MAP antibody response on chromosomes 12, 8, 9, 11 and 27. A second study – using both faecal culture and serum antibodies as the measure of MAP infection status in 192 cows – identified loci associated with disease on chromosomes 4 and 20. A meta-analysis of GWAS MAP data with the University of Washington identified further loci on BTA 1, 6, 13, 16, 21, 22, 23 and 25 associated with disease status. Bioinformatic analyses of these data have identified potential links between the different loci by identifying genes within 1Mb of the significant SNPs, and by defining candidate genes based on their role in common physiological pathways.

Potential applications

The results provide more information on the genetics of the response to mycobacterial infections. These results may be used to breed cattle with a reduced susceptibility to TB or para-TB and hence reduce the infection at the population level. The study of the transcriptional response of macrophage to infection with mycobacteria increases our understanding of the biology of the host-pathogen interactions and help to develop better diagnostic tests for preclinical phases of disease. This information may be used to improve disease management and control programs.

By controlling disease prevalence, the outputs of the Macrosys project will contribute to improved efficiency and profitability of animal production and health and welfare, thus underpinning the competitiveness of agriculture within the overall framework of European policies on sustainability.

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Project website

www.macrosys-project.eu

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[INNATELY BETTER COWS]

A genomics approach to **increasing disease resistance** in dairy cows through improvements in innate immunity

Acronym:
INNATELY BETTER
COWS

Project number:
328205

EC contribution:
309 235.20€

Duration:
24 months

Starting date:
01/08/2013

Contract type:
Marie Curie
action: International
Incoming Fellowship
(IFF)

Keywords
Innate immunity, genomic selection, dairy cow, mastitis, endometritis.

Summary
To meet worldwide demand, a major expansion in dairy production is predicted. But increases in milk production must be achieved without compromising the health and welfare of cows, and in an environmentally sustainable manner. Cows are susceptible to infection from pathogens commonly present on farms. They access both the reproductive tract after calving and the mammary gland, causing uterine infections and mastitis. Avoiding infection is difficult; it can only partially be controlled with antibiotics, vaccine and biosecurity measures. Poor health reduces longevity, requires farmers to keep more animals for the same milk output, and encourages high reliance on antibiotics. The project is seeking novel approaches to disease prevention.

The INNATELY BETTER COWS approach is to breed for disease resistance to a wide range of pathogens by selecting the 'fittest' innate immune system. Ongoing work has found evidence that innate immune systems differ between breeds in their ability to kill bacteria. This suggests there are genetic differences between animals which can be incorporated into selection objectives. Genomic selection based on high-density single nucleotide polymorphism (SNP) genotype information is increasingly used in breeding programmes to select high genetic merit animals. This method can highlight regions of the genome associated with traits of interest, which can then be scrutinised to identify possible causative mutations and genes.

Problem (background)
Immunity of the bovine mammary gland and endometrium is mediated by both non-specific (innate immunity) and specific defences (acquired immunity). Innate immunity predominates during early infection and is activated quickly by numerous stimuli. Modern dairy cows experience a period of nutrient shortage (negative energy balance) in early lactation as body reserves are mobilised to support a rapid increase in milk output.

This transition period from late pregnancy to early lactation is associated with a compromised immune status, as maintaining an ongoing microbial defence system is energetically demanding. The hypothesis is that genetic selection for high yielding dairy cows has been associated with reduced innate immune responses. This predisposes cows to endometritis and/or mastitis, present in about 15% and 20-50% respectively of all dairy cows. Both diseases decrease fertility, while mastitis also reduces milk production and milk quality and is the main driver of antibiotic use in dairy production systems.

It is currently hard to control either disease using conventional control strategies. The causative bacteria are developing resistance to antibiotics, and long-promised vaccines are still in their infancies. Certain aspects of the immune system are, however, genetically manifested and may provide suitable targets for enhancing genetic resistance. A change in breeding strategies could be used to incorporate 'genetic elements' into new disease management strategies. The recent innovations in molecular genetics for farm animals offer significant potential for major breakthroughs in selecting animals with improved disease resistance.

Aim
The project team at the Royal Veterinary College, together with a visiting professor from Huazhong Agricultural University, will perform genome wide association studies in both UK and Chinese cows to identify regions of particular chromosomes associated with health traits (resistance to mastitis and endometritis). Comparative genomics will then be used to identify candidate genes associated with the innate immune response.

The selected genes will be sequenced in different cattle populations to identify novel SNPs. The functional importance of these genes will be tested using *in vitro* responses of uterine cells and blood cells towards selected bacterial pathogens. Finally, the relevance of these genes will be validated by association studies related to disease resistance within two new populations of UK and Chinese dairy cows.

Expected results
The scientists expect to identify genes and pathways involved in the innate immune response developed when fighting mastitis and/or endometritis. This information can then be incorporated into future breeding programmes to select more robust cows and improve profitability for dairy farmers.

Potential applications
The results can be used to develop genetic markers for disease resistance in dairy cows. These markers could be incorporated into breeding programmes.

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[EADGENE_S]

Strengthening the implementation of **durable integration** of EADGENE

Keywords

Animal health, animal genomics, disease control, genomic tools.

Summary

Animal health issues are of critical importance for European citizens, affecting their health, well-being and lifestyle choices in many ways. Disease control has traditionally relied on interventions. However, animal health is now faced with new challenges and opportunities. By integrating key European teams in genomics, bioinformatics, animal health and animal models, the Network of Excellence (NoE) EADGENE (2004-2010) brought together a critical mass of scientists with unique access to complementary resources, including host and pathogen models and functional genomics. Building on these benefits, EADGENE_S ensures the long-term integration of European resources in animal disease genomics by grouping together the leading institutions.

Problem

Animal health research is facing new challenges and new opportunities. The new challenges include existing and emerging diseases that affect human health – as well as decreasing options for treating these infections – and non-zoonotic animal diseases that impinge on the quality of animal-derived food. New opportunities have arisen through major advances in genomics and related technologies, which have the potential for detailed investigation and understanding of host-pathogen interactions.

These technologies offer new opportunities for diagnosis, intervention and the selective breeding of animals, including fish. They can promote better adaptation to infection, and in some cases improved disease resistance. Before the EADGENE NoE, these opportunities were under-exploited due to fragmentation in research efforts and in access to the necessary genomics and analytical tools, for example at the host/pathogen level, across species and across pathogens and target solutions.

Aims

The network aims to strengthen a sustainable core research group of European centres of excellence, committed to integrating their resources and national facilities. By sharing and upgrading research tools and platforms for high quality joint research on animal genomics and genetics, EADGENE_S provides opportunities for further funding, and for consolidating skills and expertise through a programme of workshops, training courses and short-term missions. It also ensures efficient technology transfer to industry.

Acronym:
EADGENE_S

Project number:
265663

EC contribution:
€ 999 810

Duration:
24 months

Starting date:
01/06/2011

Contract type:
Coordination and support action

Three thematic priorities were identified by the EADGENE_S scientific community:

1. Studying the genome – environmental interactions and the resulting physiological processes that underlie health traits and are significantly modulated by environmental factors, in particular pathogens.
2. Identifying molecular variation (genes, DNA markers) and molecular 'signatures' (transcriptomic, proteomic, metabolic profiles) associated with disease susceptibility traits using high-throughput genomics technologies.
3. Developing tools and strategies to modulate the biological processes underlying health traits.

Results

The team developed and shared research tools and platforms, allowing the partners to coordinate activities and research priorities. Several dedicated workshops were organised and an international conference on Mastitis resistance was held. Mobility grants were awarded for exchanges between EADGENE_S partners and with external institutions.

Collaboration between the partner institutes, both formal and informal, is extensive and ongoing. Major consortia for the last FP7 calls were built around EADGENE partners.

Industry Days were organised allowing exchanges between the European animal breeding sector and scientists, promoting potential applications for breeding.

Potential applications

The applications are more efficient research efforts through the coordination and integration achieved by the participating scientists, who were able to integrate their resources and facilities, leading to sustainable and integrated research efforts. The expected long-term impact is more structured research in the field of animal disease genomics.

Project website

www.eadgene.info

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[QUANTOMICS]

From sequence to consequence – **tools for the exploitation** of livestock genomes

Keywords

Genomics, DNA tools, software, diseases, livestock.

Summary

QUANTOMICS is a large collaborative research project involving 17 leading research groups and businesses. It aims to deliver a step-change in the availability of cutting edge technologies and tools for the economic exploitation of livestock genomes. The project will provide the tools to identify rapidly the causative DNA variations underpinning sustainability in livestock, and for industry to exploit high-density genomic information. Its adaptable, quantitative and genomic tools will together form a powerful integrated pipeline with wide application in all farmed species. The project is expected to leave a legacy of resources for future research.

Problem

The sequencing of the genomes of major livestock species places animal agriculture on the threshold of a new era. The development of genomic tools has provided the ability to map genes associated with health, welfare, productivity and product quality. However, the application of these findings in breeding programmes has been hampered by two bottlenecks:

- The problem of finding genetic markers sufficiently closely associated with the causative DNA sequence differences to be fully effective in selective breeding.
- The challenge of identifying the causative DNA polymorphisms themselves to provide an optimally informative and portable tool for selection, breeding and understanding of trait biology.

This project is developing a set of technologies and tools designed to maximise ability to bridge the gap between trait variation and DNA sequence – and thus remove the two bottlenecks.

Acronym: QUANTOMICS

Project number: 222664

EC contribution: €5 999 000

Duration: 54 months

Starting date: 01/06/2009

Contract type: Large-scale integrating project

Aim

QUANTOMICS has five major research objectives:

1. To provide the tools that combine information from reference genome sequence, mapping, comparative genomics, annotation, functional studies and dense sequence data from the latest hyper-parallel re-sequencing technologies. These tools will be able to identify rapidly the causative DNA variation underlying important traits in livestock species.

2. To provide the methodologies and software tools to exploit effectively and efficiently genomic information in sustainable breeding programmes.

3. To determine the benefits and constraints relating to the effective application of these tools to health and welfare traits in chickens and cattle – thus providing information across contrasting breeding schemes that span the breadth of livestock improvement.

4. To create a framework for moving from genome sequences to commercial applications for all livestock species, which can be expanded to include other forms of information such as epigenetic effects where their importance has been established.

5. To disseminate the results of the project to ensure broad and long-term beneficial impacts on European competitiveness and EU policies on animal health and welfare and sustainable agriculture.

Results and potential applications

QUANTOMICS will have applications for all farmed animal species and leave a legacy of resources for future research. Generating quantitative and genomic tools based on cutting-edge technologies, it will create a powerful integrated pipeline. It should enable genomic information to be used efficiently in sustainable animal-breeding programmes. Applying the new genomic tools in dairy cattle populations will greatly increase the effectiveness of procedures that are currently supported more modestly by existing biometrical tools.

Going far beyond this, successful application of QUANTOMICS' new genomic tools to commercial broilers will provide a completely novel approach to genetic improvement of commercial, crossbred breeding stock – by applying genomics at the level of the commercial crossbred animal, instead of at the level of the parent pure lines. This 'inverted-pyramid design', if effective, will be truly revolutionary in its impact in farm animal species, where crossbreeding is common.

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Project website

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- Landbruk og Fødevarer, DK
- Commonwealth Scientific and Industrial Research Organisation, AU
- Associazione Nazionale Allevatori Bovini della Razza Bruna, IT

[3SR]

Sustainable Solutions for Small Ruminants

Acronym: 3SR

Project number:
245140

EC contribution:
€ 2 997 726

Duration: 42 months

Starting date:
01/05/2010

**Contract type: small
scale collaborative
research project**

Key words

Sheep, goat, genomics, mastitis, nematodes, ovulation, breeding.

Summary

Mastitis and nematode worm infections are the two biggest health and welfare threats to sheep and goats in Europe and beyond, causing huge economic and productivity losses. Previous research has indicated that susceptibility to both infections is at least partly under genetic control, and the 3SR consortium was formed to investigate these genetic factors. Understanding the basis of genetic control to susceptibility will help direct breeding programmes to produce more resistant and, therefore, healthier and more productive animals.

Ovulation rate is the key factor determining the number of lambs per litter for sheep. Some particularly prolific breeds have been identified along with some important genes that affect fertility. The consortium is using cutting-edge genomic technologies in order to discover the main causative mutations affecting prolificacy (the production of offspring). This knowledge may assist breeders to produce animals with enhanced prolificacy, delivering significant benefits to productivity within the sheep farming industry.

Problem

For a variety of reasons, most notably the fragmented nature of the industries globally and their lower economic worth in the United States, sheep and goats have lagged behind other major livestock species in the development of comprehensive genomic information that can inform selective breeding. It is only recently (and aided by the work of the 3SR consortium) that high quality, draft reference genome sequences for sheep and goats have been published. With 100 million sheep and 11 million goats in the EU and a combined global population of around 1.94 billion heads, these species are of considerable economic, social and environmental importance. This is particularly the case in marginal areas, and the benefits that can be delivered by better understanding the genetic basis of health and welfare traits are highly significant.

Mastitis in sheep is conservatively estimated to cost the EU around €37m annually, while each year parasite infections cost more than £80m in the UK sheep industry and $500m in Australia.

Aim

The aim of the project is to discover selectable genetic markers (single nucleotide polymorphisms (SNPs)) and causative mutations – where possible in commercial populations – for traits that are critical to sustainable farming; namely mastitis susceptibility, nematode resistance and ovulation rate. Once identified, the consortium will verify the markers in additional commercial populations.

The overall objective is to deliver:
- Selectable genetic markers for the 3 traits that can be affordably applied by sheep and goat breeders.
- The tools and resources needed to achieve the first aim and provide a lasting resource.
- A wide-reaching dissemination of results to ensure a broad and long-term beneficial impact on European competitiveness and EU policy

In order to deliver on these aims, the consortium works closely with the complementary global efforts ongoing through the International Sheep Genomics Consortium (ISGC) and the International Goat Genome Consortium (IGGC).

Expected results

The close collaboration with these two Consortia (ISGC and IGGC) has led to significant improvements in the genomics resources available for sheep and goats. Sequencing is being carried out to improve the quality of the reference sheep genome, while large scale RNA sequencing has been performed to help with the sheep genome annotation. A whole-genome radiation hybrid map has been produced for goats, containing more than 30 000 markers ordered across the chromosomes.

As well as the reference genomes, the genomic tools (for example genotyping arrays) have also been greatly advanced throughout the duration of the project. A high density (50k) SNP chip has been developed for goats which has enabled over 2000 animals to be genotyped for the selectable genetic markers of interest.

Around 4000 sheep from 11 populations with relevant phenotypic data have been genotyped, using the 50K ovine SNP chip. A further 3 400 genotypes from the same populations and funded by other national projects, have been made available for analysis in 3SR.

Analysis of the data has led to the identification of genetic regions correlated with mastitis susceptibility (determined by somatic cell count), nematode resistance (determined by faecal egg count). These genetic markers are now being verified in commercial populations and further research is undertaken to explore the functional mechanisms of resistance.

For ovulation rate in sheep, some causative mutations have been identified and functional work is being carried out to understand how these mutations affect the structure and performance of the protein produced.

Potential applications

The 3SR partners are developing a low density SNP chip, which, once verified in commercial populations, could be used by breeders to identify animals with specific markers for susceptibility or resistance to mastitis and nematode infections. Knowing which animals are particularly susceptible or resistant to infection will help breeders make decisions about how to breed animals in the future.

The advances made to available genomic resources and to the basic understanding of sheep and goat genomes will guide future research efforts and boost our knowledge of these species.

The legacy of 3SR will hopefully be an improvement in the health, welfare and productivity of sheep and goat breeds in Europe and globally. This will be underpinned by a better understanding of the genetics controlling their resilience to disease generally and their productivity in a farming context.

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- Universidad de León, ES
- University of Thessaly, GR
- Teagasc –The Irish Agriculture and Food Development Authority, IE
- Warsaw University of Life Sciences, PL
- Commonwealth Scientific and Industrial Research Organisation, AU
- Huazhong Agricultural University, CN
- Instituto Nacional de Tecnología Agropecuaria, AR

Sustainability and Robustness

Sustainability and Robustness

Whether a breeder is seeking to optimise milk or egg production, meat quality or robustness – or to reduce emissions – genomics has the potential to revolutionise animal production. It can also help to meet increasing demands – the population is currently predicted to grow faster than yield.

Traditionally, animals are selected for breeding based on specific traits. But even the best phenotypic assessments cannot guarantee that offspring will inherit all desired traits. More knowledge is still needed on traits at the biological level and on traits that remain difficult to measure, such as behaviour or welfare.

The full sequencing of most economically important livestock species has led to the discovery of millions of single nucleotide polymorphisms, which are now being deployed in DNA microarrays, enabling genome-wide association studies to identify genotype-phenotype correlations for both simple and complex traits.

Genomics allow a holistic approach to improving production at large, while simultaneously improving animal welfare and product quality.

The projects outlined in this chapter seek to balance health and welfare while meeting demands for high quality milk, and investigate practical technologies to modify selection criteria or to develop new genetic tools. They will ensure a better use of whole genome sequence information, new phenotyping methods as well as upcoming epigenetics data.

[RobustMilk]

Innovative and **Practical Breeding Tools** for Improved Dairy Products from More Robust Dairy Cattle

Keywords
Dairy cattle, genomic selection, breeding goals, milk quality, genomics.

Summary
For centuries, animal breeders have been very effectively selecting livestock species making use of the natural variation that exists within the population. With breeding goals now broadening, the RobustMilk project was designed to develop new practical technologies that allow breeders to re-modify their selection criteria to include milk quality and dairy cow robustness.

Problem (background)
Since the mid-1990s, most leading EU dairy cattle breeding programmes have expanded their breeding goals to include health and fertility traits in addition to milk production. RobustMilk focused both on the robustness of cows and milk quality.

Robustness is a broad term and has a range of connotations. The RobustMilk team defined robust dairy cows as healthy, fertile and profitable (i.e. maintain homeostasis) under a range of commonly accepted and sustainable farming systems. From this overall definition of robustness, two priorities were selected: energy balance and environmental sensitivity.

The quality of milk comprises organoleptic, technological, nutritional and hygienic (safety) aspects. For this project, the nutritional and hygienic elements of milk quality in relation to human health were the focus.

The challenge for genetic selection is not to select for more robust cows or healthier milk alone, the challenge is to select simultaneously for robust cows with improved milk quality. However, what might be good for human health is not necessarily good for dairy cow health. Careful and thorough evaluation of the consequences of selection is therefore key.

Aim
The objective of RobustMilk was to develop new useful and practical technologies to allow dairy farmers and the dairy industry to refocus their selection decisions in order to include additional traits such as milk quality and dairy cow robustness.

Acronym:
RobustMilk

Project number:
KBBE-211708

EC contribution:
€2 968 000

Duration: 48 months

Starting date:
01/04/2008

Contract type: small scale collaborative research project

Results

The project delivered knowledge and tools in four areas:

- a common database for institutes across Europe,
- phenotyping using Mid-Infrared Red (MIR),
- statistical utilisation of existing data and
- tools for genomic selection.

The database includes unique and rarely recorded phenotypic measurements (feed intake, body condition scoring and detailed health and fertility recordings), as well as the genotypes. The results are summarised in a special issue of the journal *Advances in Animal Biosciences* published in 2013.

Applications

The database has enabled genome-wide association analyses, unravelling the genetics of energy balance, feed intake, fertility and milk quality. But the impact of the database goes much further. The database set the stage for several subsequent inter-continental genetics and genomics projects.

The RobustMilk team developed new methods for accurately and routinely predicting milk quality at little or no extra cost, involving the infrared spectroscopy of milk machines. The methods have been taken up in the UK, Ireland and Belgium.

The team also developed ways to predict energy balance using mid-infrared spectra. This could be important for breeders wanting to include energy balance in breeding objectives.

RobustMilk looked into environmental sensitivity and developed models able to estimate if the offspring from some sires are more sensitive than those from others. Furthermore, the project developed new criteria for selection, going beyond the current lactation average somatic cell counts (SCC). These statistical tools have the potential to significantly impact how SCC is evaluated genetically, and could help to improve udder health.

Genomic selection is now considered to be the optimal method of genetic evaluation in international dairy cattle populations. Progress in genomic selection for some traits is hampered by access to sufficiently large datasets with phenotypes. Robust-Milk has demonstrated the potential of genomically selecting for traits notoriously difficult to measure (e.g., feed intake) but has also proven that by combining information from multiple traits, the accuracy of using genomic selection can be increased, thereby increasing genetic gain.

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Project website

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[GREENHOUSEMILK]

Developing **genetic tools** to mitigate the environmental impact of dairy systems

Acronym:
GREENHOUSE-
MILK

Project number:
238562

EC contribution:
€2 173 481

Duration: 48 months

Starting date:
01/12/2009

Contract type:
Marie Curie Action:
Networks for Initial
Training

Keywords

Greenhouse gas emissions, between-animal variation, genetic tools, whole farm models.

Summary

Many EU countries have specific and binding commitments on the reduction of greenhouse gas (GHG) emissions and all sectors of the economy are under scrutiny in relation to their contribution to meeting the emissions target. GREENHOUSEMILK will increase understanding of the role of energy efficiency and partitioning in the overall GHG output of dairy systems, develop innovative tools to help farmers select "environmentally friendly" bulls to suit their systems, and show how to manage those bulls' female offspring optimally.

GREENHOUSEMILK will harness statistical and genetic tools to elucidate the genetics of emissions in dairy cattle, and develop innovative and integrative tools that address the environmental impact of dairy farming.

Problem

The EU25 produce approximately 132 million tonnes of milk from 24.3 million cows on 1.76 million farm holdings. Ruminant animals account for up to 20% of the world methane production with the EU25 dairy population producing approximately 3.2 million tonnes of methane (CH4) per year. Many EU countries have specific and binding GHG emissions reduction targets.

Technical solutions to reduce enteric methane emissions have been, and continue to be, extensively researched. Animal breeding that exploits natural animal variation in methane emissions is an additional mitigation strategy that is cost-effective, permanent, and cumulative. Nonetheless, little work has been done on the role of dairy cow genetics in dairy system emissions, particularly considering the role of genetics in the whole farming system, including feeding strategy and management policies (e.g., energy balance, housing periods, fertilisation and manure management).

Aim

The team will use statistical and genetic tools to shed new light on the genetics of emissions in dairy cattle. The project focuses in particular on the causes of variation in GHG emissions in dairy cows; genomic tools to help select for reduced GHG emissions; and how best to integrate animal GHG emissions into farm systems models.

Expected results

Causes of variation in GHG emissions
Improvement in production and functional efficiency of dairy animals and systems will result in a sustainable decrease in emissions at a fixed level of output. Models will be developed to describe the biological functions involved in energy usage (e.g. lactation, body energy change, growth) and wastage (e.g. emissions, premature culling). Emissions and environmental impact traits will be defined. Potential predictors of these traits will be studied and the relationships between emissions and other traits (e.g. milk fatty acid composition, health and fertility traits) will also be explored. Variation in performance will be examined, both within the cow (i.e. over her lifetime) and from cow to cow. Critical points for environmental impact will be identified.

Genomic tools to help select for reduced GHG emissions
Selection for traits that are directly or indirectly related to GHG emissions, like methane output, energy balance and cow wastage, is hampered by a lack of available data (direct or indirect) for genetic evaluation purposes. Tools that exploit genomic information may help to reduce the requirement for widespread and detailed phenotypic measurements. The availability of new genomic tools (high-density SNP arrays and Genomic Selection approaches) opens up the possibility to include genome-wide information in breeding values. The potential of using genomic selection to reduce dairy emissions, via selection of traits that are indirectly related to GHG emissions, will be examined.

Integrating animal GHG emissions into farm systems models
Models will be developed that can predict system emissions accounting for specific farm variables (e.g. genetic and dietary). The models will be parameterised to account for different EU dairy systems (e.g. feeding and/or grazing regime, genetic merit, system intensity). The impact of different variables in specific system types will be modelled. This information will be useful in guiding policies that encourage shifts over time to systems that have lower environmental impact.

Potential applications

For farmers, the results will increase efficiency and thus competitiveness. The findings will also help all countries in their efforts to meet greenhouse gas emission targets.

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Project website

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[SOLID]

Sustainable **Organic and Low** Input Dairying

Keywords

Dairy, organic, low-input, sustainable, efficient.

Summary

Organic and low-input dairy farming systems are increasingly seen as delivering multifunctional benefits to the agricultural industry and society, but technical and economic constraints prevent widespread adoption. SOLID will deliver an innovative toolbox of novel methodologies that will contribute to the competitiveness of the dairy industry and increase the effectiveness with which these benefits are delivered. The project is investigating the use of breeds and feeding strategies to maintain productivity and improve animal health and welfare, while meeting the market requirement for high quality milk.

Problem

In the rapidly changing environment in which Europe's agri-food industries must prosper, new knowledge-based farming systems are required that are profitable at a farm level, that produce the competitive food products markets demand, and that are environmentally sustainable and energy-efficient. In dealing with the challenges facing agriculture – such as climate change and biodiversity loss – the multi-functional potential of agricultural systems is now as important as productivity for a sustainable future for European agriculture.

Aim

The objective of SOLID is to support development and innovation in organic and low input dairy systems, thus optimising competitiveness while ensuring a sustainable and profitable dairy industry in Europe. At the same time, the project seeks to maximise the potential of these systems to deliver environmental goods and enhance biodiversity.

SOLID provides an effective forum of key stakeholders from across Europe who are working together to develop the sustainability and competitiveness of the organic and low input dairy sector and to meet the expectations and demands of EU consumers and EU policy.

Expected results

The outputs and potential impacts of SOLID include:

- Scientific evidence as to whether genotypes which are perceived by the dairy industry to be 'adapted' to organic and low-input management systems are actually different from the predominant conventional breeds. Evidence of differences will be examined in terms of metabolic balance, fertility, health and product quality. This, and the identification of indicators for «adaptation», have the potential to impact on the future direction of breeding programmes for organic and low-input production systems, with a subsequent improvement in the overall competitiveness of these systems.

Acronym:
SOLID

Project number:
266367

EC contribution:
€5 955 858

Duration:
60 months

Starting date:
01/04/2011

Contract type:
Large-scale collaborative research project

- Identification and evaluation of novel feed components, together with a newly developed decision support tool to improve the self-reliance, and hence the competitiveness, of European organic and low-input dairy farmers. Making linkages between non-agricultural supply chains and dairy production will emphasise the multifunctional potential of organic and low-input dairy production systems.
- A life-cycle assessment framework that will allow decision-makers along the dairy food chain (farmers and processors) to improve their environmental performance. At the same time, environmental benefits will be communicated to consumers – an important impact factor helping consumers acknowledge the added value of such production systems.
- Improved competitiveness within the organic and low-input dairy sector through identification of optimal strategies for introducing acceptable innovations that enhance competitiveness and sustainability along the whole supply chain.
- Findings from relative-efficiency-analysis, which will show improvement margins and reveal pathways that ensure a win-win situation for both economic and sustainability criteria. User-friendly modelling and planning tools will be developed to encourage the effective adoption and geographical adaption of organic and low-input farming production.

Potential applications

In addition to the above, SOLID will work actively with stakeholders in a participatory approach to assess innovative strategies developed by organic and low input dairy farmers and producer groups in relation to roughage-based feeding strategies, animal health issues and product quality. This participatory approach will encourage the effective adoption and geographical adaption of innovative strategies of organic and low input farming.

Project website

www.solidairy.eu

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[LowInputBreeds]

Development of **integrated livestock breeding and management strategies** to improve animal health, product quality and performance in European organic and 'low input' milk, meat and egg production

Keywords

Organic and low-input livestock farming, dairy, beef, lamb, pork and eggs.

Summary

The project 'LowInputBreeds' aims to develop integrated livestock breeding and management strategies to improve animal health and welfare, product quality and performance in European organic and 'low input' milk, meat and egg production. This will be achieved through research, dissemination and training activities. Research will identify robustness and product quality traits, as well as innovative breeding concepts.

Problem

Almost without exception, breeding goals in livestock production have in recent years been dominated by demands for intensive systems striving for higher yields. Thanks to progress in animal breeding, today's dairy cows, pigs and poultry are capable of high outputs, but only when receiving high nutritional and veterinary support.

Under organic or low input management, product quality, health, welfare and fertility deteriorate with modern genotypes. Unfortunately, reduced input systems are in the minority and there is insufficient demand to encourage breeding companies to address these weaknesses. Instead, they attempt either to minimise the negative impact on high input animals, or use traditional unimproved breeds – neither of which is ideal.

Acronym: LowInputBreeds

Project number: 222623

EC contribution: €6 000 000

Duration: 60 months

Starting date: 1/5/2009

Contract type: Large-scale collaborative project

Aim

It is increasingly recognised that breeding priorities differ between high and 'low input' systems and the latter tend to be neglected. Recent studies (e.g. the FP6 project QualityLowInputFood, www.qlif.org) found that livestock breeds (and breeding systems) developed for 'high input' conventional production lack specific:

- 'robustness' traits required for optimum performance in organic and 'low input' production systems (e.g. extensive outdoor grazing and free range);
- product quality traits (including nutritional, sensory and animal welfare related quality parameters) demanded by the organic and 'low input' sector.

However, breeding concepts, methods and programmes focused on the needs of organic and other 'low input' systems have not been fully addressed by R&D. This project is developing: 'robustness' (resistance to biotic and abiotic stress factors, survival of young animals, longevity, fertility; and 'product quality' traits (including ethical qualities related to animal welfare and environmental impact related traits) that have a higher priority in organic/'low input' compared to 'high input' conventional systems.

The project has four main science and technology objectives:

- Develop and evaluate innovative breeding concepts for five livestock production systems (dairy cows, dairy and meat sheep, pigs and laying hens) and design species-specific breeding strategies for different macroclimatic regions in Europe.
- Integrate the use of improved genotypes with innovative management approaches that include improved diets, feeding regimes and rearing systems. This will focus on issues (e.g. mastitis and parasite control, animal welfare problems) where breeding or management innovations alone are unlikely to provide satisfactory solutions.

- Identify potential economic, environmental, genetic diversity/plasticity and ethical impacts of the project to ensure they conform to societal priorities and consumer demands/expectations, and are acceptable to producers.
- Establish an efficient training and dissemination programme aimed at rapid exploitation and application of project deliverables by the organic and 'low input' livestock industry.

Expected results

Many studies are ongoing, although some findings have been published. Provisional findings are:

Dairy cows

- The accuracy of genomic selection is greater for high heritability traits such as milk yield. But the expected benefits, in terms of relative gains in accuracy of estimated breeding values, are likely to be greater for low heritability traits, such as those related to fertility.

Sheep

- Sainfoin is effective in parasite control in pre-lambing ewes, reducing the faecal egg output by about 70% compared to forage without tannins. However, this effect is transient, disappearing within two weeks of feeding ending. Tannin-rich concentrates given at this time are not effective in reducing egg output.
- The timing of pasture access for lambs in Sicily influences meat quality. Lambs restricted to grazing during mornings only have higher levels of indol in carcase fat compared to those with access to pasture in the afternoons or throughout the day. The latter have a healthier fatty acid profile compared to housed lambs, or those with restricted access to grazing.

Pigs

- Sow productivity and carcass quality of traditional breeds appear unsuitable for the commodity pork market. But, for niche markets, the quality of meat for these breeds adds value. Additionally, the dark skin of many traditional breeds offers a greater resistance to sunburn and might be an advantage in hotter climates.
- Heat stress tolerance can be measured by reproductive performance. This has been identified in a large dataset (100 000 records) collected on farms in Portugal and Spain. For farrowing rate, heat stress heritabilities range from 0.02 to 0.05.

Laying hens

- Farmer workshops in Switzerland and the Netherlands identified an 'ideal hen' for low input systems. This hen should have a lower peak production and higher eating capacity, relative to modern hybrids, and would not display smothering behaviour or feather pecking. Many participants described the ideal hen mentality as 'optimistic', 'not stupid', 'bold and assertive'.
- A dataset of 276 free range and organic poultry units in Switzerland, France and the Netherlands shows a wide range of genotypes with clear differences in flock and farm size, and housing system, between the three countries. Production was similar, except for organic flocks in the Netherlands with a lower egg production and a higher mortality. Comparing countries and production systems, white hens and mixed flocks (in Switzerland) perform relatively well in contrast to silver hens, which showed higher mortality and more poorly feathered birds

Potential applications

The project will help reduce production problems and improve animal health and welfare in European organic and 'low-input' production systems, while improving the quality of milk, meat and eggs for consumers. Many findings could also benefit for livestock systems currently relying on high inputs. As pressure on prices for feed, fertiliser and other resources increase worldwide, many intensive units are now starting to question high inputs.

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Project website

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[SABRE]

Cutting-Edge Genomics for **Sustainable** Animal Breeding

Keywords

Livestock, genomics, epigenetics, dna tools, breeding strategies, animal health and welfare, mastitis, boar taint, gut health, eggshell quality, fertility.

Summary

SABRE will provide fundamental knowledge on 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 EU policy.

Problem

As benefits from selective breeding are cumulative, even small increases to the rate of annual improvement can have very large impacts over time. The application of new genomic technologies in practical breeding can increase the rate of genetic improvement by up to 50%, particularly for some traits, and is essential to improve the EU's food supply. In combination with enhanced relationships with industry, this leads to increased economic returns and more sustainable agro-production.

Aim

The SABRE project combined the power of gene mapping technologies, gene expression studies in target tissues and modern bioinformatics tools, with available and expanded genome sequences. The results can be used to determine the origin of genetic variation in quality, safety, health and sustainability traits in real-world livestock populations.

Research was clustered in three areas:

- development of underpinning technologies and knowledge, including mathematical genomics, epigenetics and sequencing
- understanding the genomics of key biological systems, concentrating on fertility, mammary function and the intestine
- tackling focused breeding goals, including meat quality, reduced incidence of zoonotic infection and improved animal well-being.

Results

The mammary gland, the digestive system and fertility were the focus of separate basic research packages, with more applied research aimed at enhancing eggshell quality for food safety; improving animal behaviour linked to welfare; and eliminating boar taint in pig meat. SABRE has provided fundamental knowledge of genomics and epigenetics in these topics, along with the selection tools required to implement this knowledge in breeding programmes. The project also demonstrated that genomic selection can actually be used in practice. SABRE provided €1.6 million in funding towards the draft sequence of two chromosomes of the pig genome.

The results have been reported in more than 450 publications, of which at least 120 featured in refereed journals. The knowledge gained has allowed animal breeders to increase the emphasis given to animal health, welfare, food safety, product quality and ultimately sustainability within ongoing breeding programmes.

SABRE's research has also contributed to changes in EU policy on sustainable animal breeding, particularly by contributing to the elimination of boar taint in pig meat by genetic means and thereby working towards abolition of castration of piglets. This will improve both animal welfare and economic sustainability benefits for the EU pig industry.

Potential applications

Poultry and food safety

The EU's 370 million laying hens produce 9.9 million tonnes of eggs each year. Poor egg-shell quality can lead to substantial waste through cracked or damaged eggs, as well as early culling of hens. Cracked eggs are also more susceptible to bacterial infections that can cause Salmonella. SABRE developed a number of tests that will help breeders to select hens that lay eggs with stronger shells. If this results in even a 10% (or 14 000) reduction in human Salmonella infection cases across the EU, it could save about €400 million annually.

Pigs and animal welfare

Boar taint is an unpleasant odour and taste that affects meat from around 5-15% of uncastrated male pigs. To avoid the problem, approximately 90 million male piglets are castrated in the EU every year shortly after birth. The EC and many pig industry stakeholders wish to end castration in Europe by 2018 so as to improve pig welfare. SABRE has contributed to the development of a genetic test for boar taint, which makes selective breeding a realistic alternative to castration, without reducing meat quality.

Cattle and disease resistance

Mastitis is a painful inflammatory reaction in the mammary gland due to invasion and colonisation by diverse pathogens. It is also one of the main reasons for antibiotic use in dairy production and affects 6.9 million dairy cattle in Europe at an annual cost of €2 billion. Through the SABRE project, genes and genetic pathways involved in the immune response to bovine mastitis have been identified. This information can now be used to help breeders identify and select for cows that are more resistant to mastitis, thus simultaneously improving animal welfare, food safety, product quality, economic returns and reducing the need for antibiotic use.

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[Gene2Farm]

Next generation European system for **cattle improvement** and management

Keywords

Cattle industry, SME, genomic selection, sequence data, novel phenotypes, dissemination.

Summary

The Gene2Farm project is addressing the needs of the cattle industry for an accessible, adaptable and reliable system of genetic selection which uses new genomic knowledge to underpin the sustainability and profitability of European cattle farming. The comprehensive programme of work includes the development of statistical theory, genome sequencing, and assessing new phenotyping approaches. The project will sequence the genome of key animals and exchange data with other international projects to create a comprehensive bovine genome sequence database. The breeding tools created by the project will be tested in collaboration with dairy, dual purpose, beef and minority breed organisations.

Problem

The phenotypic characteristics of individuals are governed both by the environment and by their genetics. These characteristics include not only their overall appearance, but also other important characters, such as their susceptibility to diseases, propensity to obesity, growth rate, physical strength and fertility. With increasing understanding of genetics, sophisticated statistical methods have been developed to predict the genetic quality of individuals using information from daughters, parents and other relatives, not just measurements on the animal itself. These approaches have been very successful in selecting for traits such as growth rate or yield, e.g. of meat or milk. Milk yield of dairy cows has increased dramatically over the past 40 years, but in parallel, other traits have been lost, such as fertility and health.

With the availability of the bovine genome sequence and SNP (single nucleotide polymorphisms) panels, it is now possible to estimate the effects of each genomic region on any trait for which data is recorded. In theory, using this information, it should be possible to predict the genetic component of an individual's phenotype directly from the genotypic data. This method has been taken by the dairy cattle breeding industry, using genome-wide DNA markers to estimate a 'genomic breeding value' for

bulls. The approach is quite attractive as the best bulls can be identified and used for breeding much sooner, compared with traditional phenotype based methods.

So genome-based approaches have the potential to speed up the rate of genetic progress, reduce the infrastructure costs of large-scale progeny testing, and in principle improve selection strategies for less numerous breeds. It is now possible to derive 'prediction equations' to estimate the breeding values of other animals lacking phenotypes. This has been demonstrated in the Holstein breed, with reliabilities of prediction up to 80%, for some traits. But genomic selection can only be exploited in breeds with very large population sizes, when phenotypic and genotype data on a sufficiently large reference set of animals are available. Attempts to use predictive information derived from Holstein in other breeds has met with limited success.

In addition, using genomic information it should possible to address a wider range of commercially important traits and reduce inbreeding, hence controlling the loss of genetic diversity.

Aim

The objectives of the Gene2Farm project are to derive complete genome information for identifying variations among bovine genomes, to optimise SNP genotyping panels and explore further the use of bovine genomic selection. With this in mind, the consortium is producing new genotyping data, together with whole genome sequence data, on a certain number of individuals within various European cattle breeds.

The project is also developing the tools to impute higher density genome information from lower density genotype data, and to make exchange information among data types easier. It is measuring a wider

range of biological variables underlying important commercial traits, in order to provide data for use in genetic selection for improved robustness, and developing appropriate statistical models and applications to use genomic and phenotypic information in order to optimise and customise genetic selection strategies. An important objective is to disseminate the results to SMEs, the wider cattle breeding industry and to end users.

Potential applications

Detailed analysis of genome sequences will identify variations in genome structure, shared alleles, allele frequencies and haplotypes present – within and between populations. This information will be used to optimise the SNP panels and select SNP to tag haplotypes, thus enhancing the use of genotype information. The results will also be used to predict full genome sequence from low density genotype data and ensure that this approach is optimised both within and between breeds.

Technological developments have provided farmers with on-farm electronic remote sensors and management systems to record, in real time, production data (yield of fat and protein content of milk), milk somatic cell scores, weight, movement, body condition, rumen temperature, and pH and hormone levels and more. If such data were available to inform genome-based selection models, improvements could be possible in a wide range of important traits, which would impact on e.g. efficiency and longevity. Gene2Farm will develop standardisation protocols to work towards the unification of data collected in diverse systems and create structures that the industry could use for centralised data collection and management at the appropriate level, from local systems to international exchange.

The project will therefore work towards a new system for the more effective selection of cattle for improved productivity and robustness to underpin a sustainable farming system.

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Project website

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[PIGENDEF]

Towards **marker assisted selection** against congenital defects in pigs

Keywords

Genetic defects, pig, linkage disequilibrium, causative mutations, marker assisted selection.

Summary

Genetic defects in pigs cover a wide range of undesirable conditions, such as hernias (umbilical and inguinal/scrotal hernias), cryptorchidism and splay leg, and to a lesser extent intersexuality, anal atresia and progressive ataxia and spastic paresis. These defects are fairly common in swine, leading to poor animal welfare and economic losses. They are therefore a significant problem for pig producers and breeding companies. The PIGENDEF project sought to increase knowledge of the genetic background to those defects in pigs so as to pave the way for effective marker-assisted selection. It focused in particular on scrotal/inguinal and umbilical hernias, and cryptorchidism.

Problem

Together, hernias, cryptorchidism, splay legs, intersexuality, anal atresia and progressive ataxia, and spastic paresis affect around 3% of pigs in commercial populations worldwide. In Europe, the economic loss due to these congenital defects is estimated at EUR 200 million per year. In addition to economic loss, these defects also have a serious impact on animal welfare and health. Some of the defects cause direct piglet mortality, while others lead to their culling.

Hernia inguinalis and hernia scrotalis occur within the pig population at frequencies from 1.7% to 6.7%. These numbers are averages and in practice percentages up to 10% are recorded in offspring of particular boars. However, breeding organisations select against inguinal/scrotal hernia within their own lines, independent from each other. Thanks to this selection, they can keep the prevalence of hernias below 2%. Nevertheless, despite years of selection, hernias remain present. Although the percentage of hernias can be fairly well controlled within lines, the results of certain combinations, over breeding programmes, can be disastrous, with incidences of over 10%.

Animals with scrotal/inguinal hernia show an increased incidence of cryptorchidism and are difficult to castrate. This has a cost for the pig producers since they must pay the slaughter house a fine for cryptorchids and boars (EUR 12.50 per

Acronym:
PIGENDEF

Project number:
262247

EC contribution:
€732 600

Duration: 30 months

Starting date:
01/01/2011

Contract type:
Research for SMEs

animal). As pork producers do not buy affected animals, the piglet producers must raise them themselves or sell them as slaughter piglets. The average loss per pig can be estimated at EUR 50.

Pigs that develop this type of hernia need more medical attention compared to healthy animals, and the extra labour and drugs invoke extra costs for the pig producer. On top of that, mortality rates are higher for animals affected with scrotal/inguinal hernia as a result of the strangulation of the small intestine in the scrotum. It is estimated that only 50% of affected animals reach slaughter.

Last but not least, pigs with inguinal/scrotal hernias display inferior zootechnical performance parameters. They cannot feed efficiently and their growth is affected. This leads to higher feed costs, slower throughput, lack of product uniformity and a consequent loss of income with a higher ecological impact.

Altogether the economic losses due to scrotal/inguinal hernias in the European pig population (153 million animals) are close to EUR 50 million/year. These estimations were based on a prevalence of 2% with half of the pigs being slaughtered and fined (EUR 19.2 million). The other half will survive and cost the pig producer approximately EUR 20 per affected piglet due to inferior performances, drugs and mortality during the growing period (EUR 30.6 million).

Aim

The process of selection for livestock improvement is widely accepted by the public, so a selection strategy for reducing the prevalence of scrotal and inguinal hernias is seen positively. The aim of the project is to map the chromosomal areas that have an effect on genetic defects – and possibly identify the causal mutations that underlie these defects. This will involve:

- Collection of phenotypic data and biological material from affected animals, litter mates and their parents;
- Identification of genetic markers associated with the sensitivity for the congenital disorders;
- Validation of the genetic markers found in crossbred lines;
- Functional analysis of the uncovered genetic markers for congenital diseases.

Pigs were genotyped using the 60K Porcine Illumina SNP chip, and analysed using the newest, tailor-made genome-wide association analysis software.

Results

The research should lead to markers in linkage disequilibrium or causative mutations for the congenital genetic defects studied.

Potential applications

The markers will be implemented in a practical test for selection against congenital genetic disorders in pigs.

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Project website

www.pigendef.eu

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[SelectionForWelfare]

The potential of behavioural play markers to **improve welfare** in farm animals through selection

Acronym:
SelectionForWelfare

Project number:
277031

EC contribution:
€75 000

Duration: 36 months

Starting date:
01/04/2011

Contract type:
Marie Curie action:
International Re-
integration Grant
(IRG)

Summary

The farm animal of the future is meant to be robust, adapted and healthy. 'Robustness' requires an ability to combine high production potential (growing or reproductive) in an range of environmental conditions with resilience to stressors. This project integrates animal behaviour and welfare with genetics, nutrition, immunology, reproduction and physiology to analyse whether play behaviour – a key indicator of absence of stress – could be used to improve and ensure welfare.

Problem

For livestock species, breeding goals focus primarily on improving production traits. However, selection for high production efficiency has often resulted in reduced welfare in terms of health and fitness. This has raised questions about what is ethically acceptable in animal breeding. As a result, there is a growing interest in the potential practical, economic and ethical issues involved in genetic selection for behaviour, in addition to selection for production traits.

Aim

Among farm animals, a number of behavioural traits, such as aggression, sociality, stereotypy, fear and maternal behaviour are believed to be heritable.

Play behaviour has been proposed as a new and promising potential indicator of animal welfare; animals play only if they are healthy, safe, well-fed and in a relaxed state, but not if they are under stress. Play behaviour is related to the development of strength, motor coordination and physical resistance, learning of novel environmental information and creativity, and the acquisition of social skills, enhancing flexibility and versatility of animal actions so that they are prepared to handle future real-life situations. Therefore, play behaviour can be used as an indicator of animal welfare. To date, very little information is available on play behaviour in animal production systems.

This multi-disciplinary investigation into the phenotypic expression and the genetic background of play behaviour in piglets will investigate the feasibility of including play behaviour measurements in the breeding goal. It will also investigate the phenotypic and genetic relationship between play behaviour, and animal production traits and welfare.

In addition, the project is investigating the behavioural elements involved in play behaviour in piglets. The study is also investigating the phenotypic and genetic correlation between play behaviour and animal production as exemplified by growth traits and food efficiency, immunology, learning ability and adaptability, and stress response.

Breeding for behaviour presents a number of serious challenges, and breeding for welfare even more. It is difficult and time-consuming to directly measure behaviour in the consistent and reliable manner needed to evaluate the large numbers of animals necessary for a breeding programme.

The major obstacle to genetic solutions is determining which trait(s) to select for in order to truly improve animal wellbeing, either through direct measurements or through indirect measurements that are strongly correlated. This research is tackling the problem by analysing photographic and film images with specific programmes to provide objective measurements on play behaviour in different contexts.

Expected results

This investigation will result in an ethogram of behavioural elements displayed during social play in piglets. The final objective of this study is to investigate which behavioural elements are the best candidates for use in a selection programme in pigs aimed at improving animal welfare in addition to improving animal production traits.

Potential applications

SelectionForWelfare is expected to result in further insights into the need for considering behaviour and welfare traits in breeding objectives for farm animals.

Breeding companies will be able to apply the findings to breeding strategies. For, farmers higher levels of animal welfare are expected to result in higher levels of production. For the livestock industry, higher levels of animal welfare will improve the image of livestock production. And pigs will be raised with a higher level of animal welfare.

References/publications

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Breeds and
Biodiversity

Breeds and Biodiversity

Livestock animals have been gradually shaped over time by domestication and selection intended to accentuate various traits for human benefit. For each farm animal species, an array of breeds have been developed worldwide with distinct characteristics adapted to specific environments.

Recent innovative breeding methods have brought very fast and remarkable increases in production traits, such as milk, meat or egg production. But this intensive selection process comes with drawbacks, such as increased inbreeding and a partial destruction of genetic diversity. Selection for production traits can also lead to reduced performance in other traits, such as fertility, perinatal mortality or robustness.

Many molecular mechanisms supporting genetic selection are still poorly understood. A better understanding of livestock population genomics will help build long-term sustainable breeding schemes. The identification of neutral and adaptive/selective genetic variability can be used to assess the rate of inbreeding and structure breeding programmes accordingly. The objective is to maximise the use of adaptive variation to ensure animals are suited to their environments and optimised for selection goals, while preserving neutral genetic variations at the same time.

In this chapter, several projects go back in time to investigate the impact of domestication on animal groups, look into neutral and functional genetic variation in livestock populations, and assess the use of whole genome data to develop and optimise the conservation and genetic management of livestock diversity – as well as that of endangered livestock species.

[NEXTGEN]

Next generation methods to **preserve farm animal biodiversity** by optimizing present and future breeding options

Keywords

Whole genome sequencing, genetic resources, biodiversity, landscape genomics, wild ancestors, disease resistance, breeding programmes, cattle, sheep, goat.

Summary

NEXTGEN proposes the bold step of using whole genome data to develop and optimise conservation genetic management of livestock diversity. The rationale for choosing whole genome data is to 'future-proof' DNA-based analysis in livestock conservation against upcoming changes in technology and analysis. Thus, in the context of whole genome data availability, the NEXTGEN global objective is to develop cost-effective optimised methodologies for preserving farm-animal biodiversity, using cattle, sheep, and goats as model species.

Problem

There is a growing awareness that threats to biodiversity are increasing, whether measured in terms of extinction rates, destruction of ecosystems and habitat, or loss of genetic diversity among the domestic species used in agriculture.

During the last century, the European livestock sector underwent striking changes as large-scale production expanded. The formulation of the modern breed concept during mid-1800s and its application to breeding and husbandry practices led to the formation of well-defined breeds, exposed to intense anthropogenic selection.

The progress of livestock management practices, the introduction of artificial insemination and embryo transfer, the improvements in feed technology and the use of vaccines and therapeutics against endemic diseases have fostered the spread of industrial breeding. This has led farmers to progressively substitute the less productive, locally adapted, autochthonous breeds with highly-productive cosmopolitan breeds, and to progressively abandon agriculture in marginal areas. Therefore a significant number of cattle, sheep, and goat breeds have already disappeared and many are presently endangered. This same process is now taking place in Africa and Asia.

Acronym:
NEXTGEN

Project number:
244356

EC contribution:
€2 999 999

Duration:
48 months

Starting date:
01/04/2010

Contract type: small scale collaborative research project for specific cooperation actions dedicated to international cooperation partner countries

Aim

NEXTGEN will generate whole genome data in selected populations of sheep, goats, and cattle. The consortium is developing the required bioinformatics methods and tools, taking advantage of the 1000 human genomes project, and focusing on the identification of genomic regions under recent selection (adaptive versus neutral variation). In addition, the project is developing methods for optimising breeding and bio-banking – taking into account both neutral and adaptive variations – and innovative bio-banking methods based on freeze-dried nuclei.

The team aims to provide guidelines for studying disease resistance and genome/environment relationships in a spatial context, and to assess the value of wild ancestors and breeds from domestication centres as genetic resources. In addition, it will evaluate the performance of a surrogate system compared with that of whole genome sequence data for preserving biodiversity.

Expected results

NEXTGEN will produce better biodiversity-assessment in sheep, goats, and cattle by using whole genome, with a special focus on traditional breeds and wild ancestors where they still exist. The project will develop new strategies for improving current breeding programmes.

Traditional livestock breeding programmes tend to emphasise genetic improvement for performance traits with little concern for genetic variability beyond the short-term avoidance of inbreeding. Various methods for optimising marker-assisted selection while maintaining diversity have been developed and tested; NEXTGEN will take these advances a step further, considering genomic information in approaches to maintain genetic variation while optimising selection response in breeding programmes.

The methodologies developed will enable precisely targeted selection at loci with selective variation, while maintaining variability at neutral loci and genomic regions such as the MHC. The project will also produce innovative approaches to preserving both adaptive and neutral genetic variation.

Potential applications

NEXTGEN's results will boost the conservation of the most valuable traditional breeds, as well as wild ancestors of sheep and goats that can act as genetic resources in the future. The project will promote the implementation of breeding programmes that target both the improvement of performance traits and genetic diversity.

Publications

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Project website

http://nextgen.epfl.ch/

Keywords

Whole genome sequencing, genetic resources, biodiversity, landscape genomics, wild ancestors, disease resistance, breeding programmes, cattle, sheep, goat.

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[SelSweep]

Molecular characterization of **genetic factors** in the pig under selection during speciation, domestication and breeding

Keywords

Pig, selection, whole genome sequencing, speciation, domestication.

Summary

Ever since Darwin's first description of the theory of evolution, the forces that act during speciation and, to a lesser extent domestication have attracted much attention. However, details about how speciation events have shaped genomes and, vice versa, how changes in the genome affect speciation and domestication, are still poorly understood. The SelSweep project aims to address these questions in detail at the molecular level in the pig.

The pig is of particular interest because domestication and selection have resulted in a large number of distinct breeds worldwide with very distinct characteristics. A unique feature is the availability of 12 closely related pig species that have diverged over a time span of 1 to 10 million years. The SelSweep project will substantially advance knowledge of evolutionary biology at the molecular level, while the identification of genes affected by selection opens up new directions for further improvement of this important livestock species.

Problem

Understanding the molecular mechanisms underlying genetic selection and how the genome is shaped by selection, is an important central theme in population genomics, with many crucial aspects still poorly understood. The SelSweep project is addressing these questions by analysing the complete genome sequences of a large number of closely related species, breeds and populations.

Aim

The overall objective of the SelSweep project is to understand the genomic forces acting during speciation, domestication, and breeding. This overall goal can be further broken down into the following specific objectives:

1. Providing insight into genes and regions contributing to speciation.
2. Identifying the genes under strong selection during domestication, and breeding (identifying selective sweeps).
3. Giving further insights into the relative contribution of the different kinds of variation (SNP, CNV) during selection. This will also enable a better assessment of the degree to which these different types of variation affect phenotypic differences.

Results

With SelSweep entering its fourth year, the project has completed the sequencing of the whole genome of over 200 individual pigs from a large variety of European and Asian breeds and wild boars, as well as the genomes of 18 other individual Suids from Southeast Asia and Africa. The analysis of the first 55 individuals has already provided a much clearer view of the events that shaped the genomes of these animals. The results show genomes that are shaped by a complex pattern of admixture events, both natural and human mediated. A higher nucleotide variation can be observed in the Asian pigs compared to the European pigs, and the team has estimated the divergence between the European and Asian wild boar took place around one million years ago.

The D-statistics analysis of the complete genome of 10 individuals from the genus Sus (Eurasian wild boar and related species), representing five well defined species and three individual sub-species from insular and mainland South-east Asia, revealed that the genomes of these closely related (sub) species are shaped by a myriad of past evolutionary events such as extensive intra- and inter-specific gene flow.

The team has been able to trace each speciation event back to a precise geological stage, highlighting the importance of cyclical climatic fluctuations in driving and reversing the process of speciation. In addition, results showed that humans played a role in the repartition of these species across ISEA and MSEA by translocating pigs. The results demonstrate the power of genomic analysis to decipher a highly detailed speciation history of a complex system.

The sequencing results confirm earlier studies based on mitochondrial DNA sequences that the pig was domesticated independently in Europe and Asia. Admixture analysis of European breeds clearly identified the admixture of Asian breeds in the 18th and 19th centuries. Findings indicate that up to 35% of the genome of the European breeds has an Asian origin.

Potential applications

The knowledge about genes and pathways under selection in the different breeds can help to identify potential targets or potential variants to be implemented in new breeding programmes. In this respect it complements the genomic selection currently being used by the pig breeding industry. The results also provide a catalogue of genetic variation and haplotypes that are segregating within current breeding populations. These results can be used for imputation of additional genetic variation in individuals genotyped with medium density SNP chips (i.e. the Illumina porcine 60K beadchip).

References/publications

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[NEUTRADAPT]

Estimation of neutral and **adaptive/selective** genetic variation in farm animal species

Keywords

Next generation sequencing, sheep, goats, cattle, neutral and adaptive variation, sequence analysis.

Summary

Increasing amounts of genomic data offers new insights into genetic variability in animal populations. Genetic variation can be differentiated into functional variation and neutral variation. Estimating the relative extent of functional and neutral variation will increase understanding of the biology underlying genetic adaptation and selection, and help devise breeding strategies to improve specific traits while preserving genetic diversity at neutral sites. The objectives of the NEUTRADAPT project are to estimate neutral and functional genetic variation in livestock populations, and explore possible applications of this knowledge in animal breeding and conservation programmes, using data on sheep, goat and cattle populations.

Problem

Advances in DNA sequencing technology allow genomes to be sequenced rapidly – and relatively cheaply. The genomes of all the major livestock species have either been sequenced, or are being sequenced.

Projects have identified an enormous number of genetic variations: e.g. many millions of single nucleotide polymorphisms (SNP) have been described and large panels of thousands of validated SNPs (50k, 800k SNP-chips) are now available. In addition, whole-genome sequences of many individuals are becoming available. This huge amount of genomic information can be used for fine-scale analysis of the effect of genetic variations on the phenotypes of farm animals, and for the definition and study of biodiversity.

Genetic variation can be differentiated, within the boundaries of current scientific knowledge, into functional and neutral variation. While functional variations include genetic mutations that play a role in the adaptation of farm animals to their environment (adaptive variation), or that have been under directional selection for traits of agricultural interest in farm species (selective variation), neutral variation has no apparent influence on adaptation or on the traits under selection. Both are inherited through linkage or genetic drift.

Acronym:
NEUTRADAPT

Project number:
276699

EC contribution:
€45 000

Duration: 36 months

Starting date:
01/06/2011

Contract type: Marie Curie Action: International reintegration grant

Estimating the relative extent of neutral versus adaptive/selective genetic variation in farm animals is of interest for conservation genetics, biodiversity assessment and animal breeding. However, the definition of neutral variation poses significant theoretical problems, not least of which is that variation that is neutral in one environment may be adaptive, or under selection, in another.

Aim

The NEUTRADAPT project aims to increase understanding and to use adaptive/selective and neutral genetic variation in animal breeding. The project has the following main objectives:

- To estimate neutral and adaptive/selective genetic variation using whole genome data in cattle and high density SNP markers in sheep and goats;
- To use the estimated neutral and adaptive/selective genetic variation to design selection methods that maximise genetic gain while limiting the rate of inbreeding in cattle, sheep and goat populations;
- To develop approaches for the preservation of genetic variation based on differentiating between neutral and adaptive/selective genetic variation, and compare the success of these approaches with traditional methods to limit the rate of inbreeding.

Expected results

The project should increase understanding of the potential of the various forms of genetic variation in animal breeding.

Potential applications

The genomes of all mammalian species show a high level of polymorphic variation from single nucleotide variations, through copy number variations to large segmental duplication. The functional relevance of the majority of these variations is unknown: many may indeed not have functional effects, while others have profound effects on the phenotype. The distinction between variations with an effect, and their specific effect from those with no appreciable phenotypic effect will enable genomic data to be better used in the selection of livestock, e.g. for productivity, while maintaining the long term viability of the population under selection.

Selection – both traditionally based on pedigrees, and recent approaches based on genomic information – has brought about rapid and impressive genetic improvements in farm animal species. However, selection has the drawbacks of increasing inbreeding and obliterating genetic diversity. Knowledge of the neutral and adaptive/selective components of genetic variation could be used to focus selection on adaptive/selective variation. In this way, neutral variation would not passively follow selection for target traits, due to linkage, but would be actively preserved and limit the rate of inbreeding and the conservation of genetic variability (lower Bulmer effect). More efficient selection schemes could therefore be devised for farm animals based on the estimation of neutral and non-neutral genetic variation.

Knowledge of the distribution of variations will be essential in designing conservation programmes for endangered breeds or populations. The genetic variation will not only be quantified by summing up the entire genome, but will be classified into different components: genomic regions with an adaptive or selective meaning, and genomic regions that appear to be neutral with respect to these evolutionary processes. This information will identify populations at risk of extinction and help to quantify the risk and manage breeding programmes.

References/publications

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[CodeX]

Decoding domesticate DNA in **archaeological bone** and manuscripts

Keywords

Archaeology, palaeogenetics, Neolithic, genomics, domestication, early farming, prehistory.

Summary

The major domestic animal species emerged in the remarkably innovative, early agricultural communities of the Near East over 10 000 years ago, and came to dominate aspects of life such as food, economy and culture. Through domestication humans profoundly altered their relationship with nature, controlling the breeding of their major food sources for material, social or symbolic profit. Understanding this complex process is a compelling research aim and CodeX is developing new high-resolution genetic tools to put flesh on the bones of this two-millennium- long transition.

Aim

CodeX is taking advantage of very recent scientific advances: targeted next-generation DNA sequencing, high through-put screening of expertly-provenanced archaeological samples, and emerging knowledge of modern cattle, sheep and goat genome science, including their genetic geographies. Combining these, the project aims to develop an ancient DNA data matrix for which there is no current parallel in archaeological science. These data will help unlock the key genetic changes that accompanied domestication and identify the breeding structures that are a consequence of human management. The 10 000 year genetic matrix for each species will function as a standard spatiotemporal reference grid on which any subsequent bone or animal artefact may be placed i.e. via genetic postcoding.

Genes are expected to vary smoothly in space and time and discontinuities in the matrix will thus highlight points of strong historical interest, such as the emergence of new trade networks, migrations and periods of economic turbulence – perhaps driven by climate fluctuations or plague outbreaks. The bulk of sampled material to identify suitable cattle, sheep and goat bones will be obtained through archaeological collaborations. However, CodeX will also investigate manuscript parchment samples – made from animal skins – with a uniquely dated series that will enable correlation of genetic changes with historical events, for example cattle plagues in the 14th and 18th centuries in Europe.

Expected results

CodeX is an interdisciplinary project that seeks to deliver the first comprehensive temporal genetic cartography of domestic animal history and prehistory. For each species the project will correlate the domesticate genetic matrix with known events from the human past and will uncover episodes of social change that may not be inferable from other sources.

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Novel
Technologies

Novel technologies

High-technology is not often associated with farming. Yet here – as in almost every other sector – impressive advances are changing the way food is produced. Biological, chemical and agricultural innovations are helping to increase production while increasing quality, reducing environmental impact and providing for animal welfare.

Precision Livestock Farming (PLF) is one new approach. The idea is that farmers reconnect with each individual animal, while using technology to get the most from each pig, cow, sheep, goat or chicken. The term is relatively new and very few farms are currently organised in this way.

Two of the projects presented in this chapter delve deeper into PLF, assessing what has been achieved thus far, identifying future research needs and drafting a blueprint on applying PLF at farm level.

A third project looks at the viability of smart farming technologies for pig farming, while a final project seeks to bridge the gap between biology and modern technology by training talented biologists, veterinarians and animal scientists.

[BrightAnimal]

Multidisciplinary Approach to **Practical and Acceptable Precision** Livestock Farming for SMEs in Europe and worldwide

Keywords
Precision Livestock Farming, animal farming, traceability.

Summary
Rising protein intake in developing countries, as well as rising concern over animal health and welfare in developed countries, present serious challenges to farmers. Precision Livestock Farming (PLF) aims to enable the farmer to re-connect with individual animals or small animal groups in spite of growing intensification. It uses technology to give farmers additional hands, ears and eyes.

BrightAnimal was set up to assess what has been achieved so far in PLF, and to highlight future research needs. The goal was to identify *practical* and *acceptable* PLF. This was done by a multi-disciplinary team of experts from all five continents involving experts on business and ethics, as well as biologists and engineers.

Problem
Precision Livestock Farming (PLF) has in recent years found itself in the crossfire between engineering, natural sciences (especially biology) and livestock farming. Regular conferences on PLF suggest that the science is now being taken into account.

The original hope was that PLF, by applying precision methods, would reduce resource needs and improve the efficiency of livestock farming, improve animal health and welfare, and reduce the gap between producers and consumers. We now need to know whether or not this has happened.

The BrightAnimal partners believe there are two main reasons why PLF has not produced the results expected: it is seen as neither acceptable nor practical.

Livestock farming is influenced by four main stakeholder groups with different interests in PLF: governments, through food laws and regulations; animal and human welfare interest groups (e.g. NGOs); consumers, through their purchasing patterns; and farmers, many of whom have small scale operations.

Acronym:
BrightAnimal

Project number:
227138

EC contribution:
€997 425

Duration:
24 months

Starting date:
01/04/2009

Contract type:
Coordination action

Of these, consumers and farmers are key to influencing improvements in the management of livestock farming. Consumers are the main driving force for the food market. Their decisions very much drive innovations on the farms, be it to meet expectancy of low food prices by improving efficiency, or by providing information to the consumer via labels, traceability or other means. Farmers of course have a major influence. They have to make the decision to implement PLF.

Aim

BrightAnimal had the mission to produce a framework for European and non-European SMEs on effective and acceptable precision livestock farming, and to create an international, interdisciplinary network for further development and dissemination. The focus was on fish from aquaculture, cattle, pigs and chicken.

Results

The project produced:
- The book "Practical and Acceptable Precision Livestock Farming";
- A Precision Livestock Farming Wiki as a basis for Good PLF Practices, accessible via brightanimal.pbworks.com;
- A leaflet for farmers on PLF, together with a five-minute smart farming diagnostic;
- A network of professionals from academia and industry, including from other EU projects and outside the EU.

The team also developed and presented a series of recommendations for precision livestock farming in several public conferences. The recommendations cover pathways for marketing and penetration, research objectives, research fund expenditure distribution, transparency in the food business, a new farm evaluation scheme and education.

Potential impact

By raising awareness of the commercial, social and ethical advantages to be gained from properly applied PLF principles and producing a framework for their implementation, together with guides for best practices and the monitoring of standards, BrightAnimal will make a significant contribution towards the creation of more profitable, efficient and socially acceptable livestock and aquaculture sectors.

BrightAnimal brought together previous research findings to identify gaps in knowledge and research and recommend future actions. This alone has given PLF a higher profile among relevant stakeholders, who for the first time now have an authoritative point of reference for making judgments on the application of PLF, and for obtaining guidance and information.

References/publications

In addition to the book, the project resulted in over 20 other publications.

Project website

www.brightanimal.eu

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[BioBusiness]

BioBusiness—Training in Research, Product Development, Marketing and Sales in **BioBusiness**

Keywords

Training in livestock technology, animal health, animal welfare, behaviour monitoring.

Summary

Merging new technologies and biology offers many opportunities. The main barrier is that talented biologists are unaware of the potential of modern technology. At the same time, those developing technology are not following bio-processes. The objective BioBusiness is to train scientists with a background in biology to collaborate with technology-driven people. The project is training them in research, product definition and development, marketing and sales for bio-business in the EU. The goal is to fill the knowledge gap among veterinarians, animal scientists and bio-engineers, introducing them to emerging technologies and encouraging them to put them to practical use.

Problem

Veterinarians, animals scientists, ethologists are not familiar with the potential of modern technology (sensors, cameras, microphones) and the variables that can be measured continuously in a fully automated way.

Aim

The network will focus on research that will enhance animal welfare and health management. The aim is to train Fellows with an 'animal background' in the potential and the use of modern technology. Based on this training, the Fellows will develop three new ideas, and deliver proof of concept for new products to monitor animal welfare. The project is doing this by placing Fellows within a team that is developing a new product for biological processes.

The participating Fellows have also been encouraged to obtain a PhD and follow relevant courses run by the affiliated doctoral schools. Additional training events are foreseen to cover topics considered to be of significant importance. The main areas of interest are behaviour monitoring, disease detection and monitoring, growth monitoring and management.

Expected results

The research will lead to new knowledge and understanding. Mathematical modelling techniques will be used, allowing the results to be quantified whilst providing insight into biological processes.

Individual Fellows' results will be evaluated by industry. Researchers that complete the training programme will be able to continue their career, using their new skills, in different sectors within the EU, such as industry, the civil service, academia, teaching or research institutions.

Potential applications

The Fellows are combining biology and technology to develop three innovative tools/procedures:
- an automatic lameness detection system for dairy cattle
- an automatic aggression monitor for pigs
- a procedure to shorten the hatch window of chickens incubated in large industrial incubators

References/publications

- Van Hertem T.et al (2013), Comparison of segmentation algorithms for cow contour extraction from natural barn background in side view images. *Computers and Electronics in Agriculture,* Volume 91: 65-74.
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- Tong, Q. (2013), Embryonic development and the physiological factors that co-ordinate hatching in domestic chickens, accepted for publication in *Poultry Science.*

Project website

www.bio-business.eu

Coordinator

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Partners

- The Royal Veterinary College, UK
- French Agency for Food, Environmental and Occupational Heath Safety (Anses), FR
- University of Veterinary Medicine Hannover, DE
- Livestock Research Wageningen UR, NL
- The Agricultural Research Organisation of Israel – The Volcani Centre, IL
- Universita degli Studi di Milano, IT
- DeLaval International AB, SE
- Fancom B.V., NL
- Petersime NV, BE

[EU-PLF]

Bright Farm by **Precision Livestock** Farming – Animal and farm-centric approach to Precision Livestock Farming in Europe

Acronym:
EU-PLF

Project number:
311825

EC contribution:
€5 895 357

Duration: 48 months

Starting date:
01/11/2012

Contract type: large scale collaborative research project

Keywords

Precision livestock farming, animal key indicators, socio-economic measures, animal health and animal welfare.

Summary

The objective of the EU-PLF project is to deliver a validated blueprint for an animal and farm-centric approach to innovative livestock farming in Europe that is proven through extensive field studies. This blueprint will be a reference tool, offering pragmatic guidance on how Precision Livestock Farming (PLF) systems can be applied at farm level in order to create value for the farmer and other stakeholders. EU-PLF is investigating the use of continuously automated measurements directly on the animal, or its environment. The recorded data (e.g. body movements, sounds, etc.) can be used for monitoring and management of livestock and translated into key indicators for animal welfare, animal health, productivity and environmental impact.

Problem

A modern farmer is confronted with increasing pressure to care for a larger number of animals in order to have an economically viable business – pressures which will become more acute in future years. Due to scale, farmers dispose of less time for caring for each individual animal, while society expects animals to receive more individual attention.

It is increasingly difficult for European farmers to pay sufficient attention to individual animals and build a stronger relationship with them – not only in production-intensive sectors like poultry and pigs, but also in dairy production. This problem must be faced in the context of wider challenges, including increasing concerns about links between animal and human health, the need to reduce the environmental load of livestock, and the need to optimise the productivity of livestock farming to respond to a growing world population.

Aim

EU-PLF aims to deliver a validated blueprint for an animal and farm-centric approach to innovative terrestrial farming. The blueprint will be shaped as a 'manual' with online website support It will describe how to turn PLF technologies into robust, operational systems at farm level and how to use these technologies to create value for the animal, farmers and other stakeholders in the food chain. The project will define Key Indicators (KIs) at farm level and corresponding gold standards. These will allow the capture of quantitative information directly from the animal or its environment related to animal welfare, animal health, environmental load and productivity.

The partners will identify 50 high tech SMEs or potential start-ups who will be informed about the project's potential for helping them innovate within the European livestock market by bringing their high-tech products into PLF systems – which can be commercialised by existing market players. They will be challenged and encouraged by a competition to put in place the idea of 'PLF as a service'.

Potential applications

The validated blueprint – the main deliverable of the project, will be made available to all interested parties. Different stakeholders in the food supply chain can use the blueprint to create new PLF products and services. The blueprint will document the process of starting from an idea to delivering a product with proven added value. Although the project uses pigs, poultry and cattle as demonstrators, the applicability of the blueprint extends to other species and services in the sector.

References/publications

- Aerts J.-M. et al. (2003), Active Control of the Growth Trajectory of Broiler Chickens based on On-Line Animal Responses, *Poultry Science,* 2003b, 82(12): 1853-1862.
- Wathes C. et al. (2008), Is precision livestock farming an engineer's daydream or nightmare, an animal's friend or foe, and a farmer's panacea or pitfall? *Computers and Electronics in Agriculture,* 64(1): 2–10.
- Blokhuis, H.J. et al. (2010), The Welfare Quality® project and beyond: safeguarding farm animal well-being. *Acta Agriculturae Scandinavica A, Animal Science,* 60: 129-140.
- Gregersen O. et al. (2011), Economic aspects of PLF. In *Acceptable and Practical Precision Livestock Farming,* Vol. 1, 149-178 (Eds I. G. Smith and H. Lehr). Halifax, UK: European Commission.
- Viazzi S. et al. (2013), Analysis of individual classification of lameness using automatic measurement of back posture in dairy cattle, *Journal of Dairy Science,* Volume 96, Issue 1: 257-266.

Project website

www.eu-plf.eu

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- University of Bristol, UK
- Institut National de la Recherche Agronomique, FR
- Universita degli Studi di Milano, IT
- The Agricultural Research Organisation of Israel, IL
- Teagasc, IE
- The Royal Veterinary College, UK
- Stichting Dienst Landbouwkundig Onderzoek, NL
- Fancom B.V., NL
- SoundTalks, BE
- PLF Agritech Europe Ltd, UK
- Xenon New Technologies, BE
- Abrox Tecnic SL, ES
- Syntesa sp/f, DK
- Nutrition Sciences NV, BE
- European Association for Animal Production, IT
- M&M Corporation, BE
- Wageningen Universiteit, NL
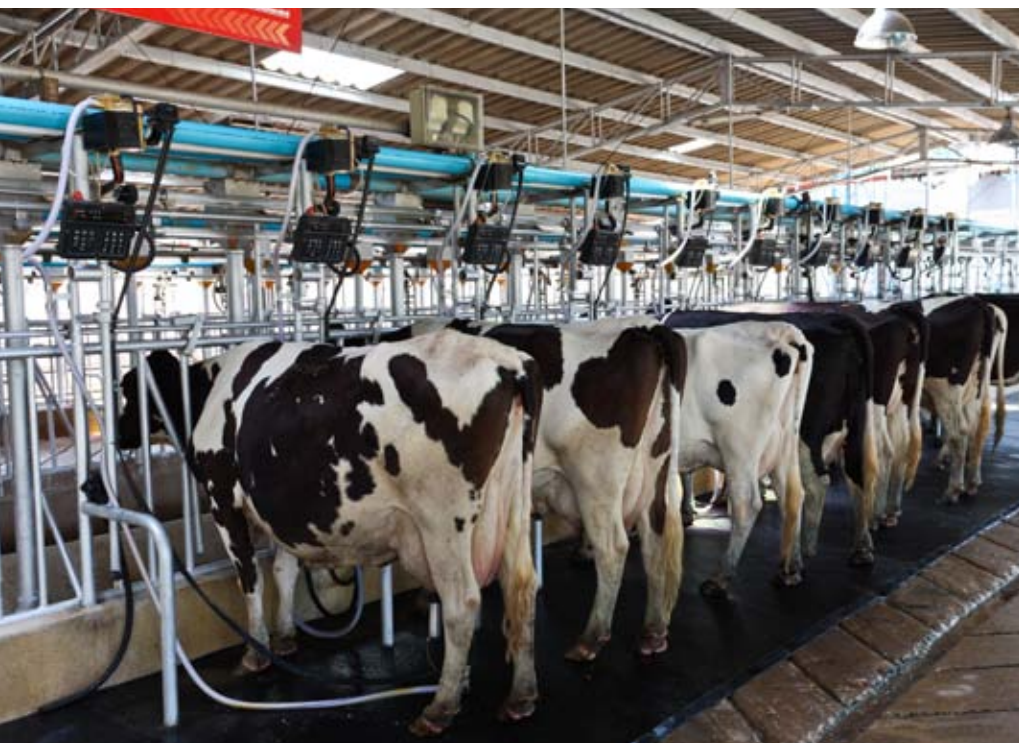
[ALL-SMART-PIGS]

Practical implementation of precision livestock technologies and services at **European pig farms** using the living lab methodology

Keywords

Pigs, fattening, PLF, SmartFarming, livestock technology.

Summary

The EU funded ALL-SMART-PIGS project will demonstrate the viability of smart farming technologies in European pig farming. The project will use an innovative LivingLab to co-create smart farming applications ready for commercialisation on European pig farms. These applications will be provided by innovative SMEs, which will test and validate their technological prototypes and services in real life conditions, together with pig farmers and other stakeholders. The project will monitor health, growth rate, feed usage and environmental conditions.

Problem

The worldwide demand for meat products is expected to increase by over 40% in the next 15 years – a serious challenge for worldwide livestock production. Simultaneously, the total number of livestock farms is steadily decreasing. The combination of these two trends means that the size of the average livestock farm continues to rise and, as a consequence, modern farmers have less time to spend with individual animals. There are major concerns about the impact of this on animal health and welfare, and the environmental sustainability of animal production for large herds.

In order to guarantee accurate and continuous monitoring of individual animals at a modern livestock farm, farmers today need reliable and affordable technologies to assist them. When the principles and techniques of process engineering are applied to livestock farming in order to monitor, model and manage animal production, it is called 'precision livestock farming' (PLF). PLF seems the only realistic way to support farmers and other stakeholders in the livestock production chain in the near future, whilst at the same time coping with the rising demand for meat.

Acronym:
ALL-SMART-PIGS

Project number:
311989

EC contribution:
€767 073.75

Duration: 24 months

Starting date:
01/11/2013

Contract type: small scale collaborative research project

Aim

A consortium of three high-tech SMEs, an established provider to the European farming community, regional R&D partners and an experienced SME and Living Lab facilitator will implement the project, assess PLF's economic costs and benefits, develop a business model for future smart pig applications and showcase that the Living Lab methodology can pave the way to the market for innovative technologies.

Potential applications

A new service concept for pig farmers labelled SMART Pig Farming Application will be developed by the project. A business model showing how this service concept can be commercialised in the future will be another key deliverable.

In addition, ALL-SMART-PIGS will showcase traceability as a means to optimise feed usage in the feed-animal-food chain. Improving communication between the supply chain partners will have great economic potential for feed providers, farmers and slaughterhouses alike.

ALL-SMART-PIGS will also showcase how to get new scientific knowledge and technologies to the market through user-driven innovation processes. This will be done using the Living lab methodology, where key performance indicators are identified and PLF technology and service concepts are co-created together with the main users: pig farmers, feed providers and slaughterhouses.

Project website

www.all-smart-pigs.com

Coordinator

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Partners

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- PLF Agritech Europe, UK
- IRTA, ES
- St. István University, HU
- Fancom BV, NL
- Nema, FO

This catalogue brings together key information on projects recently funded by the European Commission addressing animal production issues. The projects tackle topics ranging from food efficiency, animal fertility and new selection schemes to biodiversity of breeds and innovative management systems. Research in this field not only creates new scientific and technical knowledge, but also relies increasingly on advanced technologies – recently further upgraded – such as genomics tools, robotics, high-speed telecommunication and other automatised systems. Several instruments finance these multi-disciplinary projects, such as integrated collaborative research grants, Marie Curie actions, individual grants for excellence science and dedicated support for SMEs. The results obtained can be used to improve production efficiency while reducing the environmental footprint of livestock. Research and innovation in this area will guarantee food security and food quality and minimise environmental impact.

Publications Office