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Sustainable
Farm Animal Breeding & Reproduction Technology Platform

Strategic Research Agenda

Annex I Expert Reports

Working Group "FABRE Technology Platform"
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FABRE Technology Platform

Sustainable Farm Animal Breeding and Reproduction Technology Platform

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Cattle and Buffalo

1 Key opportunities and challenges – The role of research and development

In most European countries, efforts undertaken in the past using animal breeding technologies have focused on increased output on a per animal basis. Recently, breeding programmes have been modified to increasingly include functional traits and product quality traits. Under European conditions with high costs (for labour, buildings, and land), and high product prices, per-animal production will continue to be of high importance. However, with Europe's cattle production increasingly becoming part of a global market, breeding programmes must give increasing attention to cost reduction and larger scale production units. From a consumer and wider society perspective, demands are expected to concentrate on environmentally friendly production, and an increasing awareness of food safety and quality, including nutritional and organoleptic quality. Cattle breeding programmes have become global and individual programmes find themselves in fierce competition.

Biotechnology has been directed mainly towards reproductive technology and has lead to the widespread use of artificial insemination. Other reproductive technologies, like embryo transfer, sexing of semen and cloning have seen some development and limited application but without a major breakthrough yet.

Major developments have occurred in the field of molecular biology and have lead to an increasing awareness of the potential for the application in animal breeding of marker-assisted selection, gene-assisted selection and genomic selection. These technologies provide opportunities to meet the demands of farmers, processors, consumers and society.

Challenges lie in the development of a cost-effective application of the technologies for use by farmers and breeding organizations. The role of the European research community will be to lead the way in this process by providing the tools, knowledge, and skills needed by the animal breeding sector to make effective use of these new technologies. This will involve basic research, largely connected with other research activities in the field of life sciences, as well as applied research. The importance of applied research originates from two sources: Firstly, from the need of validation and verification of results from basic research in the field, and secondly, from the need to developing methodologies which can be applied in the field of cattle breeding on a routine basis.

2 Gaps to be filled

The fields of future research can be divided into three categories: i) trait-orientated research; ii) the development and evaluation of new technologies; and iii) other issues including biodiversity and economic analyses.

In trait-orientated research, one of main focuses should be the development of cost-effective schemes for the recording of traits associated with health, animal function and product quality on large numbers of cattle. This trait-orientated research is especially important as the major breakthrough of molecular approaches like genomic selection has yet to occur and will rely heavily on accurate phenotypes to be matched with genomic information. Cost effective trait measurement can also facilitate the incorporation of a broader range of traits in cattle breeding schemes using existing technologies.

With respect to molecular genetic technologies, there is a need for better integration into breeding programmes. The focus needs to move from a focus on single QTL approaches to take the genome as an entity including all interactions between genes as well as the interactions of genes with the environment. This is important in cattle breeding due to their limited female reproductive capacity and thus an industry structure in which commercial animals are an integral part of breeding schemes. The commercial cattle even in the future will be managed and housed in a variety of environments. Reproductive technologies could have substantially beneficial impacts for the production process itself and also for meeting the large variability of demands of the consumers across Europe related to culture and alimentary habits and traditions. At present, little is known of the limits of cloning technology as further developments have to deal with the complex field of epigenetics.

Decisions on the application of new technologies to produce more rapid gains must consider the economic impact on all sectors and the impact on longer term gains. It is imperative that research on these aspects accompany all technology developments.

3 The problem of stasis

If no research or development occurs in the fields mentioned above, the impact will be severe in a number of fields. Firstly, livestock farming in Europe will loose its competitiveness compared to other regions in the world where advantages due to low costs of production already exist. In some parts of Europe the occupation of land is closely linked to livestock production and in this situation a loss of competitiveness will have a very strong negative societal impact. Secondly, this situation will eventually lead to a drastic increase in imports of livestock products and create longer term dependencies. Thirdly, since animal breeding already is a global business, scenarios in which only very few breeding organizations take over the entire market, as is already the case in poultry breeding, may be envisaged. Given that it is desirable to have multiple genotypes of cattle, suited to various environments and product demands, it is highly questionable whether a few breeding organizations would be willing to supply these genotypes or to take care of long-term goals like maintaining biodiversity. A future scenario as described above may only be dealt with by using public funds to increase research activities which will be to the benefit of many regions and conditions within the European states. Finally, new technologies, be it biotechnology, or molecular approaches, or others, bear the ultimate chance for increased quality of production (cattle and buffalo products), food safety and welfare of animals. This opportunity should not be overlooked.

4 Short, medium and long-term opportunities/needs for research

5-year horizon
a) Trait-orientated research
- Improvements for the recording of health and functional traits (in nucleus herds, contract herds, in the field); with integration into molecular approaches like metabolomics
- New and better traits for beef and milk quality
- Recording of welfare and health traits, docility (human x animal interaction)
- Reduced cost of data (trait and identification) recording at farm level

b) Technology
- Full integration of bv estimation procedures with molecular approaches including SNP data
- Improvements in reproductive technologies like semen sexing and cloning, and reproduction tools such as oestrus detection or synchronisation (substitutes of hormones)
- IT-solutions for integrated data-bases from farm to central/distributed computing

c) Other issues
- Improvements of concepts for maintaining genetic diversity
- Economical assessment of new technologies and their associated risks

15-year horizon
a) Trait-orientated research
- Mechanisms of disease resistance
- Physiological traits as alternative indicators; metabolomics

b) Technology
- International genetic evaluations using genomic information
- Genotype x Environment interaction including massive genomic information
- Further research on cloning

c) Other issues
- Implementation of concepts for maintaining genetic diversity including genomic information
- Local breeds and specific regions issues

25-year horizon
For this horizon, it may be very difficult to speculate about future research needs, some topics could be:
- Efficient prediction and capturing from gene x gene and gene x environment interactions
- Expert systems for on-farm as well as networked genetic evaluations
- Designer food (milk, beef) from transgenic animals
- Embryonic selection; use of stem cell technology for reproduction

4 December 2006

Sheep and Goats

Introduction

Sheep and goats are among the most extensively farmed livestock species in Europe. The most extensive systems utilise marginal areas, not suitable for other forms of agricultural production, and provide an important source of income for the rural population. Sheep and goats maintain natural landscapes and have a very 'green' image. There are currently no major health and welfare problems.

Because of their small size and low reproductive rate, sheep and goats are less efficient than competing species in the production of meat and milk, and commercial production therefore depends on a premium price. As a consequence, often but depending on the farming system, the environmental footprint expressed per kg produce is higher than for other species.

With declining subsidies, and in order to stay competitive, sheep and goat producers seek to create special markets for quality products and increase efficiency. For dairy sheep and goats increased efficiency is achieved through increased production, while for meat sheep reduction of labour input is actively pursued. Depending on its quality, wool can be a source of income in some systems, but is a cost in others.

Based on elaborate consultation with industry and academic experts, this document identifies the problems and opportunities for sheep and goat breeding in Europe, describes the problem of the status quo and prioritises research and development needs for the near and long-term future.

Problems, knowledge gaps and opportunities

- Improved Quality: Milk quality of sheep and goats in terms of human nutrition is poorly described. A variety of measures of meat quality exists but none is suitable for routine use. As lamb is mainly eaten by older consumers, there is a need to develop products appealing to younger generations. There are opportunities to improve the nutritional value of both milk and meat, for instance through the fatty acid composition. There is an emerging market for kid meat.
- Increased Efficiency: Approaches to increase efficiency need to switch from increased production per animal to a whole flock basis, including functional traits, health management and labour costs.
- Health and Welfare: Efforts to increase production and reduce labour input have the potential to create health and welfare problems that do currently not exist. The reliance on chemicals to control diseases like sheep scab and internal parasites are incompatible with sheep and goats' 'green' image and in the case of internal parasites unsustainable because of increasing resistance of worms to anthelmintics. There are great opportunities to tackle major diseases through quantitative and molecular breeding. Aspects of animal welfare, like lambing ease and lamb survival can be tackled likewise.
- Food safety: The current situation around scrapie, including classical and a-typical is confusing. While it seems increasingly likely that these diseases have no effect on human health, this needs to be confirmed.
- Environmental impact: There is a lack of knowledge on the impact of sheep and goats on the environment including green house gases, and opportunities to change this in a positive way, for instance through selection of animals that emit less methane. Sheep and goat could serve as a cost-effective model for cattle.
- Biodiversity: Many sheep and goat producers still rely on traditional local breeds, but there is a trend for a small number of breeds to become more dominant. At the same time new composite breeds are being created in response to changing production and marketing environments. There is a need for a rational system to decide on which breeds need to be conserved. Breeders require support to manage within breed diversity.
- Breeding and Selection. Breeding and selection costs for sheep and goats are relatively high because they breed seasonally, AI is relatively inefficient, litters are small, animals are small and breeding generally takes place in small family farms. On the other hand, breeders participate in central testing and are organised in group breeding schemes, thus combining flexibility with the advantages of larger populations. Individual breeders are too small to invest in R&D. Breeders have been very responsive to programmes aimed to change scrapie resistance, and are likely to be equally keen to take up new opportunities.
- The advent of molecular genetics offers great opportunities in the field of improved disease resistance, quality and efficiency. There is a lack of research in this area on traits of specific European interest and verification of results in European breeds as well as a lack of tools to integrate molecular genetics with current systems based on performance recording. The cattle genome has the potential to deliver valuable tools for use in small ruminants.
- Export of genetics: Europe depends on overseas imports for a significant part of its lamb. Where European consumers will increasingly demand lamb to be of a specified quality in terms of food safety, meat quality, nutritional value and animal welfare there are opportunities for European breeders to export genetic material to lamb producing and exporting countries.

Problem of the status quo

In the absence of research and development in the sheep and goat sectors in Europe and given decreasing subsidies, these industries will quickly loose out to the competition (imports and domestic alternatives) on price and quality. In the case of lamb demand will fall. Sheep and goats will be disproportionately affected by regulations aimed at limiting green house gas emissions. Animal health and welfare will suffer as a result of efforts to increase production and reduce costs. Loss of significant parts of the sheep and goat industries will lead to neglect of traditional landscapes and loss of income for the rural population in less-favoured areas, while biodiversity will suffer as a results of survival of only a few highly selected breeds. European consumers will depend on imports, which may not necessarily correspond to their requirements. Foreign research will only address these issues to a limited extent.

Short, medium and long-term opportunities and needs for research

5 year time horizon, in order of priority

1. Research into the definition, understanding and estimation of genetic components (both quantitative and molecular) of new traits contributing to sustainable production, especially those related to global warming and other environmental aspects, animal health and welfare at low labour input (lambing ease, lamb survival, disease resistance). The cattle genome can serve as a basis in many aspects, but specific small ruminant work will still be required. There is a need to validate genetic markers developed elsewhere in European breeds and environments. Europe – Specific (but certain traits and genome is similar to cattle).
2. Research and development of more cost-efficient animal recording and selection technology, including DNA collection and (in collaboration with other species) software that integrates molecular information in existing evaluations (Marker Assisted BLUP). Global – general [simple and cheap DNA technology is useful to everyone, and may be even more so in developed countries]
3. Development of new tools and optimise existing tools to manage sheep and goats cope better with internal parasites, this should include host-genetics and sustainable management tools. Global – Specific.
4. Research to develop objective measures of milk and meat quality for routine use in breeding stock and having relevance to eating quality and human nutrition, including their genetic components. Developed countries – General.
5. Research into the improvement of fertility of sheep and goats, especially efficiency of AI, a-seasonal breeding and opportunities for females to deliver and rear larger litters. Developed Countries - Specific.
6. Government and industry databases on for example animal diseases need to be developed and linked to selection programmes and gene discovery research. Global – General.
7. Development of decision support tools for conservation of rare breeds, methods of *in situ* and *ex situ* conservation and genetic variation within a selection programme, this should be based on a better understanding of functional biodiversity Global – General..
8. The effect of scrapie on human health (if any) needs to be established. Europe – Specific.

15 year time horizon

- Sequencing of the sheep and goat genome Global – Specific.
- Major research in development of genetic solutions to diseases, leading to development of generalised immunity Global – General.
- Development of breeds or lines that perform well in specific lamb exporting countries (e.g. tropical) but adhere to all requirements of European consumers. Developed – Specific [this is European breeders exporting breeding stock, while European market declines]
- Adapt sheep and goat to changing climates as a result of global warming. Develop a strategy so that breed development keeps pace with global warming. Global – General
- Research in reproductive and embryo technologies to increase efficiency of breeding programmes. Developed - General
- Effective methods to either improve quality of wool or create shedding or hair sheep as part of a selection programme for milk or meat. Developed - Specific

25 year time horizon

- Development of sheep and goat products adapted to specific human genomes. Developed - Specific

Sheep and goat breeders tend to be more traditional and operate on a much smaller scale than breeding companies in other species as a result they would find it difficult to develop and apply scientific results for their own enterprise. It is therefore important that breeder representatives participate in research at an early stage and implementation will be an essential part of most projects. 20 April 2007

Pigs

1. Context - opportunities and challenges

Pig production. Pork is the most widely consumed meat in the world. A dominant production system aims at producing worldwide a rather standard type of animals and products, with an increasing competition between production basins in a more and more global market. Yet, alternative production systems exist and may play a significant role at a local or regional level. European pig production has to face a number of challenges such as the decreasing use of antibiotics or hormonal treatments, environmental, sanitary and welfare regulations, which are crucial for its social acceptance but may hamper its competitiveness. It consequently has to be technically excellent and/or promote the development of better quality products than its competitors.

Pig breeding. European pig breeding organisations are SMEs. A trend is visible of concentration, with currently about 10 global players and a significant number of smaller local breeders. A limited number of purebred animals of specialised sire and dam lines in nucleus herds are the basis for crossbreeding for the production level. The breeding goals have evolved from highly heritable traits such as growth, feed efficiency and carcass composition to sustainability related traits such as litter size, piglet vitality, sow longevity and meat quality. Breeding has become more and more technology-intensive, with an increasing use of computer and information technologies for real-time treatment of large amounts of family information, sophisticated buildings and controls to ensure a high sanitary status of artificial insemination (AI) centres and nucleus herds, the generalisation of AI and the development of new reproduction technologies (embryo transfer, semen/embryo freezing) for transportation and conservation purposes, the use of molecular tests for parentage testing, the control of chromosomal/genetic abnormalities, the selection of known alleles with favourable effects.

Research. Research in genetics and breeding has been revolutionized by the irruption of molecular technologies. Whole genome marker maps have allowed many chromosomal regions with measurable effects on traits of interest and some causative polymorphisms to be identified. The development of high throughput genomics and proteomics offers very powerful tools to investigate the mechanisms of gene expression, of cell, tissue and whole organism biology, of host-pathogens interaction. The current sequencing of the porcine genome will be the next major step in the development of system biology.
Strong synergisms have been developed between molecular and quantitative genetics to make an efficient use of genomic information for thorough analyses of genetic variability and, though to a rather limited extent in pigs, for genotype or marker assisted selection. In parallel, the improvement of statistical methods and algorithms for a more efficient use of phenotypic data, in particular those with non standard distributions, has remained a very active research field. Finally, increasing research efforts have been devoted to the characterisation and an improved management of genetic diversity. Research on reproduction has also been very active, with significant progress on fresh and frozen semen technologies, the development of embryo freezing and somatic cell cloning.

2. Future scenarios - gaps

Society. The size of pig farms / enterprises continues to increase due to labour costs, scale savings, investments related to environmental regulations. Society will go on questioning the acceptance of established treatments such as castration, hormonal treatments or even housing systems (e.g. constrained sows) and rejecting environmental nuisance such as unpleasant smells and pollution. Genetic aspects of these issues will be of increasing importance (e.g. reduction of components of boar taint by selection without impairing reproduction efficiency).

Breeding objectives and traits. Breeding objectives will further evolve, with the need for animals that are robust, are easy to manage in less constrained housing systems, with as few interventions (treatments, assistance) as possible, and have a good adaptability, i.e. remain productive and healthy in a wide range of production environments. Progress in our understanding of the underlying genetic mechanisms of the corresponding traits is a clear necessity. Standard production traits such as growth rate, carcass composition or feed efficiency will have a decreasing importance. However, exploitation of technological improvements in the measurement of these traits or of strong QTL / major genes affecting these traits remains important. The quality of pig meat should further increase for both standard and high-quality production and including human health aspects, with the use of sophisticated quality control approaches and utilizing new insights in the genetics of sensory and dietetic characteristics. Prolificacy remains an economically important trait but should be selected jointly with maternal ability traits that are net yet well understood. The impact of the diet, in particular suboptimal diets (with regard to energy and nitrogen, but also micronutrients) on the environment (manure composition) remains poorly known.

Technology. Artificial insemination using fresh semen has become a major tool for both the creation and the dissemination of genetic improvement. Frozen semen and embryo transfer techniques have improved, but there is need for substantial further improvements in order to be useful on a larger scale. Cheap and fast techniques of semen sexing would clearly have a major impact on pig production. More advanced techniques such as stem cell lines, cloning and gene transfer should also be developed, though their practical application is not currently straightforward.
The imminent availability of the pig genome sequence will clearly have important impacts on selection, parentage control and traceability, as well as on sciences in “omics”, which are likely to be very helpful to investigate complex issues such as host x pathogens interactions. Full and optimal exploitation will require a lot of efforts in bioinformatics and models to accurately predict the efficiency of marker or genotype assisted genetic improvement programmes.
The joint use of advanced modelling tools and automatic data recording systems should allow the development of highly efficient advanced management and selection systems.

Need for research to remain competitive (problem of stasis). The knowledge-intensive animal breeding sector increasingly depends on new technologies / improvements of existing technologies directly stemming from research that require more and more investments as well as skilled people with a strong scientific background to understand and make an efficient use of new technologies. Yet, the breeding organisations should essentially remain SME, that rely on a strong pre-competitive research sector to remain competitive. If no research or development occurs in Europe, only very few globally acting breeding organisations will survive and the SME in pig breeding will disappear and as a consequence diversity of breeds/genotypes suited to various environments and local market needs will be lost.

3. Short, medium and long-term opportunities/needs for research

Targets on a 5 year horizon:

- Availability of a high quality annotated genome sequence of the pig, of high density SNP panels, whole genome linkage disequilibrium maps and full genome expression arrays;
- Identification of an increased number of causative polymorphisms;
- Use of marker assisted selection based on linkage disequilibrium and of genotype assisted selection in pig breeding; use of markers for the maintenance of genetic variability;
- Improved knowledge on the genetic variability of immune competence / disease resistance;
- Genetic evaluation for sow longevity, piglet survival/mothering ability; studies on sow reserve mobilization;
- Ban of boar castration in some countries; fine mapping of QTL associated with components of boar taint;
- Insight in environment sensitivity traits and genotype x environment interactions;
- Improved pork quality by utilizing new knowledge on underlying genetic mechanisms;
- Development of automatic recording systems; increasing use of data from multiplication/production herds.
- Thorough definition of welfare indicators.

Targets on a 15 year horizon:

- Fully annotated genome of the pig including a catalogue of all functional elements;
- Identification of complex regulatory networks and epigenomic mechanisms at the whole-genome level;
- Identification of large numbers of causative polymorphisms; identification and modelling of gene x gene and gene x environment interactions ;
- Extensive use of genomic information at the different levels of the breeding pyramid to exploit additive and non additive genetic variation, with resistance to disease, robustness and behaviour as major target traits
- Exploitation of gene x environment interactions (e.g. by variation of the feed) for producing varying product qualities or producing under varying environmental conditions with one genotype of animals;
- Use of genomic tools (e.g. herd sanitary status evaluation) and complex models to optimise herd management;
- Large scale development of semen sexing;
- Development of models for the co-evolution of hosts and pathogens.
- Increased use of pigs as a model in human medicine (e.g. polyfactorial diseases, tumor therapy).

Targets on a 25 year horizon:

- A near complete catalogue of diagnostics for currently known inherited diseases;
- Progress towards modelling the likely impact of new mutations;
- Utilisation of complete genome sequence from all breeding animals;
- Full understanding of the implementation, impact and consequences of genetic modification;
- Development of a genetic identity card for each animal.

24 March 2007

Poultry

Introduction

The major part of the poultry industry is at a significantly more mature stage than those of other species both in terms of production systems and specific knowledge in respect of breeding. In part this is a result of basic research carried out in Europe over the last 40 years which also explains a significant concentration of the worlds commercial poultry breeders in Europe. These companies and industries are significant wealth creators and must be supported to maintain their European bases. There will be significant spin-off for minor breeds and other species from fundamental work carried out on chickens.

For these reasons the approach and needs of the poultry sector may be viewed differently from the other species.

Species Groups

Several distinct species of poultry are farmed in Europe and whilst there are several synergies in research there are also a number of species specific issues. This sector is driven by the chicken about which there is most existing data and which is massively more important in economic terms than any of the other species. For clarification the groups are as follows :

Layer chickens

Broiler chickens and Turkeys

Waterfowl: Ducks (Pekin ducks, Muscovy ducks, Mule ducks) and Geese

Other poultry: Guinea fowl and Quail

Game birds: Pheasants, Partridge and Wild Ducks

Grouping is based on economic relevance and current knowledge. Chickens are split into layers and broilers, due to differences in breeding practices. Whereas broilers and turkeys have much in common as far as breeding practices, in terms of genomic tools available, they can't match and turkeys are thus closer to the other poultry. One underlying issue for all other species will be to either improve the usability of the tools developed in chicken or develop specific ones.

B. Research priorities

1. Scientific issues short and medium term

Animal disease and Welfare will continue to be major issues in poultry with an increasing focus on “genetic” solutions which must be identified and understood. Research must be “solution” and not “problem” oriented

1.1. Animal disease: in addition to traditional diseases there are re-emerging diseases as a consequence for example of the ban on the use of antibiotic growth promoters. In particular we require a deeper understanding of gut physiology and its interaction with gut microflora and hence overall gut health.

1.2. Animal welfare and behaviour: Within the EU improvements in Animal welfare remain high priority; beak trimming; food restriction especially in the rearing period of breeders; broodiness in turkeys; research in order not to kill animals of one sex at birth such as male roosters of laying strains and female mule ducks

1.3. Food quality: this is a critical issue and the basis for retaining animal production within the EU. It involves both mandatory food quality (laboratory inspection) and the market quality (consumers, retailers, etc).

1.4. Sustainable production: management of genetic variability and genetic diversity, use of local resources and economic development of local biodiversity (local strains and raw materials) and development of niche market productions.

1.5. Environment: pollution, monitoring and reduction of effluents; biological efficiencies and the energy costs of animal production (direct and indirect) will require a fundamental review and solution.

There are clear synergies between “Environmental, Economical and Societal Research” and with the proposals of the “Plants for the Future” group.

2. New knowledge and basic information

2.1. Host-Pathogen interactions: routes of infection by viral, bacterial and parasitic pathogens; host gut interactions.

2.2. Integrative biology: male and female reproductive physiology; combining data from various sources to understand function, rather than a simple reductionist approach. This will be fundamental to explaining many of the associations determined from a genomic approach

2.3. Socio-economic research: for example, how we deliver new knowledge and technologies, especially to small poultry breeders and to provide objective data for society.

3. New technologies

One important thing that will have to be done for all species will be to either improve the usability of the tools developed in the chicken or develop species specific ones.

3.1. Genomics: whole genome SNP panels; genome tiling arrays; improvements in the speed and cost of sequencing and direct genomic selection.

3.2. Phenomics: phenotyping methods and data acquisition in new production systems (electronic ID of animals).

3.3. Advanced modelling: combining mathematical models with experimental data; systems and traits; predictive biology/systems biology; operational genetics; new analytical tools in quantitative genetics, population biology and epidemiology.

3.4. Biotechnologies for research and management of genetic resources: semen storage (including refrigeration and cryopreservation), embryo sexing, preservation of bird gametes and embryonic cells, transgenic technology.

3.5. Animal science; quantitative genetics, whole animal biology and Genotype x Environment interactions.

4. Information resources

4.1. Animal resources, phenotypes and biological samples: phenotypes/genotypes of pedigreed commercial and experimental lines and crosses; epidemiological data and genetic profiles of pathogen infections. Development of field databases for the latter two topics which can be standardised across the EU.

4.2. Information required for large scale analyses: Genome sequence, structural and functional annotation, Gene Ontologies, QTL maps, etc.

8 March 2007

Horses

Introduction

Problems- Key opportunities – Issues: Horses are becoming more popular in the **growing industry** of sports and leisure, and ‘hobby' farming whereas racing industry is still flourishing. Furthermore, horses are used in therapy or tourism, and there are niche markets for horse milk for people having allergies and for meat in only few member states. There are no major ethical objections against horse breeding. In some (west) European countries **maintaining rural landscape is taken over by horses**. As herbivores equine compete with ruminants as well as with plant production for natural resources and territories. Different demands of the public on horse breeding cause **the development of a diversity of horses which fit the needs of many groups of people** who potentially would like to work with or enjoy horses. **Insufficient standards of education of breeders and owners** requests to be urgently improved to meet the same standards as in other farm animals industry. **Knowledge and technology transfer between EU countries should be extended** as well throughout a European network for Equines.

Horse breeding industry and research in the Central and Eastern Europe (CEE) have to cope with several severe structural problems and need support from EU and other European industrialised countries to reorganise their equine chain, renew education and research in equine science and to benefit of technology transfer from industrialised countries.

Based on consultations of and discussion with horse breeding industry and scientists, challenges, knowledge gaps and opportunities for the horse breeding in Europe are summarised, the problem of stasis is briefly described and research priorities are presented for the short, medium and long-term future.

Challenges, Knowledge gaps and opportunities

- Performance, Health and Welfare: Breed athletes and leisure horses requires to define traits and breeding goals especially with regard to performance (gaits, jumping, velocity and endurance), health and behavioural (temperament) traits as well as to determine the interaction between genotype and environment (husbandry systems, riding systems and nutrition)
- Phenomics: phenotypes have to be more accurately recorded. This requires objective systems for judging and breeding as well as the development of traits to improve performance, disease resistance and behaviour of the horses
- Genomics: The Improved annotation of the horse genome sequence and new functional genomic information and associations with traits under selection will contribute to the identification of genes associated with performance, health, behaviour and other functional traits (national/European/ Global)
- Breeding and Selection: The development of statistical evaluation methods should be continued to improve performance, health, welfare, behaviour and functional traits by genetic selection. A further step will be the development of well defined breeding schemes that can also include molecular information
- Biodiversity: the diversity of and within breeds, region and states should be maintained or/and managed either in small endangered populations or large populations where inbreeding is increasing
- Reproduction: Improvement of payable and safe application of reproductive technologies such as AI, ET or sexing may help to solve fertility problems. This requires more reliable indicators of fertility as well as maternal and foetal well being during pregnancy and peripartum
- The technologies for long term freezing of semen and embryos need to be improved and will also play a central role in strategies to preserve biodiversity
- Technology and knowledge transfer: the renew of breeding industry and research in CEE states is requested at regional and national level. The Improvement of education of users, breeders and extension officers and the cooperation between scientists and horse users should be organised in most of the European countries and definitely coordinated at European level.

Problem of stasis

If no research or development occurs in Europe, the expected impact on industry and EU citizens may be: The loss of international leadership in sport horse breeding and competition, the breeding of horses which impair with the rising demand of citizen for e.g. hacking or agritourism, a loss of diversity of breeds and the minimisation of the complete horse breeding industry in some CEE countries, deteriorated animal welfare, limited contribution of horses to sustainable farming and sociocultural life, and economic losses in breeding industry and related business and employment in agriculture, riding education, horse exhibition, competition, races and linked historical patrimony.

For equines the following opportunities/needs for research are foreseen in the short- medium and long term to improve performance (such as gaits, jumping ability, velocity, endurance), functional traits (e.g. longevity, fundamental stability), disease resistance (e.g. Equine influenza, Rhinopneumonia), fertility, behaviour (e.g. temperament), and a to reduce hereditary diseases (such as OCD, myopathy, roaring).

Research needs for the 5 year horizon:

Breeding and genomics

- Identification and parentage control using modern tools and European identification system (UELN);
- Record more precise phenotypes using conventional and modern tools;
- Define reliable objective traits focused on performance, behaviour, health resistance evaluated with modern technical and biological data and then implement genetic analysis;
- Analysis of interactions between genotype and environment (nutrition-husbandry systems-health) with phenotypes and traits using the new knowledge obtained in those scientific fields in and for horses
- Improve information on horse genome (genome assembly, full-length cDNAs, annotation) create, develop and maintain public genome databases
- Identify genes for the main genetic (hereditary) diseases(OCD, Myopathy…) diseases resistance and underlying biological mechanisms
- Estimation and management of biodiversity of equines

Reproduction

- Improvement of chilled transported sperm (use for larger number of stallions) and of frozen sperm
- Better knowledge of stallion physiology (sperm production, nutrition and environmental factors, aetiology and inheritance of some reproductive disorders, techniques allowing sub-fertile stallions to be bred with more efficiency)
- Better knowledge of mare physiology (oestrus detection, ovulation time, pregnancy, foetal and neonatal losses, nutrition and environmental factors)
- Tools for diagnosis and therapy of fertility problems

Research needs for the 15 year horizon

Breeding and genomics

- Identification of genes, which are responsible for differences in performance (gaits, jumping ability), temperament, fertility, growth development;
- Identify genes for the main genetic (hereditary) diseases
- Development of early and reliable predictors for longevity
- Development of basic knowledge in the main biological functions to decipher muscle, skeleton and nerve development and physiology then Identify bottlenecks in metabolic pathways and related functional genes involved in the performance;
- EU production and use of equine microarrays
- Develop proteomic methodologies
- Develop bioinformatics pipelines to answer scientific questions and Implement traceability
- Genetic analysis of quality of horse milk and meat
- Development of breeding systems including new traits: biomechanics, performance, temperament, growth and fertility ability, and the effects of training, welfare and horse judging systems.

Reproduction

- Fertility prediction of a stallion per ejaculate (frozen or chilled) as soon as correlations between in vitro sperm parameters and fertility will be understood
- Improvement of efficiency of oocyte freezing techniques
- Increase of research in pregnancy and neonatal period to minimise bone disorders and neonatal disease;
- Identify genes for fertility traits
- Improvement of reproduction efficiency (animal and breeders' welfare!)
- Improved knowledge and understanding of technologies for semen sexing and cloning

25 year horizon

- Produce horses devoid of genetic diseases
- Include molecular information in horse selection
- Genetic monitoring of horse breeding at the stud and breed levels
- Integration of epigenomics in equine genetics

27 March 2007

Aquaculture

Problems, knowledge gaps and opportunities

- ***Feed source*:** There is limited protein and fat available from animal and wild-fish origin, and the life-long performance (from fry to slaughter) of improved strains in a range of rearing environments and diets (GxE) is unknown. Without strains that can handle feed composed of alternative, more sustainable plant ingredients, the industry will not be able to develop with the continued dependency of animal-based diets.
- ***Health and welfare***: Existing and new diseases and production related welfare problems will erode productivity and hence profitability and development of the industry. Breeding goals focussing only on growth will result in unwanted correlated responses and production disorders resulting in unethical production. Therefore, more knowledge about diseases, heart and bone deformities and homeostatic development is needed. Health and welfare traits must be defined and included in the breeding goals of current breeding schemes, and their relation to production traits must be established for different strains under different rearing conditions (offshore cages, low-energy, high-intensive and recirculation systems, ponds, stress levels etc.). This will enable strains to be developed that are robust to the commercial conditions in which they are reared. Important health and welfare traits are: resistance to specific diseases (pancreas disease (PD), Infectious Salmon Anaemia (ISA) and flavobacteriosis in salmonids, adenovirosis in sea bass and koi herpes virus in common carp) wide antigen recognition, adaptation to environmental changes (water temperature, turbidity) and rearing conditions, stress and behaviour.
- ***Genomic technologie****s*: Today, there is not enough genomic information (genetic markers, genetic maps, QTL, gene expression, sequence data, etc) and selection methods to efficiently use this information (genomic selection, gene-assisted and marker-assisted selection and the use of fingerprinting in breeding practices), although there are high expectations that these technologies will revolutionise current breeding practices. Knowledge is also lacking on the relationship between genotypes and phenotypes for important traits.
- ***Evaluation and selection methods***: Conventional evaluation and selection methods are still not developed for typical aquaculture breeding programs. Examples are investigation into possibilities of line and crossbreeding schemes to exploit heterosis and specific combining ability, definition of selection criteria for disease resistance, analysis of challenge test data, programs to control rate of inbreeding, optimisation of mating structures, integration of nucleus and grow-out producer units, and tailor-made breeding programs adapted for SME's.
- ***Product quality***: Efficient and non-lethal systems to measure product quality traits are unavailable, although they could be used to incerase accuracy of selection for these traits. Important product quality traits are: meat/skin colour, texture, fat, processing traits, flavour and taste, but also muscle size in bivalves could be included here. Examples of value-added traits that could be included in the breeding goals and which are important for increased choice and health effects for consumers are omega-3, low fat and specific amino acids.
- ***Environment***: Escapees from aquaculture stocks pose a major threat to aquaculture production, because of the unknown genetic impact of cultured stocks on wild stocks and because cultured stocks are host for diseases that affect natural stocks. Restocking is a related topic. The aquaculture industry will continue to suffer from a negative image if these environmental issues are not fully addressed through sustainable aquaculture practices such as improving health with minimum therapeutic medicine, improving feed efficiency and the use of publicly accepted methods to produce sterile fish and shellfish.
- ***Reproductive techniques***: Improving reproductive management is necessary to increase the breeding success of many European species (meagre, oyster, mussel, scallops), but also an increased number of high-valued tropical species that are kept indoors in EU, e.g. tilapia, cat fish. In addition, sufficient knowledge on alternatives to hormonal treatment to control maturation, e.g. light and other treatments is lacking, as is the knowledge about factors that determine gamete quality and survival of fertilised eggs. Without this knowledge, traditional or new species can not become cultured in a structured breeding regime. Knowledge about environment and genetic sex determinism is poorly understood for many species (cod, sea bass, halibut, molluscs) but have the potential to reduce production costs and improve flesh quality. Aquaculture species have reproductive features that are suboptimally used in current production systems, but which have a potential to increase efficiency of production, breeding practices and the power of QTL detection. Examples of such features are triploidy, tetraploidy and double haploids.
- ***Production efficiency***: Production efficiency will remain very important for competitiveness of the European aquaculture industry. Important traits related to production efficiency, for which we need more knowledge and early predictors, are: feed efficiency, nutrient retention, amount of slaughter waste, survival, growth and fertility (on non-animal diets), environmental tolerance (temperature, salinity, turbidity) and production related diseases are: homeostatic development, heart and skeletal deformities, lordosis, metabolic and reproductive disorders.
- ***Food quality****:* Certified tracing systems must be developed to trace products through the production chain. This will ensure both food safety and consumer confidence for the protection of branded seafood products from European seafood. Genomics tools could be used in these tracing systems.
- ***Knowledge transfer*.** Very little knowledge is being transferred from research bodies to the aquaculture industry and to developing countries. This is particularly true for new technologies in the area of genomics. It is important that industry partners have well educated personnel in the areas of breeding and genetics to ensure high quality communication between research and industry partners.

Priorities for activities that need to be successfully addressed in the next:

5 years

1. Estimate genetic parameters for feed efficiency, nutrient retention, amount of slaughter waste and meat quality on animal and non-animal diets during different life-stages of the fish (from fry to slaughter)
2. Investigate relationship between production (including systems and locations), disease resistance and welfare traits
3. Implement breeding programs adapted to the size of the industry and the biological capacity of species, e.g. genomic selection for Atlantic salmon, rainbow trout, sea bass and sea bream, breeding programs based on natural mating systems (sea bream, sole, tilapia) and more traditional breeding applications for species of limited development (turbot, halibut, cod, meagre, charrs, molluscs, etc.)
4. Develop and implement novel evaluation and selection methods for aquaculture breeding populations, e.g. line/cross breeding, selection programs with control on the rates of inbreeding, MAS/GAS/genomic selection methods, evaluation of challenge test data and life-history traits
5. Develop molecular genetics resources for important species, e.g. Atlantic salmon, rainbow trout, sea bass, sea bream, common carp, Pacific oyster and mussels
6. Develop tools for non-destructive, rapid, low-cost, and high resolution (biochemical) measurements of meat quality, e.g. fat%, pigmentation, texture, muscle size of bivalves, and disease resistance traits
7. Development of standardized methods for sperm quality assessment and cryopreservation schemes for new species
8. Develop techniques to produce sterile fish and shellfish to minimise environmental impact.
9. Facilitate education of students and industry representatives in the area of breeding and genetics
10. Initiate collective investments by producers supported by public founds (regional, national, EU)
11. Survey fertility changes in breeding programs
12. Conservation of genetic diversity by the development of European, regional and private cryobanks and research into their best deployment, in special cases also live gene banks

15 years

1. Improve knowledge on biological basis of breeding goal traits and sex determination
2. Develop new techniques for female and embryo cryopreservation
3. Develop new reproductive techniques to exclude genetic introgression of farmed genes in wild populations
4. Set up European Standard Certification Procedures to assess distinctness between commercial strains
5. Access to and application of above techniques to new species

25 years

1. Genomic information (and nano and other technologies) applied in a practical and cost effective way to breeding systems

11 May 2007

Other farm and companion animals

The species discussed in this summary (in alphabetical order: dogs, fur animals, honeybees, and rabbits) were chosen for their organized breeding and/or extensive European economic revenues. As it is impossible to give an exhaustive survey of each species in this summary, an additional report was produced for each of the species that contains further details.

Key challenges and opportunities and problem of stasis

Europe is internationally leading within fur animal, honeybee, and rabbit research, breeding and production, and plays globally an important role in breeding of dogs for police/army/customs. Despite the leading role for each of the four species, it is a challenge to increase or even maintain the present European production and market share. Increased competition from non-EU countries with much lower production costs (fur animals), importation of cheaper products of lower quality from outside the EU (rabbits), indigenous species being threatened by diseases and intercrossing with imported breeds (honeybees), and the low level of organized working dog breeding in Europe, which is established elsewhere, threatens the competitive advantage Europe has now.

Even though dogs for companion by far are the largest group of dogs, working dogs are more expensive and losing market. Dogs for police, army and customs, stasis will give USA and Australia the opportunity to further develop their professional breeding programmes, making import of the genetically better dogs from Europe redundant. Within Europe, the demand for high quality working dogs will increase due to the increasing fear of terrorist attacks. At the moment there are insufficient numbers of high quality dogs, resulting in high prices and not always dogs of sufficient quality on the jobs. In fur animals and rabbits, stasis will give other countries, such as China, the opportunity to increase the market share at the expense of Europe. This threatens the European production with a potential negative impact also in the quality and safety of animal products. In honeybees, there are very large losses due to diseases. If nothing is done soon the honeybee population will be seriously impaired. An important consequence is the loss of pollination of agricultural crops and wild flora. Unintended crossing of imported breeds to indigenous honeybee races results in a loss of biodiversity and more aggressive hybrid colonies. The indigenous races constitute an important export product to countries outside Europe and an invaluable recourse of genetic variability for future needs. This market will require a solution for this unintended interbreeding and conservation of the endangered races.

Gap analysis

Research is required in order to maintain the leading role. This can be divided into two main areas1) study of traits and the techniques required to do so, and 2) development of efficient breeding schemes, including improved reproductive technologies and management. Health, reproduction, behavior, biodiversity, product quality, and efficiency are the most important categories of traits. Techniques to develop or further specify these traits are needed, as well as genomics tools for understanding animal biology and for selection. For some species techniques to set up organized breeding schemes still need to be developed. Table 1 shows gaps in knowledge and technology in the species. Specification is made with respect to overall gaps or gaps in some countries/breeds.

Table 1. Gaps in technology and knowledge in dogs, fur animals, honeybees, and rabbits; an x indicates a gap in that field.

	Species							
	Dogs		**Fur animals**		**Honeybees**		**Rabbits**	
	A	B	A	B	A	B	A	B
Technology								
Application of DNA technology	X		X		X		X	
Genetic evaluation	X			X		X		X
Artificial insemination		X		X		X		
Cryoconservation		X	**X**		X		X	
In vitro cultivation of somatic cells					X			
Knowledge								
Education of breeders	X					X		
Reproduction biology,Embryo Mortality, fertility		X	X				X	
Geno.x Environ. Interaction	X		X		X		X	
Selection criteria	X			X		X	X	
Genetic parameters	X			X		X	X	
Efficient breeding programmes	X			X		X	X	
Transparency about new technologies to the public	X		X		X		X	

*A = gap in general; B= gap in some countries/breeds;

Needs for research

5 years:

- *Education:* in **dogs** (all countries), **honeybees** (some countries), related to the importance of recording systems and agreement on the breeding goals
- *Practical issues:* in **dogs** related to improving the recording system and set up organized breeding programmes; in **honeybees, rabbits** related to developing techniques for cryo-conservation of semen; in **rabbits** related to Improvements in reproductive technologies: oestrus synchronization and reproduction management, semen processing and quality evaluation
- *Genomics:* in **fur animals** related to the construction of a genome map, study of impact of new mutations; in **dogs, fur animals, honeybees, rabbits** related to QTL and microarray studies, development of new methods for incorporating genomic information into selection schemes
- *Health:* in **honeybees** related to developing selection strategies to improve resistance to the most important parasites and diseases: *Varroa destructor, various viruses* and *Paenibacillus larvae*; in **rabbits** related to improving quality of available vaccines using recombinant marker technologies and develop selection strategies to reduce doe losses; in **dogs, fur animals, rabbits** related to investigating the genetic background of health related problems
- *Performance:* in **dogs**: Develop methods to measure behavior objectively; in **dogs, fur animals, honeybees, rabbits** related to estimating of breeding values for new traits
- *Biodiversity:* in **honeybees** related to conservation of genetic diversity, developing techniques for detecting and maintaining pure races; cryo-preservation of semen and embryos; in **fur animals** related to cryo-conservation of semen (alopex-types), live populations (mink)
- *Ethics:* in **fur animals** related to keeping the production very transparent to the public; in **dogs** related to investigating ethical aspects to the use of dogs for various tasks (e.g. assistance dogs for disabled people, dogs for explosives detection, etc), and of breed specific and desired anatomical malformations (e.g. skull shape)

15 years:

- *Education:* in **dogs** related to the importance of prioritizing selection criteria and genetic evaluation
- *Technologies:* in **honeybees** related to developing technologies for in vitro cultivation somatic cells for functional genetics in breeding for resistance; in **rabbits** related to in vitro cell technology and cryo-banking of embryos and female gametes
- *Genomics:* in **dogs, fur animals, honeybees, rabbits**, related to the use of DNA-technologies (e.g. transcriptomics, proteomics, etc) to understand the biology of the animal, both with respect to improvement of the traits under selection, as well as to understand and predict consequences of selection.
- *Health:* in **honeybees** related to developing selection strategies to improve resistance to the parasites: *Melissococcus pluton* and *Nosema ssp., Ascosphaera apis and if necessary Aethina tumida;* in **rabbits** related to investigating the genetic components for resistance to the most important diseases; in **dogs, fur animals** related to investigating genetic background of health related problems
- *Ethics:* in **honeybees** related to investigating the risk of use of genetically modified honeybees; in **dogs** related to investigating ethical aspects to the use of dogs for various new to be developed tasks (e.g. detection of dangerous "material")

25 years:

- *Genomics:* in **fur animals** related to genomic studies of biology of reproduction, sexual maturity and moulting; in **rabbits** related to tools for managing genomic information and likely impact of new mutations
- *Performance:* in **dogs, fur animals, honeybees, rabbits** related to selection for adaptation to changing climatic conditions; in **honeybees** related to breeding honeybees for pollination in greenhouses

21 February 2007

Genomics and bio-informatics

The state of the art in genomics and functional genomics in farmed animal species is summarised in the attached paper. A strategic research agenda to address the gaps in a) knowledge of farmed animal genomes, transcriptomes, proteome and systems and b) the tools and resources required to apply 21st century systems biology approaches to research in farmed animals, and in particular to facilitate the dissection of the genetic control of complex traits to inform improvements in sustainable animal breeding and production is set out below. Some objectives are continuous in nature.

Animals as systems – animals in systems

Biological science over the past decade and more has been dominated by reductionist approaches typified by the genome projects. With the acquisition of complete genome sequences for humans and several model organisms the emphasis more recently has returned to more integrative, holistic approaches termed systems biology. Systems biology provides an appropriate scientific context and strategy for the needs of the farmed animal sector. The growing awareness of the finite nature of the planet's resources means that changes are needed in many economic sectors, including animal production systems, to address environmental issues and more generally sustainability. It is necessary not only to understand animals as biological systems, but also the impact of animals on their environment and vice versa. Thus, the scientific strategy for sustainable animal breeding and reproduction needs to address '*animal as systems* and *animals in system*'.

Predictive models

The development and testing of models lie at the heart of systems biology research. The extent to which a model is predictive determines its value in understanding the system of interest. Ideally, the models should be not only qualitative but also quantitative. Whilst the importance of predictive quantitative models has received increased recognition with the re-emergence of systems biology, such models have been the foundation of quantitative genetics and genetic improvement of plants and animals for decades. Thus, adapting the 21st century vision of systems biology to the needs of sustainable animal breeding and reproduction will be less about alignment of philosophies and approaches and more about ensuring that the technologies and information systems customised for the target species and systems are put in place.

Five years

Phenomics – Establish standard phenotypic trait ontologies for the major farmed animal species to encompass production traits and disease traits (metabolic, inherited and infectious). Co-ordinate and standardise the acquisition of disease surveillance data at a pan-European level in a manner not only to improve the effectiveness of disease control, but also to enable research on the genetics of host responses to infectious disease (biological samples from which DNA can be prepared are required as well as the trait data). Develop incentives to encourage the use of commercial populations for high resolution genetic analyses in farmed animal species.

Genomics, sequencing – 'finished sequence' for pig, cattle (model bovid), chicken (model avian), salmon (model salmonid); draft sequence 2-6x coverage[1] aligned with appropriate model for sheep, goat, duck, turkey, trout and other farmed fish species

Genomics, variation, SNPs – SNP discovery programmes to reveal up to 5 million putative SNPs for each major farmed animal species[2]; validated SNP panels with 0.5 – 1 million SNPs for each target species.

Genomics, variation, copy number variants (CNV) – scan farm animal genomes for evidence of copy number variants – insertions, deletions and duplications. Develop clone-based and oligo-tiling-path arrays for comparative genome hybridisation (CGH) analyses. Develop assays for such variation in pedigrees to facilitate studies to test for associations with performance.

Bioinformatics – Support for continued annotation and maintenance of genome databases customised for farmed animal data (e.g. Ensembl, ARKdb, ..) as well as for generic resources (e.g. EMBL, ArrayExpress, GO, …). Development of data sharing policies to maximise the value to be extracted from complex data sets. Deployment of GRID technology for more effective integration of disparate data sets and exploitation of distributed computing capabilities. Development of appropriate data security systems that enable effective use of commercial data sources but without compromising legitimate commercial interests.

Develop or customise computational tools for the elucidation of gene-gene interactions (e.g. epistatitc QTL) and gene networks from functional genomics and genetics data.

Transcriptomics – In collaboration with technology providers refine transcriptomic tools to reflect current knowledge of the target genomes and transcriptomes and include tools for assaying alternatively spliced transcripts, alternative promoter usage and the expression of non-coding RNA genes.

Proteomics – Develop proteomics technologies for high throughput analyses in farmed animal species with an initial emphasis on tissues of economic importance, e.g. skeletal muscle, milk, egg and wool.

Develop comprehensive immunological toolkits for high throughput assays of immunological important proteins for all major farmed animal species.

Functional genomics, genetic modification –Develop systems for high throughput genetic modification, including RNAi-based gene knock-down in cell-based systems.

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[1] Horse and rabbit not listed here as these targets have already been achieved - 6.8x coverage for horse and 2x coverage for rabbit

[2] major farmed animal species assumed to be: cattle, sheep, goats, horses, pigs, chickens, ducks, turkeys, salmon, trout and other fish species cultured in Europe

Fifteen years

Phenomics –Evaluate the scope of using advanced scanning technology to acquire high quality phenotypic data for large numbers of animals (living and/or post-mortem in slaughter houses or packing plants).

Establish the capabilities and facilities as necessary to deliver high throughput detailed phenotyping on farmed animal species, including disease challenge capabilities.

Genomics, sequencing – Deploy inexpensive re-sequencing technology to evaluate the merits of genome selection, initially in dairy cattle.

Bioinformatics – Support for continued annotation and maintenance of genome databases customised for farmed animal data (e.g. Ensembl, ARKdb, ..) as well as for generic resources (e.g. EMBL, ArrayExpress, GO, …). Development of data sharing policies to maximise the value to be extracted from complex data sets. Deployment of GRID technology for more effective integration of disparate data sets and exploitation of distributed computing capabilities.

Development of pen-side / farm / slaughter house data capture systems to support phenomics targets concerned with more effective use of commercial population data.

Develop or customise computational tools for the elucidation of gene-gene interactions (e.g. epistatic QTL) and gene networks from functional genomics and genetics data.

Transcriptomics – In collaboration with technology providers refine transcriptomic tools to reflect current knowledge of the target genomes and transcriptomes and include tools for assaying alternatively spliced transcripts, alternative promoter usage and the expression of non-coding RNA genes.

Metabolomics – Exploit developments in metabolomics technology for systems biology research in farm animals and to evaluate the merits of animal products.

Functional genomics, genetic modification – Develop a range of stem cells from farmed animal species to facilitate cell-based in vitro functional genomics research, including genetic manipulation. Develop advanced technologies for genetic manipulation in farm animal species, including the capability for precision genetic modification using homologous recombination in appropriate stem cells and RNAi-based gene knockdown.

Twenty-five years

Functional genomics, genetic modification – Develop a range of stem cells from farmed animal species to facilitate cell-based in vitro functional genomics research, including genetic manipulation. Develop systems for high throughput genetic modification, including RNAi-based gene knock-down in cell-based systems. Develop advanced technologies for genetic manipulation in farm animal species, including the capability for precision genetic modification using homologous recombination in appropriate stem cells and RNAi-based gene knockdown.

16 April 2007

Animal Breeding and Genetics

Introduction

Animal Breeding aims at exploiting in a sustainable manner genetic variation within and between breeds in genetic improvement programmes to enhance competitivess and sustainability of EU animal food production. Estimation of breeding values plays a central role in most improvement programmes. These procedures need to be improved to capitalise on the increased understanding of the underlying genetic mechanisms on the one hand and the increased range of characteristics on the other. Reproduction techniques have an important influence on the optimal design of improvement and dissemination programmes that yield the desired genetic improvement while restricting the degree of inbreeding. Animal improvement programmes should focus on safe exploitation of genetic variation between animals to:

- produce better-quality, healthy, affordable, diverse food products offering consumers in and beyond Europe real options for improving their quality of life;
- ☐promote a more sustainable agriculture and aquaculture, including emphasis on non-food functions of animals such as pleasure, leisure, or use in the medical area;
- enhance the competitiveness of European agriculture and aquaculture and its organisations;
- build the basis for implementing high-quality and sustainable breeding strategies in developing countries.

Problems and opportunities

The ***keys opportunities*** underlying our action are the world wide recognition of the European strength in the field population and quantitative genetics, the availability of a wide range of genetic resources of high value, the high quality of the breeding organisation, including reproduction biotechnology centres and performance recording networks. Europe is, therefore, well positioned to rapidly transfer developments in science to a more profitable and sustainable agriculture and aquaculture.

The ***key challenges*** concern both increasing our understanding of factors contributing to genetic variation and the development of schemes that make optimal use of genetic variation while restricting the degree of inbreeding.

- The very fast progresses coming from animal genomics, with the short term availability of high density SNP filters, offer new fascinating opportunities for the genetic dissection of traits (QTL and gene detection through linkage disequilibrium and direct associations) as well as the selection programmes of animal (genome wide EBV and selection). Useable software tools need to be developed and made available.
- There is a need to develop novel methodologies for evaluation of the effects of on-going breeding-schemes and for design of new schemes that incorporate developments in fields like biotechnology (e.g. reproduction techniques and embryo genotyping), animal genomics (QTL information), and informatics (tracking and tracing) to improve efficient and to respond to demands from society (increased emphasis on quality of animal products and on animal welfare). There is a need to predict the consequences of developments in these areas on the (creation of) genetic progress and its dissemination from the top of the breeding pyramid to the production level.
- Improvement in the genetic analysis are needed that build on developments in field of statistics and of computer algorithms in order to deal with increasing complexity of (phenotypic) information due to multiple traits being measured in multiple environments and traits being measured on different types of animals (purebred and crossbreds). Incorporating traits such as disease resistance, longevity, and robustness requires novel methods (e.g. Markov chain Monte Carlo) to solve the complexity due to the large number of parameters relative to the amount of data, and due to the correlation of parameters. There is a need to explore other computational and numerical methods that have been successful applied outside animal breeding.
- Given the strong negative impact of inbreeding on reproductive and health traits, we need to find breeding schemes that generate genetic progress while maintaining appropriate genetic diversity (restricting inbreeding rate). Improved methods are needed for the design of breeding programmes, which involves predicting the consequences of alternative schemes on the phenotypic performance of a population and on the level of genetic diversity. Secondly, improved tools are needed to implement these concepts in selection procedures that aim at generating genetic progress while restricting the rate of inbreeding.
- In many species, selection for the most important economic traits has led to a reduction of fitness traits. Increased understanding of the biological background of antagonistic relationships between fitness traits and production traits is expected to enable the formulation of breeding strategies that achieve a balanced gain in multiple traits, i.e. prevent a reduction of fitness traits.
- The traits included in the breeding objectives of livestock species is expected to increase in response to consumer and social requirements and due to the introduction of new traits. Their underlying genetic variability must be evaluated, using classical approaches or new statistical techniques when they display specific distributions. This includes development of methodology that incorporates the social interactions in groups of animals associated with behavioural repertoires that are important for animal welfare and for proper functioning of the group.
- The environmental sensitivity (also referred to as phenotypic plasticity) of genotypes constrains the variability of phenotypic expression which depends on nutritional, climatic, infectious, and social environment. Increasing our understanding of environmental sensitivity is essential to take into account the dynamics of the environment in which future breeding animals will have to produce. Research should focus on defining, through population biology, which will be the most efficient genotypes for predictable environments
- Recording of phenotypes of animals will remain vital for breeding programmes. Given the high cost of phenotyping animals, research is needed to better

define the most efficient method and design to record phenotypes. This research will be important not only to improve the application of research findings, but also to conduct appropriate research in the definition of the role of genes, especially in the product quality and welfare traits. This research requires strong interaction with scientists in other disciplines such as electronic animal identification and nanotechnology.

- The application of crossbreeding has to pass from the simple estimation of level of heterosis created by crossing two breeds to the level of heterosis created by crossing two individual animals.
- Disease transmission is a crucial population-level issue which involves two players: the host and pathogen. These two players interact through infection (pathogen to host) and immunity (host to pathogen), and the pathways involved in both processes are under genetic control. Future research must focus on increasing our understanding of how variation in a population affects the overall performance of groups of animals and how changes in biodiversity are likely to influence the control of infectious disease.

Gap analysis

A number of the above challenge cannot be met without increased knowledge and improved technologies including:

- The development of conceptual quantitative genetic approaches to handle the high complexity of the phenotypes recorded as well as the complexity of the genome including the large number of genes and their interactions in contributing to the genetic variation underlying any production or functional trait.
- The development of computing resources to conduct the genetic analysis of the population to handle the increasing information on animals.
- The sequence of the genome of "minor" species such as duck, quail or fish species
- Efficient production of embryos or oocytes that can be genotyped at a large scale.

The problem of stasis

The European breeding industry can be characterised by its high scientific and technological level that ensures the high value of its products and determines its leading role in the world market. The industry is well positioned to adopt new technologies such as genome wide selection. This, however, requires a continued and substantial invest in research. The access and use of genomic information (in particular to the gene sequence linked to phenotypic variability) could be limited in the future, increasing the differences between actors competitiveness. If nothing is done, the functional and fitness traits should continue to be degraded following the selection on major characters.

Short, medium and long-term opportunities/needs for research

First 5 years

- Concerning the breeding objective and inclusion of new traits :
    - Increased understanding of genetics involved in host-pathogen interaction
    - Development and application of methodology to quantify and exploit genetics of traits measured on animals kept in groups that are influenced by social interactions.
    - Initial methods available to quantify and predict environmental sensitivity.
    - Genetic control of variation of quantitative traits
- Concerning the statistical and mathematical tools :
    - Statistical development and computer algorithms adapted to the new traits
    - Understanding the complex relationships among traits that cannot be described using standard distributions.
    - Improved inference of genetic parameters in selected populations.
- Concerning the breeding plans :
    - Development of improved methodology to maintain biodiversity and avoidance of inbreeding.
    - Genome wide estimation of the breeding values in major species
    - Improvements in animal identification and phenotype recording
    - Adaptation of breeding techniques and developing of sustainable highly productive genetic material and strategies in less developed countries (Third countries)

Longer term

- Continue development of methodologies to improve prediction of breeding values (predictive biology)
- Accounting for epigenetic phenomenon in EBV and animal breeding
- Implemention in practise of methods to select animals for desired degree of environmental sensitivity.
- Efficient prediction of phenotypic performance of animals in range of environmental conditions.
- Integration genome sequence information in the improvement of minor species
- Development of schemes incorporating large-scale genotyping at embryo or oocyte level.
- Development of sustainable breeding strategies to produce improved genetic material for less developed countries (Third countries)

28 March 2007

Reproduction

Reproductive techniques are indispensable for efficient animal breeding and have been used for decades to enable safe and efficient breeding. Efforts to develop practical methods for artificial insemination (AI) started in Russia in 1899. The first successful embryo transfer (ET) took place in rabbits in the 1890's. Nuclear transfer (NT) or gene transfer (GT) was first successfully executed in 1980. More recently (1997) the birth of Dolly - the first NT clone of an adult mammalian - was reported. AI and ET are nowadays routinely used worldwide.

The level of implementation of reproductive techniques varies not only between animal species, but also between countries. It is affected by e.g. infrastructural differences, differences in availability of the techniques (AI, ET) as a commercial service or because of lack of knowledge and practical methods in certain species, often due to anatomical and physiological limitations. Reproductive techniques are important tools to optimise breeding programmes, allowing dissemination of genes of interest. Therefore it is important to fill the gaps of knowledge and further develop practical methods in order to facilitate the use of both old and new reproductive techniques thus enhancing the competitiveness of EU farmers and food producers.

There is a need to coordinate the EU research agenda for an optimal output. Therefore national and international policymakers and research funding organisations should be encouraged to develop a coherent yet flexible European research base in animal breeding and reproduction.

The reproduction part of the strategic research agenda will focus on improving practical exploitation of reproductive techniques in order to:

- *maintain the efficiency of genetic programmes aiming to select for multiple traits of interest for sustainable agriculture, production efficiency and consumer demand.*
- *Develop programmes aiming to integrate knowledge / know how of reproductive (bio)technologies (AI, ET, IVF, embryo and gamete preservation) and new methods for genetic evaluation (including genomics)*
- *help to maintain genetic diversity in domestic species*
- *render possible the continued production of high-quality, healthy, affordable and diverse food*
- *strengthen animal agriculture and aqua culture through improved reproduction and animal breeding*
- *promote environmental agricultural and aqua cultural sustainability*
- *enhance the competitiveness of European agriculture and aquaculture organisations*
- *improve the welfare for livestock species by more sustainable selection programmes*
- *understand the consumers concerns for reproductive biotechnologies and communicate about the gains and risks of their extended use.*

In order to build a strong research base, effective technology transfer and training of new scientists are important. In the rapidly changing field of animal reproduction, there is a constant need for new scientists in the forefront of knowledge and with skills in animal reproduction and genomics based techniques.

Reproductive techniques can be based either on traditional reproductive biology or on molecular genetics/genomics. They facilitate more extensive evaluation and dissemination of specific genetics than would be possible by natural mating. The challenge is to optimise existing reproductive techniques and to improve their practicality, to develop new techniques and to implement them more widespread.

In the table below it is indicated what relevant research in the area of reproductive techniques in animals should focus on.

If no research and development takes place in the area of reproductive techniques, the development of animal breeding will be hindered. This will negatively influence the evaluation and dissemination of specific genes of great importance for the improvement of animal health and welfare as well as for the changes necessary for true sustainability in the area/ sector.

Table 1 Relevant research in the area of reproductive techniques in animals

Research Activity	prioritisation	Time frame (yrs)
Reproduction research basic (useful in AI, ET, NT, GT)		
Oestrus cycle: investigate the oestrus cycle, for some species	High	5-25
Female factors e.g. reproductive diseases) associated with the decrease in fertility and pregnancy loss	Medium	5-15
Genetic indicators for female fertility oestrus expression)	High	5-15
Gamete development and maturation	High	5-25
Fertilisation: investigation of the fertilisation process	High	5-15
Embryo development incl. maternal interaction = epigenetics and foetal growth regulation	High	5-25
Disease transfer through sperm / oocytes / embryos / nuclei / genes: ▪ swift and specific detection ▪ clinical relevance ▪ destruction of specific pathogens	Medium Medium Medium Medium	5-25 5 15 25
Feed composition and rations in relation to reproductive performance of male and female	Medium	5-15
Influence of physical environment and animal interaction on reproduction	High	5-15
Development of oestrus and pregnancy indicators milk/non milk based indicators	Low	5
Development of imaging methods ultrasonography to analyse ovarian state, early pregnancy and foetus abnormalities.	Low	5
Oestrus synchronisation reduced or non hormone use	High	5-15
Gene banking=preservation of oocytes and somatic cells	Low	5-25
Rearing efficient breeding animals	Low	15
Relevant breeding soundness evaluation	Low	5
Artificial Insemination / semen		
Semen preservation: development of new extenders, slow release semen incl. liquid semen	High	5-25
Efficient semen sexing	High	5-15
Relevant tests to measure semen quality / predictors for male fertility	High	5-15
Genetic indicators for male fertility	Medium	5-15
Timing of insemination	Medium	5
Practical non laborious insemination techniques for all species	Medium	5-15
Low dose insemination	Medium	5
Develop new AI techniques in order to improve labour efficiency	High	5-15
Embryo Transfer / embryos		
Embryo preservation	High	5-15
Embryo quality: develop tests for relevant characterisation of embryo quality	High	5-15
Develop methods for correct processing, and handling improving embryo survival/ quality	Medium	5-15
Alternatives for hormonal super ovulation e.g. egg collection from slaughtered material	High	5-15
Optimise super ovulation response	Medium	5-15
Non invasive sexing of embryos	Medium	5-15
Improved in vitro embryo production	High	5-25
Non-surgical transfer of embryos	Medium	15
Nuclear Transfer (cloning) / Gene Transfer		
Develop methods for derivation and maintenance of livestock embryonic and adult stem cells	High	5-25
Improve efficiency and safety of gene transfer methods	High	15-25
Complete functional validation of the novel candidate genes potentially affecting economically important traits	High	5-25
Gamete maturation, fertilisation, embryo-maternal interactions, or foetal growth regulation using system biology tools for transcriptome and proteome analyses	High	15-25
Establish cellular differentiation and transplantation methods	Medium	5-25
Develop advanced NT protocols	Medium	15
Develop transgenic animal models for new applications in the medical area	Medium	15-25
Risk assessment/research communication	Medium	5-25

16 February 2007

Food Quality and Safety

Priority problems and opportunities.

Consumer habits and lifestyles in Europe are changing very quickly – we need to be able to adjust selection goals consistently to meet consumer expectations or provide new product/market opportunities through selection.

We need to better understand and exploit genetic variation in resistance to infection by (current and emergent) zoonotic organisms as one of several technologies needed to ensure food safety. Food safety research should include genomics of zoonotic species to better understand host-pathogen interactions so that new or improved vaccination approaches might be developed. The safe dissemination of genetic improvement also has a role to play in ensuring food safety.

Some important sensory quality attributes of animal foods (e.g. tenderness, colour and texture of meat or albumen quality of eggs) are heritable. There are significant opportunities to improve quality and consistency of product through; a) development of better tools to measure/predict phenotypes and b) genomics research to develop molecular genetic selection tools.

Our understanding of the nutritional needs of humans continues to improve. The nutritional value of foods of animal origin is driven by macro and micro composition. There is an opportunity to improve general nutritional value and maintain and further develop niche products, through better understanding of the genetics and genomics of product composition.

Gap Analysis

The main gaps are: a) the need to identify the DNA polymorphisms, their interactions with each other and the environment controlling the heritable component of relevant traits and b) the need for the development of better, cheaper and less invasive tools for measuring phenotypes as a basis for breeding value estimation and payment systems. New 'gaps' in relation to safety may be being created by legislative changes related to the use of chemotherapeutics in animal feeds and changes to animal housing driven by welfare legislation.

The problem of stasis

Without relevant research on product safety and quality within Europe we will not be able to satisfy the increasing demand of consumers for diverse foods of high safety and quality produced in a transparent and traceable way. We risk that animal breeders elsewhere in the world gain in market share, and also miss out on the opportunity to develop differentiated value-added products to help European farmers compete with lower-cost imports.

RESEARCH NEEDS

First 5 years

The priority traits are:

Campylobacter infection of poultry meat, Salmonella infection of poultry and pig meat and eggs; identified taints of foods (especially boar taints), tenderness of beef and pork, shell quality of eggs, lipid/antioxidant content and composition of all animal foods, storage stability of fish and milk.

Priority research should be to identify the major genetic loci relevant to the heritable component of these traits and to progress from QTL to identified polymorphisms. Parallel to this work we need continued research on the biology of relevant traits, specifically, host-pathogen interactions, muscle biology, egg formation, lactation and product changes during storage. Progress in selecting for these traits would be enhanced with development of simple and cheap measurement technologies for these traits.

DNA traceability tools exist for the major species, but should be developed for minor food species.

15 years

The priority traits are:

Continued work on the traits listed under 5-years together with increasing attention to other zoonoses (especially VTEC, Staphylococcus in milk and viral infections of shellfish), food flavour characteristics, protein quality variation, processing characteristics (we expect important developments in processing in this timescale) and micronutrient composition.

By 15 years we should have sufficient knowledge of major genes for quality and safety traits **and the priority will be to research the interactions of these major effects in relation to the sustainability of specific livestock products and systems**. Advances will also be needed in genetic evaluation systems that combine novel phenotypes and multiple genetic markers inform selection decisions and product differentiation.

As an example of research relevant to nutritional composition, we would wish to see research to understand genetic variation in the digestion, absorption and metabolism of components of animal diets relevant to nutritional value and sensory quality of animal foods.

25 Years

In this timescale **priority should be given to animal fitness and adaptation as a component of perceived quality.**

The knowledge of the functional genetic elements related to food safety and quality traits will have grown significantly and research will be driven by predictive biological approaches that seek to model the interactions of genes and production systems to meet specific market needs.

From improved understanding of the genomics of host-pathogen interactions, research should include novel approaches to safety, including improved vaccines and possibly GM approaches to resistance.

Health, Welfare and Performance

Introduction

Based on elaborate consultation with industry and academic experts, this document identifies the problems and opportunities for animal breeding “Health Welfare and Production” in Europe; describes the problem of the status quo and prioritises research and development needs for the near and long-term future. Given the large topics it covers it should considered as a companion to species and technologies groups.

Problems, knowledge gaps and opportunities

- *Health:* Development of global concept of generalized immunity, is needed an indicator trait for general disease resistance. Identification of new and better disease resistance traits is only limited (e. g., immunocompetence, resistance or tolerance). Impact of selection for disease resistance vs. disease tolerance should be assessed (e.g., is it better to select for acquired or innate immunity?). Impact of improved health at population level is unknown (e.g., herd immunity). Also sociological and political issues are currently ignored (e.g., farmers may consider disease and welfare recording as intrusive because of the sensitivity of the information).
- *Animal Welfare:* Definitions of welfare with objective criteria are needed. Adaptation to consumer and general public conceptions changes and cultural considerations will be required. Typical issues are competition effects, cannibalism, reaction to stress that are considered unsolved problems.
- *Production / Reproduction:* Shift to selection for increase product quality, healthy products is considered a major challenge in all species from poultry to buffalos. More robust (e.g., fertile) animals in high producing dairy and beef cattle, interaction between reproduction and environment are often unknown. More automatic on-farm performance recording (e.g., milk ingredients and hygienic status), interaction between recording protocols and modelling of genetic and non-genetic goals are key opportunities and challenges. Expert systems for farm management based on continuous recording of important traits potentially directly on the animal (e.g., Radio Frequency Identification based) creating massive longitudinal data will need technological advances. Not well-known correlations between optimal / special conditions and “real-life” conditions will need additional research. Designing of animals optimized for economic and production environments is a key challenge. Development of adequate overall indexes integrating molecular and phenotypic data will require additional attention.
- *Economic Efficiency:* Challenges are in the reduction of labour requirements, while maintaining or improving animal health and welfare, and product quality. Given the current evolution of the European agriculture and the demand for environmental friendly production systems; adapted breeding for low input and industrial production systems will be needed, breeding should be considered in a management perspective. To achieve such goals, all methods to develop adequate multiple trait selection tools in breeding strategies should be encouraged.
- *Biological Efficiency:* Accounting for environmental impacts (e.g., wastes, diet) in the calculation of efficiency and the preservation of genetic resources, with special attention to local breeds has yet to be done. Increased consideration for the reduction of greenhouse gas and more efficient use of resources will be needed. We are approaching a plateau on some major selected traits (e.g. milk in cattle, egg number or growth in poultry) with welfare implications because high producing animals more sensitive to stress, metabolic unbalance and diseases. Environments will become less "optimised" due to welfare consideration (e.g, extensification, open air, more diverse feedstuff), genetic characteristics need to be adapted in order to avoid decrease in fitness and therefore efficiency.
- *Other issues (i.e. IT):* Development of grid-based IT technologies could allow easier data exchange between existing data bases on a herd, regional, national and EU wide level. Development of adapted IT technologies for large and distributed multi-country, multi-trait and multi-environment genetic evaluation systems is a key technology that needs to be developed.
- *Enabling factors:* Training the scientific staff, education of farmers, and enlightenment of the consumers together with the definition of more balanced selection goals (balance between production/fitness but also short/long term genetic variability) and the search for niche production (high meat quality in poultry / cattle; fatty acid in milk) should be considered important enabling factors in the next 5/15 and 25 years

Problem of stasis

Expert identified that stasis in the fields of “Health, Welfare, and Performance” will increase gap between available and needed animals in the future. Impact on the industry and EU citizens will be very important. Industry will be unable to adapt and face challenges from competitors and EU citizens will not find the quality of products and production circumstances they aspire to. Given already known and probably generalized negative genetic correlations between production and health traits, lack of research in this area will lead to continued deteriorating functionality of animals and the decrease of animal welfare because of the lack of adaptation to production circumstances.

Short, medium and long-term opportunities and needs for research

5 year time horizon by group of topics:

- Improved performance (production/reproduction), health and welfare recording for diverse commercially and socially important traits including (in order of priority):
    1. Sustainable performance recording (e.g., useful information, genetic and non-genetic, going back quickly to farmers stimulating and maintaining interest).
    2. Product quality (e.g., using innovative methods as spectral data in dairy production)
    3. Biological efficiency (e.g., waste, diets)
    4. Animal health (e. g., recording covering all animals, not only diseased)
    5. Animal welfare (e.g., developing and recording of objective welfare indicators)
    6. Linking of existing databases, easier data exchange, on a herd-level, regionally, nationally and EU wide together with public-private cooperation in this field.
    7. Obtaining data in environments closer to commercial use in all species and for all traits.

- Improved genetic evaluations for performance (production/reproduction), health and welfare traits including (in order of priority):
    1. Development of routine combined genetic evaluation of animals based on phenotypic and molecular information, enabling research towards genomic selection.
    2. Advanced genetic evaluations using optimally existing data bases on a herd, regional, national and EU wide level.
    3. Maintenance of sufficient research on genetic evaluation methodology, in particular for novel traits as product quality and animal fitness and robustness.
    4. Proper use of international evaluation results in developing countries.

- Improved breeding programs for performance (production/reproduction), health and welfare (in order of priority):
    1. Breeding for improved products and improved production circumstances will affect current breeding programs.
    2. Importance of health and welfare traits and reproduction will increase with broadening of breeding objectives.
    3. Social considerations will enter breeding programs.

15 year time horizon (in order of priority):

1. Genomic selection will become widespread.
2. Selection for alternative product quality and animal robustness traits will be widespread.
3. Advanced modelling for new and potentially massive data (e.g., longitudinal data recorded on-farm automatically) will be needed.
4. Interaction, data exchange, distributed computing and expert-systems will be developed on a herd, regional, national and EU wide level.
5. Major research in development of genetic solutions to diseases, leading to development of generalised immunity. This will be accompanied by investigations of the molecular or polygenic genetic mechanisms specific to individual diseases.
6. Integration of GxE interaction in routine genetic evaluations, selecting animals for an environment, not creating proper environments for the animals. This will be especially important in less optimised production systems and for developing countries.
7. Alternative methods to experimental challenges as those will no longer be considered ethical.
8. Molecular genetic should play a major role including the use of laboratory species (e.g., mouse) to identify disease resistance candidate genes.

25 year time horizon

Developments of technologies have the potential to change radically the direction of animal breeding for "performance, health and welfare", most influential should be increased capabilities:

1. to monitor directly biological processes to gain new inside into animals
2. to acquire molecular, gene-expression and other novel types of data
3. to analyze data and to predict genetic merit and non-genetic management related values
4. to manage animals, to select the best and to disseminate superior germplasm.

16 February 2007

Diversity and Distinctiveness

Preface: exploitation and conservation of genetic diversity

- In Europe the consistent increases in animal production have been realized by intensification of livestock systems towards high input – high output systems. The genetic resources used for these intensive production systems are only a few breeds and lines. Continuously, many local breeds and recently developed breeds and lines are set aside from the primary food production chains.

- Farm animal genetic resources are sources of genetic variation of fundamental importance to ensure future genetic improvement, to satisfy possible future changes in the markets and in the production environment, and to safeguard against disasters that give an acute loss of genetic resources. In many areas local breeds adapted to harsh conditions are unique sources of income for the rural communities. The link between local breeds and the environment where they were developed makes them key components for the management and conservation the European agro-ecosystems diversity, and important elements of cultural diversity, as they reflect a history of symbiosis of relatively long periods with mankind. Diversity of breeds and their farming systems highly contribute to European food products quality and diversity. Than, farm animal genetic resources are opportunities to maintain a vital countryside.

- European breeding organisations are strong players in the global competition. It is crucial for Europe that the breeding sector maintains and further develops its leading role. At this respect, sustainable utilisation and conservation of the European breed (and production system) diversity can play an important role.

1. Challenges, opportunities, gaps

1.1 Challenges

- To maintain within the production systems a large variety of breeds economically competitive. This includes developing sustainable local breeds.
- To develop methods and strategies to further exploit available genetic variation in livestock and at the same time implement and further develop methods/strategies to maintain farm animal genetic diversity.
- To achieve a wider participation of the stakeholders on the issues of animal genetic resources sustainable use and conservation, including the industry.
- To achieve a better incorporation of AnGR policies in policies.
- To develop low cost strategies for animal genetic resources inventories, conservation and development.
- To develop strategies for a common management of the genetic variation of worldwide distributed commercial breeds, in order to avoid losses due to the use of too narrow genetic basis.

1.2 Key opportunities

- Breed diversity is often thought just as source of genetic variation to ensure future genetic improvement. However, breed diversity is today increasingly reclaimed in Europe for food product diversification and quality, for maintenance of diversity of natural agro-ecosystems and rural culture. With the standard of living increasing, new roles upraise for domestic animals, including sport, leisure, tourism, companion, hobby; breed diversity offers opportunities in this direction.
- With EU enlargement, number of farms has more than doubled. In this process new breed diversity has also entered in EU. Across all Europe, still existing diversity is at risk of being exposed to the erosion process that generally accompanies intensification of production systems.
- Awareness for farm animal genetic resources has been raised in the last two decades within EU.
- Genomic research is making possible to localise and characterise genes and their functions. Breeds with extreme phenotypes are proving to be particularly useful at this respect. Than, breed diversity offers high opportunities for understanding genome structure and function of farm animals, and development opportunities.
- Breeds with seemingly limited competitive benefit may harbour single genes (e.g. disease resistance) of potential high value with respect to economics and animal welfare, which can be transferred through traditional breeding strategies or transgenic techniques in high efficiency breeds.
- European research leadership in the farm animal genetic resources issue can provide useful expertise for other parts of the world.

1.3 Gap analysis

- Basic technology to meet existing challenges and opportunities is already available, but needs further development in particular in the following areas:
    - systematic screening of potential unique genetic structures in (endangered) breeds, based on farm animal sequences, high throughput genotyping and comparative genomics;
    - reproductive technologies for commercial and conservation (ex situ) purposes;
    - strategies for keeping a vital countryside, including the characteristic animal production systems and associated breeds. Strategies should be based on a total economic value of breeds.

2. The problem of stasis: what will happen if no research or development occurs

- Loss of farm animal genetic diversity and of opportunities for future development of farm animal populations.
- Genes will be discovered and patented by competitors, EU farm animal industry will have no or limited access to licensed technologies.
- Loss of opportunities for keeping a vital countryside.

3. Short, medium and long-term needs for research

3.1 Five years horizon

- To develop strategies at the country level to halt erosion of farm animal diversity, within and between breeds.
- To develop strategies at the European level to halt erosion of farm animal diversity. The experience developed by some countries more advanced at this respect should be used.
- To develop models and strategies, at the European and global levels, for the management of genetic diversity when breeding is not centralised in order to avoid the risk that a too narrow genetic basis will be used.
- To develop enhanced reproduction, molecular genetic and statistic tools for preserving genetic diversity.
- To increase the efficiency of breeding for less intensive or small-scale animal farming, often associated to local endangered breeds.

3.2 Fifteen years horizon

- To study efficiency of implementation, at the country and European levels, of strategies to halt erosion of farm animal genetic resources.
- To understand and experiment the role of animal farming agriculture including the associated local breeds in sustainable rural economies and environments.
- To develop mechanisms in order to have markets recognising the non-market services of farming, including the environmental and cultural roles;
- To implement knowledge on differences in the genetic structures of breeds.

3.3. Twenty-five years horizon

- To develop models using breed diversity to understand genome structure and functions.

29 March 2007

Enclosures

More general consideration on Genomics and Bio-informatics

Genomics and systems biology

Animals as systems – animals in systems

Biological science over the past decade and more has been dominated by reductionist approaches typified by the genome projects. With the acquisition of complete genome sequences for humans and several model organisms the emphasis more recently has returned to more integrative, holistic approaches termed systems biology. Systems biology provides an appropriate scientific context and strategy for the needs of the farmed animal sector. The growing awareness of the finite nature of the planet's resources means that changes are needed in many economic sectors, including animal production systems, to address environmental issues and more generally sustainability. It is necessary not only to understand animals as biological systems, but also the impact of animals on their environment and vice versa. Thus, the scientific strategy for sustainable animal breeding and reproduction needs to address '*animal as systems* and *animals in system*'.

Predictive models

The development and testing of models lie at the heart of systems biology research. The extent to which a model is predictive determines its value in understanding the system of interest. Ideally, the models should be not only qualitative but also quantitative. Whilst the importance of predictive quantitative models has received increased recognition with the re-emergence of systems biology, such models have been the foundation of quantitative genetics and genetic improvement of plants and animals for decades. Thus, adapting the 21st century vision of systems biology to the needs of sustainable animal breeding and reproduction will be less about alignment of philosophies and approaches and more about ensuring that the technologies and information systems customised for the target species and systems are put in place.

From sequence to consequence

Predictive models are not only required for the pursuit of knowledge and greater understanding of animal systems, but also to inform improvements in sustainable animal breeding, production and reproduction. Thus, in the genomics era models should allow the prediction of consequences from sequence, i.e. nucleotide substitution(s) to the severity of epidemics, to product quality and customer satisfaction, to animal health and well-being.

Models, experiments, tools and resources

The virtuous cycle of predictive systems biology research to enable and inform improvements in sustainable animal breeding and reproduction requires:

- Modelling – the development of improved predictive and quantitative models requiring skills in theoretical / numerical / mathematical biology
- Experiments – the testing and generating of models and hypotheses requiring multidisciplinary skills and expertise in the whole animal biology encompassing the full breadth of phenomics, including host and pathogen aspects of infectious disease, molecular biology, molecular and quantitative genetics, bioinformatics
- Tools and resources – the development of the necessary molecular, biological, mathematical and informatics tools, methods and resources to enable the experimental and translational research programmes

State of the art

A primary aim of farm animal genome research is to understand the genetic control of agriculturally, economically or biologically important traits. In addition, these species have considerable importance as models for understanding important biological process, for example, vertebrate development using chickens as a model.

Status of structural genomics and resources genome research in farm animals

The ***genome*** of a farm animal consists of 1 to 3 x 10^9 base pairs of DNA containing an estimated 20,000 to 25,000 protein genes that together represent the blueprint for a cow or a chicken or a salmon. The ultimate description of the structure of a genome is its complete DNA sequence. ***Draft genome sequences*** have been completed (chicken, 2004[3]), are in progress (cattle[4], horse[5]: raw data generated, assembly and analysis in progress; pig[6]: sequencing in progress) or planned (salmon). Low coverage (2x) sequence coverage is also available for the rabbit genome[7]. Clone-based ***physical maps*** (***BAC contigs***) have been completed or are in the final analysis phase for chickens, salmon, cattle and pigs[8]. A virtual map of the sheep genome has been established by aligning sheep BAC end sequences with the human and cattle genome sequences. Extensive ***libraries*** of large fragment ***genomic*** (e.g. BAC) and ***cDNA*** clones are available. From the latter, between 37,000 and 1.14 million ***expressed sequence tags*** (***ESTs***) are in the public domain for salmon, sheep, chickens, pigs, horses and cattle[9]. The cDNA clones or EST data have been used to develop ***microarrays*** (cDNA, oligo and Affymetrix GeneChips) with

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[3] Sequence and comparative analysis of the chicken genome provides unique perspectives on vertebrate evolution. Hillier *et al*., International Chicken Genome Sequencing Consortium (2004). Nature **432**, 695-716.

[4] http://www.hgsc.bcm.tmc.edu/projects/bovine/ http://pre.ensembl.org/Bos_taurus/

[5] http://www.broad.mit.edu/mammals/horse/

[6] http://pre.ensembl.org/Sus_scrofa/index.html

[7] http://www.ensembl.org/Oryctolagus_cuniculus/index.html

[8] http://www.sanger.ac.uk/Projects/S_scrofa/ http://www.bcgsc.ca/lab/mapping/bovine http://www.genome.wustl.edu/projects/chicken/index.php?fpc=1

[9] http://www.ncbi.nlm.nih.gov/dbEST/dbEST_summary.html

up to 24,000 independent probes per array for chickens, pigs, cattle, sheep and salmon. Genome wide ***linkage*** (chicken, cattle, pig, horse, salmon, trout and sheep) and ***radiation hybrid*** (cattle, pigs, horses, chickens) maps with more than 2,000 mapped loci per map have been constructed. In addition to the 1,000 - >2,000 ***microsatellite*** markers available for each species, hundreds of thousands of ***single nucleotide polymorphisms*** (***SNPs***) are being identified as a by-product from the sequencing projects[10]. ***Bioinformatics*** resources include genome databases[11], genome sequence ***databases***[12], and web resources[13]. Similar resources are being developed for some economically important fish species – e.g. salmonids, tilapia, sea bass.

Physical mapping or even sequencing a genome, however, does not reveal its function.

Functional genomics – successes and prospects

A primary justification for genome research is to enable the dissection of the ***genetic control of complex traits***. Understanding the genetic control of such traits, whether it is carcass composition (fat / lean content) in animals or obesity in humans, or responses to infectious disease in livestock or humans, is the challenge for genetics research in the 21st century. The regions of the genome that control variation in such traits are termed ***quantitative trait loci*** (or ***QTL***). Our understanding of the genetic control of quantitative traits has been revised in the light of results from QTL mapping experiments[14]. QTL with moderate effects on traits such as growth, carcass composition, litter size and host responses to infectious disease have been found, not only in experimental populations but also in commercial populations. Identifying the ***trait gene*** and causal genetic variation within a QTL is exceptionally demanding and has been rarely achieved in better funded species such as humans and mice. Nevertheless there have been a few recent successes in which single base pair changes that are causative of major QTL effects have been identified[15] (e.g. for muscling in pigs and for milk yield in cattle). Farm animal species offer many advantages for genetics research and the dissection of the genetic control of complex traits. Livestock populations and breeds offer greater within and between population ***genetic diversity*** and variation than found in laboratory (inbred) mice. Experimental ***crosses*** between diverse breeds can be combined with analysis of segregating commercial populations for high-resolution ***linkage*** or ***recombination mapping***. – a combination not possible in human genetics. The availability of thousands of SNP markers allows the power of ***linkage disequilibrium*** based approaches to ***association studies*** in ***segregating populations*** to be pursued effectively. These advantages for genetics research can now be more fully exploited through the availability of genome information and tools (sequence, SNPs, microarrays) that are equivalent to those available to human and mouse geneticists. Advances in ***genetic modification*** technologies as applied to farm animals (nuclear transfer, gene targeting, RNAi, lentiviral vectors) offer further experimental opportunities for functional genomics research in whole animals as well as in cell-based systems.

Technology transfer

European companies are amongst the world leaders in animal breeding of pigs, poultry, cattle and cultured aquatic species. These companies are well-placed to exploit increased understanding of the genetics of economically important traits and in several cases are already using genomics technologies. For example, ***marker assisted selection*** can be used to accelerate the rate at which desirable natural variation is exploited to improve animal health, welfare and productivity. Molecular tools developed through genome research can and are also being used to provide robust traceability of products from farm to fork.

Gap analysis

Phenomics

Increasingly, the capacity to define animals in molecular terms at the DNA or genomic level, for example to the resolution of a single nucleotide, has outstripped the capacity to define phenotypes both in volume and precision. Intermediate level phenotypes – transcriptome, proteome and metabolome are addressed later. High resolution genetics, gene-gene interaction and network analyses require large numbers of animals / recombination events. These numbers are beyond the capacities of experimental animal / farm facilities for land-based animals and current labour-intensive systems for capturing detailed phenotypic / trait data.

The human phenotypes of interest to medical science largely concern non-infectious disease, including cancer and infectious disease. These data are largely acquired post-hoc from health services with the costs of the phenotypic measures borne by the health services. The phenotypes of greatest interest in the model mammal (i.e. mouse) are also disease states. Recently, large-scale coordinated efforts have been made to acquire comprehensive mouse phenotypic data in a high throughput manner[16].

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[10] http://www.ncbi.nlm.nih.gov/SNP/snp_summary.cgi

[11] http://www.thearkdb.org

[12] e.g. http://www.ensembl.org

[13] e.g. http://www.chicken-genome.org ;

[14]. Andersson, L., Haley, C.S., Ellegren, H., Knott, S.A., Johansson, M., Andersson, K., Andersson-Eklund, L., Edfors-Lilja, I., Fredholm, M., Hansson, I., Håkansson, J. and Lundstrôm, K. 1994. Genetic mapping of quantitative trait loci for growth and fatness in pigs. *Science,* **263**, 1771-1774; Domestic animal genomics: deciphering the genetics of complex traits. Andersson, L. and Georges, M. (2004). Nature Review Genetics **5**, 202-212.

[15] e.g. Grisart, B., Coppieters, W., Farnir, F., Karim, L., Ford, C., Berzi, P., Cambisano, N., Mni, M., reid, S., Simon, P., Spelman, R., Georges, M. and Snell, R., 2002. Positional candidate cloning of a QTL in dairy cattle: identification of a missense mutation in the bovine DGAT1 gene with a major effect on milk yield and composition. *Genome Research* **12**, 222-231; Van Laere, A-S., Nguyen, M., Braunschweig, M., Nezer, C., Collette, C., Moreau, L., Archibald, A.L., Haley, C.S., Andersson, G., Georges, M. and Andersson, L, 2003. A regulatory mutation in IGF2 causes a major QTL effect on muscle growth in the pig. *Nature* **425**, 832-836.

[16] http://www.eumorphia.org/

Large volumes of simple phenotypic data (e.g. birth weight, milk yield) for farmed animals can be acquired at modest cost from the industry, but the capacity for detailed phenotyping for production traits (e.g. meat quality, milk lipid composition), metabolic diseases or for immune and infectious disease traits is limited by the associated costs. Experimental animal facilities are essential for the acquisition of high quality phenomic data. Effective pooling of phenotypic data across research organisations or exploiting opportunities to acquire phenotypic data from large commercial populations will require the development of robust standard operating procedures, including agreed ontologies for phenomic data.

> Targets – Establish standard phenotypic trait ontologies for the major farmed animal species. Co-ordinate and standardise the acquisition of disease surveillance data at a pan-European level in a manner not only to improve the effectiveness of disease control, but also to enable research on the genetics of host responses to infectious disease (biological samples from which DNA can be prepared are required as well as the trait data). Develop incentives to encourage the use of commercial populations for high resolution genetic analyses in farmed animal species.
>
> Evaluate the scope of using advanced scanning technology to acquire high quality phenotypic data for large numbers of animals (living and/or post-mortem in slaughter houses or packing plants).
>
> Establish the capabilities and facilities as necessary to deliver high throughput detailed phenotyping on farmed animal species, including disease challenge capabilities.

Genomics

Genome sequencing: A completely sequenced genome is recognised as a pre-requisite for 21st century systems biology research. Although the costs of sequencing complex genomes continues to fall, the current driver for improvements in sequencing technology is the target of $1,000 for a re-sequenced human genome. Emerging technology platforms such as Solexa and 454 are of value for re-sequencing or *de novo* sequencing of simple genomes with limited repetitive sequence. The limited window of opportunity to exploit the capacity of the (human) genome sequencing centres for high throughput *de novo* sequencing of complex genome should be grasped to complete the acquisition of complete genome sequences for all the major farmed animal species (including aquaculture species) and their pathogens.

> Targets – 'finished sequence'[17] for pig, cattle (model bovid), chicken (model avian), salmon (model salmonid); draft sequence 2-6x coverage aligned with appropriate model for sheep, goat, duck, turkey, trout and other farmed fish species

Genetic variation

Genetic variation - Single nulecotide polymorphisms (SNPs): SNPs are the genetic markers of choice for high resolution genetic analyses. There is a competitive market for high throughput SNP genotyping platforms. SNP discovery programmes are required to exploit this technology for population-wide genetic analysis. As the emerging linkage disequilibrium (LD) maps for farmed animals reveal that haploblocks are smaller than expected, higher density SNP panels are required.

> Targets – SNP discovery programmes to reveal up to 5 million putative SNPs for each major farmed animal species[18]; validated SNP panels with 0.5 – 1 million SNPs for each target species.

Genetic variation – copy number variants (CNVs)[19]: Detailed characterisation of the human genome has revealed unexpected levels of insertion / deletion / duplication variation between individuals. Whilst, as yet, much of this variation appears to have no phenotypic consequences, some of this variation is associated with disease.

> Targets – scan finished farm animal genomes for evidence of copy number variants – insertions, deletions and duplications. Develop clone-based and oligo-tiling-path arrays for comparative genome hybridisation (CGH) analyses. Develop assays for such variation in pedigrees to facilitate studies to test for associations with performance.

Genetic variation – re-sequencing: The capability to re-sequence the human genome of an individual for $1,000 is likely to be achieved within the next 5-10 years or less. The necessary technology is likely to be equally efficacious for any comparable genome for which a finished sequence is available.

> Targets – Deploy inexpensive re-sequencing technology to evaluate the merits of genome selection, initially in dairy cattle.

Bioinformatics

Scientists engaged in genome research programmes require unimpeded access to databases, together with suitable tools for interrogation and analysis in order that increased knowledge and understanding can be developed from a synthesis of many individual experiments. Bioinformatics resources are essential for the analysis and dissemination of experimental data from genome research programmes and for the intelligent planning of further research, primarily to deal with the large volumes of data generated by genome research. In addition to the volume of data generated, biological research also generates complex data sets, which must be combined in sensible, meaningful and flexible ways. Thus, good bioinformatics is critical to deriving value from the funds invested in genome research. The need for bioinformatics in the analysis of the complex genomes of agricultural species spans the full spectrum of database resources, methods and infrastructures for data integration and analytical / display tools.

> Targets – Support for continued annotation and maintenance of genome databases customised for farmed animal data (e.g. Ensembl, ARKdb, ..) as well as for generic resources (e.g. EMBL, ArrayExpress, GO, …). Development of data sharing policies to maximise the value to be extracted from complex data sets. Deployment of GRID technology for more effective integration of disparate data sets and exploitation of distributed computing capabilities. Development of pen-side / farm / slaughter house data capture systems to support phenomics targets concerned with more effective use of commercial population data. Development of appropriate data security systems that enable effective use of commercial data sources but without compromising legitimate commercial interests.

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[17] 'finished sequence' has an error rate of 0.01% and generally has no gaps

[18] major farmed animal species assumed to be: cattle, sheep, goats, horses, pigs, chickens, ducks, turkeys, salmon, trout and other fish species cultured in Europe

[19] http://www.sanger.ac.uk/humgen/cnv/

Develop or customise computational tools for the elucidation of gene-gene interactions (e.g. epistatic QTL) and gene networks from functional genomics and genetics data.

Transcriptomics

Transcript profiling: The transcriptome represents the sum of gene expression at the level of RNA transcripts in the cell, tissue or organism of interest. As gene expression changes over time and in response to environmental stimuli, including infection, it is necessary to define the sample in multiple dimensions – spatial, temporal and state. Alternative splicing and RNA editing means that the transcriptome is more complex than the gene content of the genome with the number of different transcripts exceeding the number of genes.

There is a competitive market in technologies that enable massively parallel assays for gene expression at the transcript level, including spotted microarrays and Affymetrix GeneChips. These transcriptomics platform technologies have already been used in research on farmed animals. Consortia of research groups have commissioned some of the species-specific reagents and tools required for transcriptomic analyses in farmed animals. Current transcriptomic platforms largely address the expression of protein-coding genes but do not provide coverage of non-coding RNA genes. Current transcriptomic platforms for farmed animals mainly provide one probe / probe set per gene, do not address the use of alternative promoters, alternatively spliced transcripts and thus do not allow the full complexity and diversity of transcriptomes to be assayed. Exons arrays, CAGE library technology and sequencing-based methods represent currently available technologies that could be customised for farm animal studies to address the gap in current systems.

Although the primary use for transcriptome analyses may be in research, there are also opportunities to use transcriptomic data for diagnostic (health, productivity) purposes.

Targets – In collaboration with technology providers refine transcriptomic tools to reflect current knowledge of the target genomes and transcriptomes and include tools for assaying alternatively spliced transcripts, alternative promoter usage and the expression of non-coding RNA genes.

Proteomics

Protein profiling: The proteome is the complete set of proteins expressed by a cell, tissue or organism. The proteome is dynamic (cf. the transcriptome) and the source again needs to be defined in multiple dimensions. Post-translational modifications of proteins extends the scope for complexity as information flows from the genome through the transcriptome to the proteome. Analyses at the protein level are further complicated by the lack of a facile universal system equivalent to hybridisation based assays used for nucleic acid analyses. The complexity of the technologies for proteomic analyses is a significant barrier to high throughput analysis and to customising proteomics technology for the species of interest.

In addition to the gap in proteomics technology customised for farm animal species, there are significant gaps in the tools available to assay proteins of importance for immune functions.

Targets – Develop proteomics technologies for high throughput analyses in farmed animal species with an initial emphasis on tissues of economic importance, e.g. skeletal muscle, milk, egg and wool.

Develop comprehensive immunological toolkits for high throughput assays of immunological important proteins for all major farmed animal species.

Metabolomics

Metabolite profiling: The metabolome is the collection of metabolites present in a cell, tissue or biological organism and represents a significant product of a genome and its interaction with its environment. Metabolites can indicate the physiological state of an individual – growing, pregnant, lactating or sick. Metabolites can also indicate the relative merits of animal products as food, e.g. fatty acid composition. Thus, metabolomics can not only contribute to the development of comprehensive systems biology models for farmed animals, but also directly to issues of commercial importance.

Targets – Exploit developments in metabolomics technology for systems biology research in farm animals and to evaluate the merits of animal products.

Functional genomics – high throughput gene modification / knock down (RNAi)

The 'omics technologies summarised above allow the development of systems models of the species of interest. These technologies also allow the testing of some elements of the models. For example, predictions of how an animal will respond to a given environmental stimulus, including exposure to a pathogen can be tested. There is also scope to test the genetic component of the model, for example by segregation analyses or association studies. Although cause and effect can be deduced from such genetic analyses the precision with which the causal genetic variation can be defined is often limited by the size of the population. Genetic manipulation technologies offer the opportunity to test the genetic component of the models and to explore the cause and effect relationship for specific genes or genetic variants. Different genetic manipulation technologies offer a range of options of varying sophistication and precision. Some potentially attractive technologies are yet to be proven in mice, for example, RNAi-based gene knockdown in a tissue-specific or temporal-specific manner.

It is unlikely that genetically modified farm animals will be approved for entering the food chain in the next 5-10 years in Europe. However, there is greater public support for GM-based systems to produce molecules, cells or tissue for human medical use. There may be GM-based solutions for the threats posed to both animals and humans by infectious diseases. Finally, as the economic influence and power of China will continue to grow there is a need to track the development and deployment of GM-technologies in China.

Targets – Develop a range of stem cells from farmed animal species to facilitate cell-based in vitro functional genomics research, including genetic manipulation. Develop systems for high throughput genetic modification, including RNAi-based gene knock-down in cell-based systems. Develop advanced technologies for genetic manipulation in farm animal species, including the capability for precision genetic modification using homologous recombination in appropriate stem cells and RNAi-based gene knockdown.

More general considerations on genetics

Animal Breeding aims at exploiting in a sustainable manner genetic variation within and between breeds in genetic improvement programmes to enhance competitivess of EU producers and animal food. The basic tools of animal breeding are well proven and in many cases only need to be effectively applied to make a difference in recently domesticated species, however, in some cases this would benefit from more user-friendly software tools. As explained in more detail at other place, animal breeding is faced with a number of challenges including (i) the ability of animals to handle an increasingly wide range of production circumstances, (ii) the increased attention to quality of animal products, (iii) increased emphasis on animal health and welfare. Animal breeding programmes are based on a sound understanding of the role of genetic factors in the different characteristics of an animal (performance, robustness and quality). Estimation of breeding values plays a central role in most improvement programmes. These procedures need to be improved to capitalise on the increased understanding of the underlying genetic mechanisms on the one hand and the increased range of characteristics on the other. The development of high-density SNP genotyping will facilitate genome wide selection but useable software tools need to be developed and made available. Reproduction techniques have an important influence on the optimal design of improvement and dissemination programmes. The breeding programmes need to be implemented that yield the desired genetic improvement while restricting the degree of inbreeding. Improved tools are needed to support the design of these schemes. In a large number of species crossbreeding is used to capitalise on breed complementarities and crossbreeding effects. The potential use of non-additive genetic variation needs further study and development of software tools. Ultimately, we need to have:
□□software able to optimise the use of genome wide selection
□□in combination with a number of specific genes of known effect
□□for improvement of additive and non-additive genetics effects
□□for multiple traits
□□across a range of environments
□□taking into account population level traits
□□taking into account the design of breeding structures of the different species
□□whilst optimising the amount of genetic diversity.

Animal breeding and reproduction have an enormous potential to improve our lifestyles and prosperity and to enhance the competitiveness of EU farmers and food producers. In order for this future to be realised, the EU and its Member States need to coordinate the EU research agenda in the field. This process involves national and international policymakers and research funding organisations to stimulate a coherent yet flexible European research base in animal breeding and reproduction. The research agenda will focus on improving the safe exploitation of the genetic diversity of animals in order to:
□□produce better-quality, healthy, affordable, diverse food offering consumers in and beyond Europe real options for improving their quality of life;
□□strengthen animal agriculture and aquaculture through better animal breeding and reproduction and by interacting more strongly with other fields;
□□promote environmental agricultural and aquacultural sustainability, including new applications for pleasure, leisure, or in the medical area;
□□enhance the competitiveness of European agriculture and aquaculture organisations.
For building a strong research base, effective technology transfer and training of new scientists are important. In the moving field of animal genetics, there is a constant need for a flow of new scientists skilled in the latest tools into research and industry.

Breeding
Future qualitative and quantitative genetic technology will give breeders much control over the genetic makeup of individual animals selected for breeding. In other words, what can be selected with increasing precision is the genome of an individual. Yet population-level effects also deserve consideration for at least three reasons. **Firstly**, social interactions in groups of animals are associated with behavioural repertoires that are important for animal welfare and for proper functioning of the group. Impact of current selection strategies on social interactions is poorly understood. **Secondly**, the expression of production potential inherent in an animal’s genes depends on nutritional, climatic, infectious, and social environment, which also includes the important role of the breeders. This is called environmental sensitivity or phenotypic plasticity and provides a measure of genotype-environment interactions at the level of an individual animal. It is important that we increase our understanding of environmental sensitivity. It is important to take into account the dynamics of the environment in which future breeding animals will have to produce. Research should focus on defining, through population biology, which will be the most efficient genotypes for predictable environments.
Thirdly, disease transmission is a crucial population-level issue which involves two players: the host and pathogen. These two players interact through infection (pathogen to host) and immunity (host to pathogen), and the pathways involved in both processes are under genetic control. Future research must focus on understanding how variation in a population affects the overall performance of groups of animals and how changes in biodiversity are likely to influence the control of infectious disease.

There is a need for research focusing on the further development of complex statistical methods and computer algorithms for coping with multiple traits measured in multiple environments and types of animals (pure bred and crossbreds). The methodology is needed for testing different models and estimation of genetic components that increase our understanding of the population-level effects. Results from these analyses need to be implemented in methods used for genetic evaluation of animals in the population. They need information from new sources such as genomics and the study of how animals adapt to specific environments or changes in environment (robustness). Attention must also focus on the more complex, non-linear,

and difficult-to measure traits such as disease resistance, longevity, and robustness, as well as on new and emerging traits. Extensive modelling of complex phenotypes (biological traits) provides interesting and important information about environmental influences on these phenotypes for advanced management tools.
Given the strong negative impact of inbreeding on reproductive and health traits, we need to find breeding schemes that generate genetic progress while maintaining appropriate genetic diversity (restricting inbreeding rate) in populations under selection. Improved methods are needed for the design of breeding programmes which involves predicting the consequences of alternative schemes on the phenotypic performance of a population and on the level of genetic diversity. Secondly, improved tools are needed to implement these concepts in selection procedures that aim at generating genetic progress while restricting the rate of inbreeding. Finally, tools are needed to monitor the consequences of selection in order to close the planning-implementation-evaluation cycle which needs to be the basis for each breeding scheme.

The role of phenotype recording is vital for selection, as checking and measuring of the result is important. E.g. if we have data on poultry at the slaughterhouse level, we can see what is the progress in improvement of animal health and bone structure. Given the high cost of phenotyping animals, intensive research is needed to better define the most efficient way to take and handle records. This research will be important not only to better apply research results, but also to conduct appropriate research in the definition of the role of genes, especially in the product quality and welfare traits.

Future biology will increasingly require the analysis of large volumes of data (e.g. genomic data). Better numerical methods for analysis and modelling are needed to address a whole range of biological problems from the molecular to the ecosystem level. The application of crossbreeding, as a tool to overcome the problems of reproductive and health traits, must be better understood. In dairy cattle, it has to pass from the simple estimation of level of heterosis created by crossing two breeds to the level of heterosis created by crossing two individual animals. Much could be learned from pig and poultry experience who have ample experience in applying the vigour of heterosis and the vigour of using crossbred information in pure-line selection.As the need for numerical analysis and modelling spans all areas of biology, the field of animal breeding and genetics will have to adapt to its own needs some new methods developed for other purposes, in addition to contributing approaches specifically designed for farm animal problems.

Illustrations

For illustration a number of subjects are listed which are on the strategic research agenda to meet the described challenges:

Developments in Statistical Genetic Methodology

1. Multivariate Generalized Linear Mixed Models in animal breeding.There is a need to understand the complex relationships among traits that cannot be described using standard distributions. An example is the association between litter size in pigs and piglet mortality. A zero-inflated Poisson distribution may be adequate for the latter, while a Gaussian model may be appropriate for litter size. An example within cattle breeding, or other breeds is welcome?
2. Inference of genetic parameters in selected populations. Most of the data arising from a breeding program have been subject to various forms of selection. There is still a need to understand how inferences are affected when selection is ignored, what are the consequences for the efficiency of selection, and especially, what approaches are to be implemented to deal with selected data when there is incomplete information about the way selection has operated.
3. Application of Markov chain Monte Carlo methods in Genetics. Many of the hierarchical models used in modern genetic studies are extremely complex (such as the one described in point 1, above, or 5, below); the complexity arises due to the large number of parameters relative to the amount of data, and due to the correlation of parameters in their posterior distributions. Standard Markov chain Monte Carlo (McMC) methods show typically very bad behavior under such circumstances and this results in poor inferences. McMC strategies must be developed that lead to better mixing and convergence properties of the chains.
4. Heterogeneous genetic variance and GxE interactions. Animals may be observed in different environment conditions, and the environment may affect traits and genetic parameters. At lot of work is already done in order to show and investigate how environmental variation affect genetic parameters, however we still need to focus on model and method that cover the variation in genetic parameter affected by traits measured in different environment. An example is related to disease traits. In some environment (herd, countries, or areas) the infection rate estimates high genetic variation, however in other environments low genetic variation in infection rate is obtained.
5. Genetic control of variation of quantitative traits. Recent studies have suggested that environmental variation in many traits may be under genetic control and a statistical genetic model has been postulated to describe this process. This opens the possibility to select for a more homogeneous expression of economically important traits. It seems highly relevant to investigate whether there is support for the model using data on production traits and to study selection strategies under such a model. Development of statistical methods in this (as well as the other cases) needs to go hand in hand with increased understanding of the power of alternative designs for estimating genetic parameters.

Breeding schemes

1. Breeding schemes that incorporate information of a large number of markers. Information on tens or hundreds or thousands of genetic markers on each individual has become a reality. Appropriate computational methods (ie, to deal with millions of records) and models must be developed that make adequate use of this vast amount of data and to understand the dynamics of selection under this scenario.
2. A number of in particular welfare traits are influences by social interactions between animals that are kept in the same group. It has been documented that the traditional model is not able to handle interactions between animals in

an adequate manner. The quantitative genetic model needs to be extended to handle social interactions. Breeding schemes need to be designed that can capitalize on genetic variation in traits influenced by social interaction.

3. Animal are produced for a wide range of environments and markets. How to optimally select animals to meet that wide range of conditions.
4. The aim is to improve performance, welfare and product quality traits of commercial animals. In poultry and pigs these animals are often crossbreds while selection takes place in pure lines. Recording of full pedigrees is a requirement to use information on crossbred animals in genetic evaluation of pure bred animals. Recording of full pedigree, however, is often too costly. Genomic information (SNP) offers the potential to overcome the need for extensive pedigree recording.

Separate reports on the other/companion animals

Honeybees

1 General information on honeybees

1.1 Peculiarities in reproduction and genetics of honeybees

Honeybee queens mate in flight with numerous drones from diverse genetic sources. Controlled mating requires artificial insemination or island isolation, techniques that are lacking in most European countries or restricted to a small number of queens. Polyandry of the queen results in several subfamilies (patrilines = group of worker bees fathered by the same drone) within a colony. The males (drones) develop from unfertilised eggs and are thus haploid in origin. Due to the haploid/diploid sex determination system, the genetic relationship can vary within a colony or between queens from one colony between 0.25 and 0.75. In the honeybee, the sex of an individual is determined by a single locus (csd). Therefore, not only haploid individuals but also diploid individuals that are homozygous at the sex locus develop into males. However, in the latter case, the drones are cannibalised by the worker bees at an early larval stage. Inbreeding increases the probability of homozygosis at the sex locus, and, consequently, the frequency of nonviable diploid larvae (which would develop into worker bees under non-inbreeding conditions). For this reason, honeybees are strongly affected by inbreeding, and this has to be considered when developing breeding designs in the species. However, the main methodological problem in honeybee breeding is the fact that both the performance and behaviour of the colony result from the interaction between the queen and worker bees. In selection, the combined influences of the queen and workers on traits must be taken into consideration. Recent studies have shown negative genetic correlations between the contributions of queens and workers. Several traits simultaneously affect the practical use of honeybee colonies. The heritabilities of some of these traits are small, and the genetic correlations between the traits are partly hindering selection response.

1.2 Economic and ecological importance of honeybees

Honeybees (*Apis mellifera*) are primarily known as honey producers. However, the economic value of honey production plays a minor role compared to the economic value of honeybees as pollinators of crops. The increased crop yield achieved by honeybees has been estimated at $14.6 billion per year for the US. Nearly 9 billion dollars' worth of agricultural goods indirectly benefits from the pollinating activities of bees (alfalfa, milk, etc.). The annual value of each colony to the British economy has been calculated to be about €1200. By this estimate, the EU economy (25) reaps benefits totalling €13.9 billion from its 11.6 million honeybee colonies. Consequently, honeybees are considered the fourth most important agricultural livestock sector in several European countries. In addition, and equally important, honeybees significantly (ca. 80%) enhance the environment by pollinating wild flora.

1.3 Situation of beekeeping in Europe

The approximately 630.00 beekeepers in the EU (25) keep 11.6 million colonies, with Spain, Greece and Hungary having the highest percentage of professional beekeepers. Most European countries average about 10 hives per beekeeper. Therefore, most of the colonies are kept on a non-commercial scale. The average EU honey production per colony is about 15 kg. One of the most serious threats to beekeeping is the ectoparasitic mite *Varroa destructor*. Apiculturists use acaricides to protect their colonies, but as the first acaricide-resistant mites and unwanted residues in wax and honey have already been reported, breeding the honeybees for resistance is becoming more and more important. Another major threat to beekeeping is American foulbrood (AFB), a fatal bacterial (*Paenibacillus larvae*) disease attacking honeybee broods. In most countries AFB is a notifiable disease, since it is highly contagious and potentially lethal to affected colonies. Other fairly common bee diseases are European foulbrood (*Melissococcus pluton*), chalk brood (*Ascosphaera apis*) and Nosemosis (*Nosema apis /Nosema ceranae*). A new beekeeping pest not thought to be present in Europe at the moment, the small hive beetle (*Aethina tumida*), was recently reported to have caused considerable damage and colony losses in the US.

1.4 Situation of bee breeding in Europe

In contrast to other agricultural livestock, the 25 geographical races of the honeybee arose as a result of natural selection. There is only one "artificial" race, the Buckfast bee, which is a hybrid of different honeybee races. Natural honeybee populations are strongly affected by the transport of non-native races of honeybees throughout Europe. *Apis mellifera carnica* and *Apis mellifera ligustica* are most popular for beekeeping purposes. These races are exported to many countries. Due to the mating strategy of this specie (see 1.1), we found an uncontrolled introduction of genes from these races into the indigenous strains. Only very small purebred populations of the other European indigenous races (e.g. *A. m. mellifera, A. m. caucasica, A. m.sicula)* are still in existence. Performance testing and genetic evaluation for honey production, gentleness, and resistance against pathogens and controlled mating (artificial insemination or purebred mating areas protected by law) are mainly limited to *A.m. carnica* and *A.m. ligustica.* About 500,000 queens are reared by breeders in the EU each year, partly for export to non-EU countries.

2 Key challenges and opportunities

All honeybee races used for beekeeping worldwide originated from Europe. In addition to this natural genetic reservoir, there is a long tradition of honeybee breeding and selection in Europe. Most European countries have an inadequate self-supply of honey or wax. The use of advantageous methods of selection and the development of breeding schemes for endangered honeybee races provide an opportunity to:

- conserve honeybee biodiversity in Europe,
- stabilise honeybee populations in Europe,
- secure the pollination of agricultural crops and wild plants,
- improve the degree of self-supply of honey in Europe and
- improve the export of superior breeding queens to non-European countries.

3 Gap analysis

- QTL/candidate genes for traits of interest for use in maker-assisted selection (MAS)
- Use of micro-array techniques
- Use of genetic performance testing and genetic evaluation in some countries
- Impact of genotype-environment interaction on the accuracy of genetic evaluation
- Long-term storage of honeybee semen and embryos
- Efficient selection criteria for resistance breeding

4 The problem of stasis

- Losses of colonies due to several pathogens (especially *Varroa destructor*)
- Problems in food safety: unwanted residues in honey and wax
- Insufficient pollination of agricultural crops, causing deficits of billions of euros for the EU economy
- Loss of biodiversity in the honeybee
- Loss of biodiversity in wild flora due to insufficient pollination of entomophile plants
- Highly aggressive behaviour in inter-racial hybrids

5 Needs for research

5.1 5-year period

5.1.1 Breeding for resistance against *Varroa destructor*
5.1.2 Conservation of genetic diversity of the endangered European honeybees races by:
5.1.2.1 Improvement of morphometric and molecular genetic tools for testing pure breeding
5.1.2.2 Development of breeding programmes for endangered honeybee races that foster conservation of genetic variability and improvement of their beekeeping competence
5.1.2.3 Cryoconservation of embryos and eggs and long-term storage of semen in the honeybee
5.1.3 Application of smart breeding techniques (maker-assisted selection/mirco-array technique)
5.1.4 Breeding for resistance against *Paenibacillus larvae*
5.1.5 Application of recent methods of genetic evaluation in honeybee breeding (certain countries/races)

5.2 15-year period

5.2.1 Breeding for resistance against *Melissococcus pluton, Nosema ssp. Ascosphaera apis*, various viruses and eventually *Aethina tumida*
5.2.2 Development of in-vitro cultivation of cells of somatic origin for research on functional genetics (e.g. cellular resistance mechanism in the honeybee)
5.2.3 Risk analysis of the use of genetically modified honeybees (considering 1.1 above)

5.3 25-year period

5.3.1 Breeding for adaptation to changing climatic conditions
5.3.2 Breeding of honeybees for use as pollinators in greenhouses

22 December 2006

Dogs

Dogs are a special species because they are used as companion animals, but also as working dogs. Some of the opportunities and challenges hold for both categories, some are specific for one of them. In addition, especially in the south of Europe, the management of stray dogs is of major concern because they can be aggressive in a pack and transmit diseases. Even though the companion animals are the largest category, it is also the category that is most difficult to influence. Companion animal breeding is in the hands of private people and is largely non-commercial. There are breeders that earn (part of) their living by breeding dogs, but many breeders are hobbyists who own a dog or bitch and want to breed with them. Even though the studbooks can set ground rules with respect to health and looks, the actual breeding decisions lay with the owners. It depends very much on the (daily board of the) studbook whether results of research are implemented or not.

There are contacts between breed associations in different countries, but in a rather fragmented way: not all breed associations within a breed are involved. The studbooks within a country are organized in a kennel club. These kennel clubs generally define the breed standards, hold the registration of the dogs, file (sometimes at request of the government) special demands, such as for a behaviour test, or bans, such as the prohibition to breed with certain breeds, and/or have a general advisory role. When in a certain breed an increasing number of dogs appears to be aggressive, for example, they can provide advice and sometimes financial support for research.

In commercial scale dog breeding is mainly in hands of large scale breeders. In some countries these breeders have organised themselves by setting up rules and regulations with respect to health and welfare of their dogs (both bitches and puppies). This to show they are different from large scale kennels with a poor reputation because of poor practice, especially in Eastern Europe. Those kennels (also called puppy mills) produce huge amounts of puppies for the Western markets (e.g. for sale in shops in Belgium & France;

these puppies are widely available for sale in e.g. Holland too through private handlers).

There is no control of breeding, no health checkups, no consideration for animal welfare etc. so most of these puppies have poor genetics, have been weaned way too early, are diseased etc. However, these farms get a very good living out of sale of the puppies – very cheap to produce since hardly any regulations apply, and western people pay hundreds of euros for these puppies. Since the eastern countries are now part of EU, they should be included somehow - question is how to get some regulation into the business (numbers produced are BIG). This is both for ethical/animal welfare issues, as well as consumer issues and these puppy mill puppies form a serious competition for the more ethical companion dog breeders who would like to pay attention to the quality issues. Of course, puppy mills exist elsewhere too, like galgo/podenco farms in Spain and ordinary backyard breeders in farms etc. in all western countries.

Genetic research in dogs thus far has mainly focussed on genetic defects of dogs (e.g. Imperial College, London, UK and Veterinary faculty, Utrecht University, The Netherlands).

Some organisations, such as the Animal Health Trust in the UK (http://www.aht.org.uk/) already offer genetic services for dogs, part of which they have developed themselves.

Another type of genetics research is on quantitative genetics, or how to determine the heritability of important traits such as health related traits and subsequently use this information in organised selective breeding. Mainly due to the lack of organisation and the lack of high quality data, not much research has been done thus far (e.g. university of Helsinki, Finland). However this research has already lead to the introduction of standard use of estimated breeding values for hip and elbow dysplasia in all breed clubs in Germany

and Finland.

Working dogs are a relatively new field of work. The most well known example of a working dog, apart from traditional jobs such as herding and guarding, is a guide dog for the visually impaired. However there are many more types of working dogs, such as dogs for police, customs, and army (detection of a large variety of subjects, guarding, patrol work), assistance dogs for physically disabled people, dogs for deaf people, dogs for detection of mercury, dogs for companion in old people's homes or hospitals, etc. The number of jobs dogs are trained for is increasing rapidly. Currently there are even dogs of which it is scientifically proven they can sniff skin cancer (Australia) or bladder cancer.

However, most of these dogs are bred at a non-commercial basis and without a well defined breeding goal. This non-commercial basis is an important reason for the generally very low professional level of working dog breeding, within Europe but also worldwide.

Key opportunities

- Health problems occur in dogs in general, both companion animals and working dogs. This not only impairs the welfare of the dog, but also that of its owner as often high medical costs are involved and the life span of the dog often is seriously reduced. The trajectory of a puppy to become a working dog is very expensive and health problems after graduation will thus result in large losses. Research on the genetic background of health problems in dogs, therefore, is of great importance to enable improving the health of dogs through selective breeding.
- Many dogs for companion are bred with the aim to perform tasks: herding, agility, hunting, pack work, etc. Research on the genetic background of those traits will enable to better select the best dogs for breeding and thus improve the traits in the population.
- There is an increasing demand for working dogs (e.g. guide dogs, police dogs, assistance dogs). To live up to this demand, and to improve the quality as a working dog, selective breeding programs need to be developed for these working dogs.
- In addition, new tasks for dogs are developed regularly. This creates an opportunity to investigate directional breeding of dogs for more tasks (e.g. company for old/disabled people)
- Dogs are used as model for human disease genetics. Research on genetics of health related subjects, therefore, not only help improving the dogs' quality of life, but also help unravel human genetic disorders.

Key challenges

As research on dog genetics and breeding is a relatively new field of work, there are still many practical challenges. These challenges sometimes are still more important to tackle first than the research related challenges. Therefore, they are mentioned here first.

Practical challenges

- Education of the people in charge on how to set up and run a breeding program
- ☐Agreement among breeders on direction of selection
- Organise the recording so that all dogs will have a unique registration number and accurate observations on their performance, in the computer.
- All observations should always be related to the number, not the name of the dog.
- In order to do research, data should be made available for these purposes by the breed clubs or the kennel club (depending on who owns the data).
- In order to get insight in the genetic background of type of observations that are determined by more than a single gene, observations of a large number of animals is required to be able to estimate the genetic parameters. (related to importance of data recording)
- A serious practical challenge with respect to dog research is funding. As most dog breeding is performed at very small scale, there is no industry involved.
- Consequently, it is hard to find funding for dog breeding related research.

Research related challenges

- Find genetic background of health problems, both through molecular and quantitative genetic techniques
- Develop objective techniques to record behaviour related traits
- Develop objective techniques to record other types of performance traits
- Design of selective breeding programs
- ☐There are a number of ethical aspects to research as well. In some breeds the standards may need to be reconsidered with respect to anatomy. For example, in some breeds have such deformities in skull size and shape are desired that the dogs have problems feeding and breathing, whereas other run the risk of eye balls to pop out of their sockets.
- Another ethical aspect is related to the use of dogs in jobs. What type of tasks are still allowed, what is acceptable. Is it, for example, acceptable to use a dog in anti-terrorism work, or in mine detection, when there is a serious risk of injury?

Gap analysis

- ☐In dog breeding and genetics in many cases still very basic tools are missing that are prerequisites for successful selective breeding. Most important is education, especially of people in the board of breed associations, private breeders, and people in charge of breeding programs. Without their input setting up research is impossible. Of course those people already know a lot, but they should learn basics on the need of accurate recording, of design of a breeding goal and on the possible consequences of selection decisions.
- ☐In most breeds and working dog populations, data recording is of very poor quality and data recording programs (computer) need to be developed to help build up good quality data.
- ☐In many breeds and working dogs there is no clearly defined breeding goal
- Objective data recording for many traits is very difficult as there are no methods for objective measuring of those traits, especially related to behaviour (though some work has been done)

What knowledge is required to open up longer term opportunities

- Selection criteria (definition and agreement on)
- Genetic parameters
- Molecular genetic tests for monogenic disorders

The problem of stasis

- No continued molecular genetics research on health related problems. This research occurs in, for example, the UK and the Netherlands, but also in the USA. If the USA patent all genes they discover it will become very expensive to use the molecular tests to be developed.
- In addition: if we cannot test for those diseases (yet), carriers will continue to be used as parents and puppies with the diseases will continue to be born, with all emotional consequences for the owner and welfare consequences for those puppies.
- No continued research on quantitative genetics research on health related problems.
- No research on working dogs: especially in police dog breeding there are a large number of private breeders in the EU who sell their dogs also outside the EU, for example to the USA. Research on working dog breeding has been set up in the USA, so this market will disappear unless the EU will also invest in working dog breeding.
- In addition: improved working dog quality will help improve the quality and quantity of their services: guide dogs, other types of assistance dogs (e.g. physically disabled, deaf, seizure, etc), detection dogs (e.g. people (dead or alive), explosives, means of arson, drugs, mines, mercury, and many more), guard dogs, patrol dogs, etc.

Short, medium and long-term opportunities/needs for research

☐First 5 years

- Improve recording system
- Education (e.g. with respect to importance of agreeing on the breeding goal)
- Investigate genetics of health related problems
- ☐Research on objective measurements on behaviour
- Set up breeding programs for working dogs

- Ethical issues related to the production circumstances
- Ethical issues related to the use of dogs for various tasks

15 years

- Education
- Investigate genetics of health related problems
- Europe-wide regulation for all dog breeders at least on some level.
- Guidelines on how often bitches are allowed to produce puppies, minimum requirements for parents used e.g. on their health, age etc.
- Ethical issues related to anatomy

☐25 years

- Breeding value estimation on a number of polygenic health issues in all countries
- Registration of all intentionally produced puppies (both pure bred and crosses, not necessarily in kennel clubs with pedigrees but at least ids just like in cattle) and all breeders

Fur animals

Focus is on mink and foxes.

Key opportunities

The general rise in wealth has lead to a steadily increase in the demand for fur products since 1999. Worldwide the turnover of fur coats and fur accessories was 12.77 billion dollars in 2005. Europe is internationally the leading fur producer. Thus, Europe has the opportunity to meet the increasing demand for high quality fur products. It will create new jobs also in rural areas with few other possibilities. The production is mainly restricted to the Northern part of Europe including the North and Baltic countries, the Netherlands and Poland.

Key challenges

It is a challenge to increase or even maintain the present European share in a market with an increased competition from non-European countries such as China with much lower production costs. Furthermore, a continuous dialogue should be maintained with the general public and animal welfare activists' attitude should be considered.

Research or development

Europe is leading in fur animal research and development. Research will contribute to a sustainable fur animal production with healthy, efficient animals with a competitive fur quality and welfare in accordance with societies demand.

- ***Adult body size***: Size has been the most important parameter for determining prices in recent years. This has lead to selection for larger size. A better understanding of the consequences of selection for increased size is needed to maintain sustainable breeding schemes.

- ***Fur and hair quality:*** Fur quality is one of the main competitive parameters. Research into the genetics of fur quality traits forms the basis of improvement by selection.

Efficiency: Improved feed efficiency will reduce production costs and contribute to increased competitiveness. It can be obtained by more efficient use of feed and by shortening of the growth period. Improved feed efficiency will also minimise the output of nitrogen and phosphorous into the environment. Efficient use of the feed requires better knowledge of the digestive system and the genetics of nutrient requirement and metabolism. Selection for feed efficiency may be direct or indirect. Improvement will require redefinition of the nutrient requirement as well as adaptation of the feeding management.. Understanding of moulting is a part of this research.

- ***Welfare:*** Fur animals have been domesticated since the end of the nineteenth century. However, the degree of domestication is still debated in some part of the society. New insight into the genetics of behaviour and welfare will facilitate the documentation of the present status of domestication and the further improvement of domestication and adaptation to production systems.

- ***Health and disease resistance:*** Specific diseases in fur animals are expected to be at least partly genetically determined. Knowledge of the genetic background can be exploited in breeding and production.

Reproduction and kit mortality. Limited female and male fertility and high kit mortality in the first days postpartum are major limitations for an efficient production as well as a limitation to breeding schemes, with relatively low selection intensity. In foxes, prolonged *in vitro* survival of fresh semen and increased survival and efficiency of cryo preserved semen will enhance the possibilities in breeding programmes and the genetic progress as well as the possibility of dissemination of genetic progress. This will also provide the basis for increased selection intensity in males.

- ***Feed quality:*** Carnivorous fur bearing animals are fed with fish and slaughter offal. However, these resources are limited. The use of other protein sources is however often limited by anti-nutritional factors. A combination of modifying the protein source (e.g. plants) and selecting for increased tolerance to these anti-nutritional factors is likely to be the best strategy.

Technology requirements

- ***DNA-technology:***

Genome research in fur animals has been very limited and is far behind the research in species such as cattle, pigs and poultry. It makes genome research an area where Europe can be in the forefront. Genomic techniques are essential for genetic dissection of traits like fur quality, fur colours, disease resistance and behaviour. DNA-technologies are the short term priorities.

- ***Breeding programmes:*** Incorporating new information into selection schemes requires development of new statistical methods and computer algorithms. For mink, where individual recordings are not possible for all traits it is necessary either to develop models taking into account common recordings for a number of animals or to develop new recording systems. Dissemination of genetic progress is less efficient particularly in mink than in other production animals. In foxes, more efficient methods in artificial insemination will improve breeding progress. Incorporation of individual skin informations from the auction houses in the breeding programme can be a first step in improving skin traits in both mink and foxes.

Longer terms opportunities

Efficient selection for genes or genetic markers is based on knowledge of gene interaction (epistasis) and of the influence of a gene on more than one trait (pleitropi). Shortening of the growth period requires further insight into the biology of reproduction, sexual maturity and moulting. Transcriptomics and proteomics are useful in such studies.

Consequences of stasis

Missing research in fur animal production will enhance the already existing development where an increasing fur production in non-European countries with lower production costs threatens the present European position. Europe accounts at present for the majority of globally farmed pelt, and fur animal production is thus important for European income and employment.

Needs for research

5 years: Establishment of gene dense genetic maps, QTL-studies and breeding programmes for selection of genetic markers allows selection for e.g. fur quality traits. Development of breeding programmes taking into account common recordings for a number of animals will enable selection for e.g. feed efficiency. In foxes, improvement of survival of fresh and frozen semen will provide possibilities for larger genetic progress.

- ***15 years:*** DNA-technology as well as transcriptomics, proteomics and metabolomics enables the understanding of the biology of fur quality traits, efficiency, disease resistance, behaviour and reproduction as a basis for further improvement by selection. This requires further development of breeding programmes integrating information of multiple traits and new information into conventional breeding programmes.

- ***25 years:*** Genomic studies of the biology of reproduction, sexual maturity and moulting will make shortening of the growth period and further domestication possible.

- ***National initiatives:*** Due to the mainly national organisation of fur farmers, development of breeding programmes will be as a hole performed nationally or within the Nordic/Baltic countries.

- ***European initiatives:*** Development of genomic technologies requires co-operation at a European level.

- ***Traits particular for fur animals:***

- Hair and fur traits
- Feed efficiency is recorded jointly for a group of animals
- The digestive system in the carnivorous fur animals differs from other farm animals
- An annual reproduction cycle

Rabbits

Introduction

Rabbits have several desirable traits such as fast growth rate, good carcass quality, short reproductive cycle with high prolificacy and mothering ability. In addition, rabbits are easily manageable, with optimal cost and space/animal ratios; they do not require expensive housing infrastructure, and, as herbivorous, do not compete with humans for food. Rabbit meat has remarkable nutritional and dietetic qualities, being characterised by high protein levels, low fat (triglycerides and cholesterol), low energy contents, and low anti-nutritional and allergenic properties. It is also rich of polyunsaturated fatty acids (with a favourable ω-6/ ω-3 ratio) and minerals, except sodium.

Currently, about 50% (600,000 tons) of the estimated yearly world rabbit meat is produced in Europe, and it satisfies 85-90% of the internal demand. Despite the rabbit breeding sector is considered of minor importance, rabbit meat production earns a significant share of the gross value from European animal productions being comparable to those of sheep and goats and is worth 300 millions euro. Commercial rabbit breeding is unevenly distributed in the EU, being more concentrated in southern Europe (Italy, Spain, and France, with 230, 160, and $90x10^3$ tons, respectively) than in central-northern Europe (Germany, Belgium, and Nederland, with 34, 10, and $10x10^3$ tons, respectively), and eastern Europe as well (Czech Republic and Hungary, with 34 and $11x10^3$ tons, respectively). These figures closely reflect the differential pro capita rabbit meat consumption in each country.

Apart from innumerable farms where rabbits are raised for self-consuming purposes, in the EU there are approximately 35 thousands stockbreeders and at least other 12 thousands engaged in the supply-side chain as professionals, technicians, and employees in feed plants and slaughterhouses. In Europe, rabbit breeders are well organised around national-wide associations, which often interact with scientific rabbit associations.

Although in some EU countries rabbits are mainly regarded as pet animals, for the present report they will be considered as farm animals for meat, fur, and angora wool production. Rabbits are also used for special biomedical production (antibodies, proteins, and enzymes) and as models for specific human diseases or as laboratory animals. In these cases, however, their breeding (often specific pathogens free production) is very specialised, remaining restricted to few companies world-wide, and, therefore, will not be taken into account in this context.

Key opportunities

The most likely scenario in the next 25 years will show an increasing wealth and ageing of European citizens together with an increased sensibility for wellness and health-related problems, so that quality rather than quantity of food-stuff will be the main issue. At the same time, the cost of labour, production (feeds, energy, transportation), and marketing will also rise. Thus, the EU-based meat rabbit production chain, due to its low margin of profits, might be easily threatened by non-EU countries with much lower production costs. On these grounds, the following key opportunities appear logical:

1. Strengthen and maintain worldwide leadership in breed selection, commercial hybrid production, availability and conservation of different pure breeds;
2. increase the competitiveness of the meat rabbit farming through reduction of animal losses due to pathologies, improvement of reproduction and feed efficiency, development of mechanization and automatic systems, improvement of dressing out yield, and rationalisation of the production chain;
3. ameliorate both quality and safety of rabbit meat products from farm to fork through traceability, good farming practice, and certified rabbit slaughtering facilities, as well as their value-added, through involvement of transformation industries and final sellers in the marketing of cut-up and further processed products;
4. provide further full- and/or part-time work opportunity to rural society in geographical areas of Europe not suited to gross animal farming;
5. export appropriate technology and know-how to extra European and developing Countries in a global perspective necessary to provide high quality food and improve the standard of living.

Key challenges

1. Develop new rabbit breeding methods, less costly and more sustainable, by integrating, under a system-based approach, animal welfare with health issues and productive efficiency to limit the impact of undesired residues on meat products in the context of food quality and safety;
2. introduce alternative, more environmentally-friendly housing systems to reduce the environmental impact of farms;
3. improve overall reproductive efficiency by reducing losses (embryo, foetal, neonatal, and postnatal deaths) and increasing doe longevity, while maintaining high fertility rate through new management and synchronisation techniques capable of reducing the use of exogenous hormones;
4. implement new strategies for prevention and control of rabbit diseases by improving the defence responses of the immune system through feeding programs, genetic selection, pre- and pro-biotic, and new biotech vaccines;
5. extend the activity of both selection and artificial insemination (AI) rabbit Centres to effectively boost dissemination of genetic improvement;
6. extend the conservation of genetic resources to preserve currently unknown useful genes.

What can be tackled by research and development

Advances in basic science, involving a large array of disciplines from genetic to physiology, are required for improving the knowledge-base necessary to cope with problems associated with rabbit reproduction, management, nutrition, health, and welfare. Recent developments in molecular biology and genomics will boost the speed for transferring knowledge from basic science to applied fields in rabbit farming and will support the deployment of effective strategies. The emerging field of nutrigenetics and nutrigenomics is rapidly gaining importance, and studies focussed on rabbits could provide species specific insights for integrating diets for prevention of diseases. Although AI is largely employed, several aspects regarding the fertility of bucks, quality of semen, and its crio-conservation remain to be investigated. Currently, most of the production losses occurs during pregnancy (embryo deaths, abortion), and the neonatal and post-weaning periods (GI diseases) up to the first 40-50 days of life. In addition, today production systems provoke a high turn-over rate of females as a consequence of pathologies and infertility.

Gap analysis

Rabbit production systems are strongly associated with successful implementation of productive technologies and a better knowledge of reproductive mechanism.

(What is missing technology to meet existing challenges and opportunities)

- Standardized methods to assess, easily and unequivocally, welfare parameter indicators for early warning of potential stressful and harmful conditions;
- Development of rapid diagnostic tools for infectious rabbit diseases and reliable tests for the identification of "true" infected animals between those vaccinated;
- Low-cost and efficient bio-sensor technology for the detection of environmental pollutions in the farm and, through nanotechnologies, of physiological parameters in a selected group of "sentinel" rabbits;
- Low-cost, high-throughput genotyping technologies to identify, in their genetic structures, specific DNA polymorphisms associated to desired phenotypes and analyse large numbers of Single Nucleotide Polymorphisms (SNP) as molecular markers of specific traits for gene-oriented selection;
- Microarray systems to analyse on a large scale the expression of genes and the levels of proteins and metabolites for further development of functional genomic and proteomic;
- Bioinformatics applications to help handling the mass of genomic and proteomic data into physiomic, to reveal functional associations and biological mechanisms, and mathematical models to adopt the best management strategy in the specific context;
- Semen sorting and cryo-preservation techniques to diffuse genetic selection programs.

(What knowledge is required to open up longer term opportunities)

- Fundamental research, unified under a systemic and integrated approach, on several molecular, biochemical, and physiological aspects of rabbit biology involving hormone regulations of reproduction and interactions with the environment in view of oestrous synchronization in AI programs;
- Identification of key welfare indicators, both direct (animal-based) and indirect (management, housing system), and their validation for practicability and predictability of wellness in field conditions;
- Gene-environment interaction in the determination of health and disease;
- Role of genetic variation in response to diets and role of nutrients in the regulation of gene expression and long term effects on biological functions;
- Availability of the whole rabbit genome sequencing necessary to improve markers or gene assisted selection and functional genomics;
- Better biological understanding of those pathological agents responsible of several production-related diseases, including the Epizootic Rabbit Enteropathy (ERE), their interaction with the host, and immuno modulation;

(What other obstacles exist to technological development)

- Political support to provide social consensus and long-term economical resources necessary to enrol young scientists from different disciplines that work together with breeder associations, farm industries, and technological firms in a network of laboratories oriented to rabbit research and development.

The problem of stasis

What will happen if no research or development occurs, how will this impact on the industry and EU citizens

- If no research or development will be deployed to rabbit breeding and reproductive technology, the main risk is to waste the existing know-how competence. The lack of European-based projects will also favour the decline of rabbit meat production systems to step into a non-competitive market as a consequence of their poor efficiency and very low margin of profit. This aspect will also impact the EU citizens, at least in the medium- and long-term perspective, either directly with higher unitary cost for rabbit meat produced locally or, indirectly but more seriously, with the potential lower quality of rabbit foodstuff imported from extra European Countries where controls are less stringent. In addition, there will be negative effects on rural employment and income of rural families involved in rabbit rearing.

Short, medium and long-term opportunities/needs for research

First 5 years

- Low-cost recording systems and assessment of new traits for performance besides litter size, milk production, and growth rate;
- Full sequencing of rabbit genome, including the systemic study of EST and the production of high density genomic tools (SNP micro arrays);
- Improvements in reproductive technologies: oestrous synchronisation and reproduction management, semen processing and quality evaluation, gamete/embryo production and preservation, and embryo transfer application;
- Extend cryo-banking of embryos and female gametes from local breeds;

- Reduction of production losses from embryo to weaning, and culling;
- Cage size and design together with stocking density to provide good health and welfare for rabbits (young, rearing, and breeders);
- Vaccines for viral diseases using a biotechnological approach, i.e. recombinant vaccines, marker vaccines.
- Study of rabbit gut ecosystem with molecular and microbiological tools

First 15 years

- Long-term effects of foetal programming via altered maternal diets on rabbit health and performance;
- Components of the digestive immune system and improvement of the antibody repertoire;
- Definition of genetic components for reproduction, longevity, and disease resistance, and selection programs of new genetic lines;
- Gene or new markers (SNP) assisted selection;
- Introgression of gene of interest such as disease resistance, meat quality, and others;
- In vitro cell technologies;

25 years

- Tools for managing genomic information and likely impact of new mutations;
- Genomics studies of biology of reproduction, sexual maturity, disease resistance, growth, meat quality, tegument and moulting;
- Transgenic rabbits for special meat production (nutriceutics).

List of important countries for "local" meeting

1. Italy,
2. Spain,
3. France,
4. Germany,
5. The Netherlands,
6. Hungary,
7. Portugal,
8. Belgium
9. Czech Republic

Sustainable Farm Animal Breeding and Reproduction Technology Platform

FABRE TP

Priorities for Equids in Europe

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And suggestions of other European experts of the core group (see the list in table 5)

Introduction

Horses are becoming more popular in the growing industry of sports, leisure, and hobby farming whereas racing industry is still flourishing in Western Europe Countries (Eu Equus, 2001), horses are used as well as in tourism, medical therapy, social rehabilitation or social eventing. There are niche markets for horse milk for people having allergies or being fun of esthetical care using cosmetics milk based by products, and for meat in very few Member States (Belgium, France, Italy, Slovenia, Spain),(Miraglia et al., 2006). Hence the population of horses in Western European Countries (n = 15 WEC) rises to 4.3 millions of heads (11.4 horses/1000 inhabitants), and likely much more including Central and Eastern European Countries (CEEC), to meet the increasing demand of various end-users – 3.5 millions of hectares are requested in those 15 WEC (e.g. 3 p. 100 of total arable land) to feed yearly this population which is as much as the wine yard surface (2.6 p. 100) and twice that of sugar beet (1.6 p. 100) (Commission Européenne,2000 – EU Equus, 2001 – Eurosat-Poiret, 2004). And 0.2 full time people /horse are employed in the European equine industry (EU Equus, 2001).

So far there is a rising demand of end-users for horse breeding which causes the development of a large diversity of horses which should fit the needs of many groups of people who would like to work with or enjoy horses. There are 6.2 millions of people who ride in the 15 WEC (e.g. 2 p. 100 of the population) and likely this number would increase when CEEC would meet soon the same life standard (EU Equus, 2001). These figures take part of the first pillar of CAP which deals with the support to the production means.

In some WEC, maintaining rural landscape is of high concern. This concern is taken over by horses as Equids compete with Ruminants as well as with plant production for natural resources and territories. In addition breeding horses contributes to maintain population and socio-economic activities in such area which definitely fit the second pillar of CAP which deals with the multifunctionality of agriculture (Miraglia et al., 2006).

In CEEC, Horse Breeding Industry has to cope with several severe structural problems whereas there is still population of Equines and long tradition in horse breeding (Copa, 2005). These countries need support from EU and other European industrialised countries to reorganise their Equine chain, research in Equine Science and to benefit of technology transfer from Industrialised Countries. Equine knowledge in these former CEEC countries, their culture and tradition should be protected first of all by scholarships for young scientists and horsemen. The financial affirmation of new associations is important as well for the further development. The use of working horse must not be neglected in CEEC countries too as it is important for the small holders in these countries. And the increasing use of horses in forests related to nature protection is rising in WEC as well as in CEEC countries too.

As result the horse industry is more important in WEC and CEC countries as it was considered in the last decades because it belongs to both social service and food production.

Whatever the Countries, the standard of education of breeders and owners requests to be urgently improved to meet the same standards as in other farm animal industry. Similarly secondary and higher Education in Equine Sciences should be updated and promoted in all the countries (EAAP – Horse Commission – Session 24, 2005 and workshop in 2008: table 2).

Knowledge and technology transfer between EU Countries should be extended as well throughout a European net work for Equines.

In this context, consultation and discussion with representatives of European horse breeding industry and scientists experts in Equine science have been carried out to state: key challenges, knowledge gaps and the opportunities to meet the needs of the horse breeding in Europe.

The problems of stasis are briefly described then the research priorities are presented for the short, medium and long term future.

Key challenges

Four key breeding challenges have been targeted :

- **Breeding performance horses for race and sport** using most of the modern tools to maximise the efficiency of breeding and husbandry systems and to prevent the risk of health disorders ;
- **Breeding leisure horses, ponies and donkeys** for riding education, hobby, tourism and therapy implementing relevant management systems to reduce the cost of breeding and to fit the social need of the end-users: riding amateur… ;
- **Preservation of endangered breeds** to maintain biodiversity using new modern tools in the scope of strategic selection plan ;
- **Breeding horses for alternative animal products**: meat or milk and its derived products (fermented cheese, milk substitutes for newborn or adults affected by allergies, cosmetics ....) implementing accurate management systems to reduce the cost and to handle the quality of end products.

And old traditional national studs must be maintained with traditional horse breeds and cultural values in CEEC countries

Knowledge gaps

- Breeding **athletes horses** requires to define traits and breeding goals especially oriented to maximise the performance (gait, jumping, velocity and endurance) and to minimise the risk of health disorders mainly related to locomotion : joint disorders, Osteochondrosis-OCD...., muscular disorders : rhabdomiolysis ...., due to their potential heritability or/and interactivity with husbandry and riding systems and nutrition.
- Breeding **leisure horses** and **horses** devoted to **alternative usages or products** needs to define traits and breeding goals with special regards to behaviour (good temperament), capability of horses to be fed with high forage based diets and to their robustness.
- As a result **phenotypes** of those horses and breeds should be more accurately and extensively recorded to support modern approach using molecular genetics. This requires objective systems for judging and breeding as well as the development of traits to improve performance, disease resistance and behaviour of horses.
- The full knowledge of the map of the equine genome since 7 February 2007, the improved annotation of the horse genome sequence, the new functional genomic information and the association with traits subjected to selection will contribute to **the identification of genes associated to performance, health, behaviour and other functional traits**.

  The resulting breeding and selection strategy should be based on continuous **development of statistical analysis** whereas breeding schemes will also include molecular information in the very next future.
- **The diversity** of and within breeds, regions and states should be maintained, or/and accurately designed and managed either in small endangered populations (Bodo et al., 2005; Cothran and Luis, 2005) or large population where the inbreeding is increasing (Cunningham, 2005; Langlois, 2005).
- This approach should be strongly supported by the use of **new reproductive technologies** such as AI, ET or sexing to increase the progeny of genetically horses (Bruns and Koenen, 2006; Ricard and Dubois, 2006). But those technologies need to be still improved whereas reliable indicators of fertility as well as maternal and foetal well being during pregnancy and per partum should be determined and evaluated. But the **interactions between genotype and environment factors** should be determined and evaluated as heritability would explain on average only 30 p. 100 of the statistical variance of most identified traits.

Problem of stasis

If no research or development occurs in Europe, the expected impact on industry and EU citizens may be: the loss of **international leadership in sport horse breeding and competition,** the breeding of horses which **impair with the rising demand of citizen** for e.g. hacking or agritourism, a loss of **diversity of breeds** and the minimisation of the complete horse breeding industry in some CEE countries, deteriorated **animal welfare,** limited contribution of horses to **sustainable farming and sociocultural life**, and economic losses in breeding industry and related **business and employment** in agriculture, riding education, horse exhibition, competition, races and linked historical patrimony.

For equines the following opportunities/needs for research are foreseen in the short- medium and long term to improve **performance** (such as gaits, jumping ability, velocity, endurance), **functional traits** (e.g. longevity, fundamental stability), **disease resistance** (e.g. Equine influenza, Rhino pneumonia), **fertility, behaviour** (e.g. temperament), and a to reduce **hereditary diseases** (such as OCD, myopathy, roaring).

Indeed improvement of education and knowledge, dissemination of Equine Sciences and Technology transfer should be fighltly associated to the effort in research to support breeders and riders, professionals and amateurs, consumers and citizen who are increasingly involved in the Equine chain.

Research needs

Quantitative genetics and breeding programs

In a problem driven research agenda on the challenges to meet the goals of an expanding horse sector the following areas within quantitative genetics and breeding programs will have the highest priority :

1. **Behaviour characteristics** of the horse to ensure safety and pleasure to work with horses for either performance or having them for leisure or as companions
2. **Health and longevity** to make horse ownership affordable and ensuring high standards for animal welfare leading to robust and durable horses
3. **Breeding value estimations** considering multi-trait breeding objectives and international use of breeding stock.
4. **Reproduction** to ensure affordable and reliable technologies to be used considering the internationalization of breeding programs of many breeds.

- *Behaviour characteristics*

This research area would include characterization and recording of different types of temperament and behaviour in various horse breeds (Hausberger et al 2007; Lansade et al 2006 and 2007). Definition of what is good and bad temperament for various utilizations of horses will be a basic task. This research is especially important for breeds that are used to a large extent by young people and for breeds of multi-use.

The research results should demonstrate:

- measures of the relative importance of inheritance vs. environmental effects, i.e. the repeatability and heritability of temperament and behavior traits considered relevant for different horse breeds and use

- genetic and environmental parameters, including correlations of various temperament and behavioural traits with performance traits
- Possible designs of breeding programs for appropriate inclusion of mental characteristics for improvement of various horse populations.

The scientists involved must include expertise in ethology, quantitative genetics and training of horses. Research must be conducted in close collaboration with breeders and end users of the horses. Research plans should be developed for initial experimental studies and at the next stage relevant methods would be tested in recording schemes that can be applied in e.g. performance testing of stallions and at tests of young horses for different use.

- *Health and longevity*

Soundness and durability of horses are of highest priority to ensure high standards for animal welfare and to make horse ownership affordable. In most horse breeds problems arising from disorders and injuries affecting the locomotion part of the horse dominate needs for treatments and culling of horses. Some of these disturbances may have a clear genetic predisposition, although most of them have a multi-factorial background. Many other types of injuries and defects also cause harm to the horses. Several of these problems may also to at least some extent have a genetic origin. The following R&D activities have high priority from a genetic and breeding program view:

- **Skeletal disorders** need to be investigated from a genetic point of view. Such studies should include identification of relevant diagnostic criteria and recordings to be used for genetic evaluation purposes, analyses of prevalence and effects of environmental (Donabedian et al 2006; Martin-Rosset et al 2006; Van Weeren and Brama 2006) and genetic (Philipsson et al 1993; Philipsson 1996; Ricard et al 2001) origin on records of various disorders (Coenen et al 2006, Robert et al 2006). Studies on relationships with various rearing strategies and genetic and phenotypic correlations with conformation and performance will add necessary information for studies on alternative strategies to reduce problems with skeletal disorders in horses.
- **Congenital defects** and their genetic origin and tests for discovery of carrier animals. Analyses should include prevalence and importance of various defects from welfare as well as economic points. Alternative strategies for the reduction of defects in horse populations should be investigated.
- **Longevity and survival** should be studied in relation to variation in conformation and possible early predictors of soundness.
- **Epidemiology studies** based on regularly recorded disease data should be strived for as a tool to monitor the trends in different diseases and for further research priorities (Coenen et al 2006; Robert et al 2006; Valette et al 2006). Some clinical data on diseases, e.g. on certain genetic defects, could be more efficiently researched if regularly recorded at clinics.

- *Breeding value estimations*

Breeding evaluation requires continuous research to integrate new sources of information for multi-trait breeding objectives in various breeds. As international use of breeding stock has become common, the development of methods and procedures to make breeding value (BV) comparable across countries or populations is necessary (Koenen et al 2004; Thoren et al 2006; Ruhlmann et al 2006 and 2007). This research must be closely linked to research on the design of different tests of performance and selection strategies.

- *Reproduction*

Reproduction is in this context a partly genetically determined trait that largely impacts the design of breeding programs (Tunon et al 2000; Ricard et al 2003; Hamann et al 2005; Bruns and Koenen 2006; Ricard et al 2006). From this point of view the following R&D activities should be prioritized:

- Improved fertilization ability of chilled, transported semen and of frozen semen
- Development of a system for certification/quality control of semen to be transported included export of semen as regards fertilization ability.

Genetic variation in fertility results for stallions used with different reproduction technologies

Molecular approach to support breeding programs

- *The whole genome of horse has been sequenced in February 2007.*

The status of the horse has recently changed in the society and its role is becoming more important to governments and to a large number of citizens. In this species, the international scientific community has worked for decades in concert to produce basic tools for a better understanding of the structure and expression of the genome. **The European contribution to international genomic mapping** project was particularly developed at INRA, Jouy-en-Josas (France), at Animal Health Trust (UK) and more recently in Hannover (Germany) with physical mapping by large scale BAC sequencing and fingerprinting(Guerin et al 2003). Resources for the construction of genomic maps were developed with the production of polymorphic markers, essentially microsatellites, the constitution of families for segregation analysis, the construction of somatic cell (SC) and radiation hybrid (RH) panels for mapping, of bacterial artificial chromosome libraries (BACs), the elaboration and maintenance of public genetic databases(Perrocheau et al 2006). These maps are intrinsically of primary importance for each species but also allow comparing genomic data from different sources by means of comparative mapping. Several mutations responsible for Mendelian traits were identified (ex Cream coat colour: Mariat et al 2003; Epidermolysis: Milenkovic et al 2003). The large quantity of mapping results obtained and the existence of a motivated scientific community have positively oriented the decision of the US authorities to undertake **whole genome sequencing of the horse** at the Broad Institute. The sequencing part and assembly is **now achieved** with a 7X redundancy. Once annotation is completed, the sequence of all horse genes will be known and the huge polymorphism (SNPs) to be discovered will be available for screening. Regulatory sequences will also be discovered in the next step. This represents a milestone in the discovery of genes of interest especially those governing multifactorial traits and will tremendously boost the capacity of investigation of horse genetic research.

- *What are the consequences of whole horse genome sequencing?*

The main change concerns the availability in a near future of **SNP and expression microarrays for large scale genome screening.** Tracking genes of interest for horse improvement needs three components: precise phenotype recording, numerous polymorphic and gene markers and adapted statistical methods and databases. Society and horse professional requirements should first be transformed into scientific objectives. Proper animal panels should then be obtained and phenotyped with the most adequate affordable technologies to define the phenotypic status of animals. Horses are not experimental animals and the constitution of panels relies on the acceptation of breeders for obtaining phenotypes and biological samples for genotyping. Thus, **phenotyping methods should be precise, standardized and kept acceptable for the breeders.**

All sequencing data were funded by public authorities are thus regularly updated and available online. Difficulties encountered to unrevealing the genetic basis of traits, due to the population structure and reproductive biology of the horse, will partially disappear as population analysis will replace the actual need for large families in which the trait segregates. **Genomic profiling** will be used at least for high value individuals to estimate the predisposition of a horse to a particular trait in case genes are not yet identified(ex: Endurance horse Barrey et al 2006; ex: Gene expression profiling in muscles, Mucher et al 2006).

The rapid evolution in orientations and methodologies requires a change in the organisation of research. The development and use of **large scale microarray technologies** along with their bioinformatics environment will be more reliably performed on specific platforms unaffordable to single small laboratories. In parallel, **large scale phenotyping** will most probably require networks and collaboration at the European level.

- *Strategy of research for the up comings years*

Research in the next five years will concentrate on the **development of phenotyping, genotyping and methodology**. The development and the accessibility of large scale screening for polymorphism and gene expression by microarrays will accelerate the pace at which genes for complex traits are identified. Research will focus on **hereditary disease/affection transmission and disease resistance** to pathogens. There is a need for the creation and development of statistical association or linkage methods adapted to the horse population structure. These will improve the identification of genes for simple Mendelian traits or traits dependent upon major genes. The creation of **genetic databases** including phenotypes and genotypes associated to versatile software's for the retrieval and management of ongoing data production will be developed. The expanding quantity of data in molecular genetics increases the complexity of bioinformatics treatments but opens exciting opportunities to use data and knowledge generated in other species by comparative genetics and physiology.

In the horse, markers or genes involved in racing or jumping **performances** should be identified and used to propose **molecular genotyping kits** to select for these traits (Barrey et al 2006). Genetic counselling will thus be based on objective molecular data (Tunon et al 2000). Other traits such as horse meat or milk production should also benefit for marker or gene assisted selection. **Traceability** of horse products will be included in these improvements. All screening tools will also be used to better detect **doping** and will help racing authority's decisions in reducing frauds. The relations between genes and phenotypes will be partially uncovered. Identification of mutations for traits will open to a better understanding of gene function, gene regulation, and metabolic pathways interactions. Control of expression by epigenetic systems will also be of great interest to study. In the long term, the objective of molecular genetics is to integrate markers in selection schemes to produce sound horses devoid of genetic diseases and well adapted to the demand of consumers.

Reproduction

- *The stallion*

Equine is one of animal species for which selection is not primarily based on **fertility performance**. This lack of selection on reproductive success has induced large variability of fertility in equine population. Identifying subfertility in stallions before starting a sire career or a decrease in fertility before starting a breeding season is of high concern for the equine industry (Magistrini et al., 1996, Malmgrem 1997, Parlevliet et al., 1999, Sieme et al. 2004). Hence **incidence and detection of the major causes of subfertility**, originating from spermatozoa or seminal plasma, must be studied to design some tools for rapid and sure diagnosis. But fertility evaluation using *in vitro* parameters remains questionable and a great effort must be done to design predictive tools (in the next 5 years and more). Such studies could permit to find out therapy for some disorders or to manage sub-fertile stallions more efficiently.

Fertility prediction of a stallion or of an ejaculate is one of the main objectives of horse breeders to be able to optimise male management and to choose the best method of sperm storage. More research has to be conducted on **semen preservation** to improve the dissemination of European genetics within and outside Europe, and to preserve genetic diversity (Bodo et al 2005; Bruns and Koenen 2006; Ricard and Dubois 2006). At the moment, sperm from 10-20% light breed stallions or more (depending on the methods used) cannot be chilled or frozen with success (Batellier et al., 2001; Vidament 2005). This rate is much higher in cold blooded stallions. So, to improve these results, more knowledge on interactions between sperm and female genital tract, on extender protection and cooling rate and on cellular modifications induced by sperm storage (chilling or freezing) that could modify fertility potential of sperm cells is needed (Katila 2001a, 2001b, Batellier et al. 2001, Rota et al. 2004, Mari et al. 2005, Aurich 2005, Silva et al. 2006). As the best genetically stallions have the opportunity to mate 300 to 500 mares per season, it is important to optimize the management of these very valuable stallions. So studies about **stallion physiology** (sperm production, nutrition and environmental factors, interaction with sport career, aetiology and inheritance of some reproductive disorders) are needed (Sieme et al. 2004, Stradaioli et al. 2004, Stout 2005, Janett et al 2006). However such important studies will not be solved in 5 years and will have to be conducted over 5 years horizon (15 years will be more reasonable).

- *The mare*

Mare is a seasonal female, with **cyclicity** beginning early in spring. The breeding season is quite short (March to mid-July in some countries) and the length of pregnancy is long (11 months), so technical skill is needed to have a mare foaling each year at the same time of the year. At present, oestrus detection is carried out either by a stallion (but rarely present in the same farm) or by scanning uterus by ultrasonography (too sophisticated technique for common use). So, better knowledge about beginning and detection of cyclicity, about oestrus detection (Rampin et al. 2006) and about mechanisms and timing of ovulation is needed. Improvement in domains such as easy timing of ovulation period (Briant et al., 2004a), storage of semen during a long time (Heiskanen et al. 1994, Batellier et al., 2001, Vidament 2005) could induce less work for farmers, less animal examinations, less transport, so less accidents. So, all these techniques could induce a better animal and breeders' welfare. Better knowledge **on pathophysiology of the female genital tract**, particularly with ageing, would help to produce more foals (in the next 5 to 15 years) (Allen et al. 2006). Superovulation and maintenance of fertility are complicated to obtain in the mare (Briant et al., 2004b). However, this tool is really necessary to improve the efficiency of embryo transfer. One could think that new knowledge about central and local control of follicular growth will lead to understand the way to induce superovulation (in the next 15 years). **Interaction with environmental factors such as nutrition** (Guillaume et al., 2006), interaction with sport career, aetiology and inheritance of some reproductive disorders are of high concern too.

Embryonic and foetal losses rates are both around 9%. Losses rate during neonatal period (foals between 0 and 3 months of age) is also high: 12%. So intensive researches about **pregnancy and neonatal periods** could help to reduce these losses (Ousey 2004, Ousey 2006, Castagnetti et al 2007), but Europe has very few scientists in that field. An effort could begin in the next 5 years (maternal and foetal monitoring, management of mares after dystocia, perinatal pathologies (placentitis…)) and be pursued in the 10 following years (management of sick and/or premature foals, endocrine status of the pre/dysmature foal, therapies of the foal in septic shock). A network of neonatal care hospitals have to be built and associated with research units.

- *Biotechnology*

Present techniques of embryo freezing lead to inconsistent pregnancy rates after transfer of one **frozen-thawed embryo** (20-40%) (Lagneaux et al., 2000, Huhtinen et al. 2000). So further studies are needed, particularly the method of vitrification could improve the results (Moussa et al., 2005) rather soon (5 years). Embryo selection by molecular genotyping for some important traits could be done rather soon even in utero (Gerard et al., 2006) but these techniques will be really powerful when **ARTs (Assisted Reproductive Technologies)** will be available.

ARTs and early embryo culture (until day 7) have to be greatly improved (Squires 2005): very inconsistent fertility rates are obtained after **IVF** (*in vitro* fertilization) (Palmer et al. 1991, Dell'Aquila et al. 1999, Alm et al. 2001), results are higher with **ICSI** (intracytoplasmic sperm injection) (Dell'Aquila et al. 2001). By the time, too few European scientists are involved in the study of the mechanism of fertilization and in the improvement of these ARTs. The next step will be the use of these ARTs with stored or selected gametes (in the next 15 or 25 years).

At present, **sperm sexing** is developing in bovine (USA, Australia) and ovine (Australia) species. However, the rate of sorting remains low and technical problems have not been solved in the equine even if lot of interesting studies have been done (Morris, 2005). Since low numbers of sperm cells are sorted, ARTs or AI with very low doses of frozen spermatozoa will be needed to produce sex sorted embryos or foals , but these techniques are not yet reliable , so use of sexed semen would be a reality in next 15-25 years . And alternative techniques for AI using low doses of spermatozoa must be evaluated (Sieme et al. 2003). However the main question remains: what will be the demand from horse breeders to inseminate mares with sexed sperm or to get sexed embryos after ART.

As genomics will have going on, information about **important genes for reproduction** have to be studied intensively, either to understand underlying mechanisms or to include them in genetic programs (Leeb et al., 2005).

The first equine clone is born in 2003 in Italy (Lagutina et al. 2005). In 15 years, this very expensive technique will be at the disposal of horse owners to duplicate some horses with great sentimental or genetic value. But the use is still under discussion (Camillo et al., 2006).

- *The donkey reproduction*

Donkeys have physiological particularities, but scarse information is available about this species. There is a real need for **cryobanking gametes or embryos** from all European breeds. But techniques are less advanced than for horses. For instance, the frozen semen of jacks does not fertilize the jennies (Vidament et al. 2005) (progress waited in the next 5 years). **Embryo transfer** does not really work either (Panzani et al., 2006). Biotechnologies and ARTs could constitute a goal for the next 15-25 years. A European network on these aspects is important to be built.

Biodiversity and conservation

- *Conservation of horse breeds is now acknowledged*

Both, the idea of conservation of old monuments and preservation of rare wild animal species began more than a century ago. However the maintenance of traditional domestic animal breeds started at the second half of the last century. Only the World Conference of Rio de Janeiro (1992) declared that **domestic animals, horses included, belong to the global biodiversity**, and they should be protected as both living beings and human products.Thus, traditional breeds belong to the cultural heritage of mankind , some of them are threatened by extinction, some of them are not endangered. This distinction can be important for the subsidies possibly given by national governments or EU.

There are many systems to evaluate the degree of endangeredness. The most practical one is elaborated by FAO (1989). The following figures inform us about it :

The state	*number of females*
Extinct	---
Critical	< 100
Endangered	100 - 1000
Vulnerable	1000 - 5000
Insecure	5000 - 10 000
Normal	>10 000

The limit for subsidization is the female population of 7500 in the present European pratice. For the horse species these figures can be smaller. The most important is the 100 - 1000 category, because such a population can be preserved with the necessary professional breeding management.

- *The endangered or rare horse breeds*

It is not possible to register the endangered equine breeds based on FAO World Watch List (2000) or using national stud books. In this registration the international contact are not taken into consideration and some endangered national populations have the same breed mates many thousands in other countries.

A **practical, empirical grouping** is given here. However a global comparison based on molecular genetics must be taken also into consideration. Some good preliminary results can be found in the book „Conservation Genetics of Endangered horse Breeds (Bodo et al,EAAP 2005).

There are warm blooded, cold blooded horses and pony breeds, according to the well used grouping or characterization of horse breeds. The common breeding goal for warm blooded horses is now the sport purpose including jumping, dressage and eventing. The distance riding, the driving sport, polo and voltige are only secondary sections. The race horse (gallop and spacer, trotter) is another category. For cold blooded horses the breeding goal is more and more the meat or to some extend milk production instead of the work. Some pony breeds are suitable for riding and driving of children.

There is now an international gene basis for the sport horses, (Cor de la Bruyère or Ramiro can be found in the pedigrees of Selle Français, German or other national Sport horse breeds). The genetic basis for the improvement of the given new breeding goal is the English Thoroughbred. The same tendencies are in the development of different national riding pony breeds using small sized Thoroughbreds or some Arabian genes impact the development.

Therefore those breeds out of these global tendencies should be considered as rare breeds.

The first valuable group is that one improved only by Arabian and empty from Thoroughbred genes. The best example is the Shagya Arabian founded at the Bábolna stud. Other similar breeds are the Terskaya and Karabah in Russia and the Caucasus region. The breeding and selection is made separately from purebred Arabian.

In the group of warm blooded horses there are some Spanish orignated breeds (Lipizzan, Lusitano, Andalusian), which were improved by Arabian, but never with Thoroughbred.

Another group is the halfbred group E.g. Cleveland Bay or Furioso, Gidran in Hungary or the Wielkopolska in Poland. and many others. They were improved by more or less Thoroughbred genes, however the breeding and selection run separately from the international sport horse gene basis.

The cold blooded group segregates upon geographic situation. There are British breeds (Shire, Clydesdale, Suffolk Punch), Western European continental breeds (Auxois, Poitevin etc), they can be considered as local breeds, however they are spread all over the world.

Another local group is that of the Alpine region the Noric with the Franche Montagne and Murinsulaner.

The modern history of ponys is interesting. The use of small horses for children is depending only on the life standard of the countries. Hence some pony breeds are saved and multiplied for the children and others are endangered by extinction and the international riding pony is developed for competitions. E.g.: The Connemara and Welsh pony are well used also nowadays but the Fell is endangered.

The small horses living in extensive natural conditions like the Hutzul or Bosnian Pony ot the Sorraia or Retuertas represent a special value in the families of horses.

The only living ancestor, the Przewalski horse can be the basis of many scientific work in geneticcomparison with the other horses.

- *Key challenges for development and tasks for research :*

1. The role of natural extensive systems for local horse breeds joined to nature protection in pasture areas is very important
2. Characterisation of local horse breeds at European level isrequested. It should be elaborated in the framework within of an EU project.
3. A well organized molecular genetic comparison at international level. Is necessary. Up to now there were only sporadic work but it must be a comprehensive one This extensive work of laboratories must be based upon the preliminary characterization of the breeds by specialised laboratories funded for that purpose.
4. Artificial insemination and embryo transfer should be developed for the preservation of genetic resources of horse species as well.
5. The old traditional breeds belong to the cultural heritage of humanity and therefore the old traditional buildings, stables, houses, yards etc. belonging to the old studs, must be protected as well. The developing movement of old traditional national studs of Europe must be protected.
6. The supply of horse breeding units with pastures and feed producing areas is the key for the breeding.
7. The utilization of alternative products and the cooperation with tourism should not be neglected to help breeding traditional horse breeds.
8. Elaboration of the conditions to implement such programme supported by a EU budget devoted to rare horse breeds.

Dissemination and transfer

- *Dissemination of knowledge*

Teaching Equine Sciences has decreased tremendously in WEC while it has continued to some extend in CEEC since the last world war. As a results education in Equine Sciences is rather low or/and heterogeneous in most Countries whereas there is still a long tradition of horse breeding in EU and strong know-how of breeders.

But Equine Industry is changing increasingly as the social demand is new and the economic pressure is higher. So far updated higher education should be implemented to promote new knowledge in equine industry. Different countries have implemented Master of Equine Sciences (Germany, Sweden, and UK). Other Countries are on the way to design such a higher education system (France, Italy…). It would be likely very relevant to coordinate at EU level such initiatives through a European Master of Equine Sciences. A workshop entitled: "Higher Education in Equine Sciences: New prospects" is scheduled in 2008, and organised by the Horse Commission of EAAP. Hence exchange of knowledge between WEC and CEEC would be performed as well.

For extension officers a certificate of qualification in Equine Sciences should be obtained after those people should be thought Courses in the scope of special horse programme. This step is of high concern to secure the harmonisation of knowledge, then to stimulate a better understanding and use of the new technologies to promote European Equine Industry in the world context.

- *Transfer of technology*

Two Situations should be considered: WEC and CEEC whereas the needs are different.

In CEEC the situation of Equine Industry is still very weak. The size and the quality of horse population are very significant but they should be preserved and oriented adequately to the new utilisation of horses in the scope of new Industrialised Countries. But breeders associations have been established only after recent political changes. So far they have to be secured and extensively invited to participate and to be supported by European Organisations, ex. Copa – WBFSH – EAAP The conditions for the transfer of modern technologies routinely implemented in WEC : parentage control AI – ET – Electronic access to electronic stud books ... etc, should be determined at EU level for CEEC.

In WEC technology transfer is working according to the general regulation stated in EU. But this transfer should be increasingly discussed in Europe (WEC and CEEC) in the very next future as far as there will be innovations generate by the research in molecular genetics: microarrays…

- *Cooperation*

It arises either for education and innovation that a strong cooperation in research is requested too in Equine Sciences as in other farm animals.

Different attempts have been implemented successfully to initiate Cooperation for research between researchers and professionals.

Interstallion is a European Working Group (WG) which has been established in 1998 and placed under the umbrella of WBFSH(World Breeding Federation for Sport Horses) EAAP (European Association for Animal Production: Horse Commission) and ICAR(International Committee for Animal Recording). The objectives of the WG are to "improve accessibility, understanding and comparability of foreign breeding informations across countries". At present two projects are in progress: one is leaded by the Swedish University in Agricultural Science (SLU, Uppsala, Sweden), 4 Countries are involved (DK, G, NL, and SW); and the other one is leaded by National Institute for Agricultural research (INRA – France), 5 Countries are participating (BE, DK, IRE, FRA, SW).

A European WG focused on Behaviour and Welfare has been designed by Horse Commission of EAAP in 2003. This group is publishing a book which summarise new knowledge in the field (EAAP 2007).This book will constitute the platform for further discussion and cooperation throughout a network.

Nutrition WG is a European Working Group which has been established in 2000 and is conducted by EAAP (Horse Commission) with the participation of Feed industry. This WG has published three books which contribute to the harmonisation of the knowledge in the field to promote exchanges of horses throughout EU to compete with world production using updated knowledge in Nutrition and Husbandry (EAAP 2002-2004-2006).

Hence Networks are already workable in these different fields to study genetics-reproduction and the interactions with nutrition and management factors. They would be good support to promote research in cooperation with an increasing contribution of representatives of Equine Industry.

Discussion-Conclusion

Equine Industry is facing to new challenges. The performance of the athlete horses in EU should increase to be still competitive with horses bred in other Countries such as North America for race and sport horses, Australia and Brazil for sports horses to take part with this promising market. The booming development of leisure riding and the diversification of usage of horses, and the increasing role of horses in the use of territories are of high concern for European and local socio-economy.

The approach of **breeding** should be designed and implemented to day **across the scientific disciplines** even genetics will lead the programmes as the questions which have been raised by Industry and Scientists are multifactorial. The answer to Equine Industry should be given in respect of integrative biology where Genetics – Physiology – Nutrition – Behaviour – Pathology are combined throughout consistent breeding systems where the impact of new knowledge and technologies should be evaluated. These evaluations are presented and discussed either in the scope of scientific meetings (table 2) or/and joint meeting between industry and scientists (tables 3, 4).

Priorities have been proposed (table 1). These priorities should combine the identification of new traits and corresponding identified genes consistent with phenotype referred with representatives of Equine Industry to meet adequately the demand. WBFSH – EAAP – ICAR could be constituted the working group to manage these priorities and related programmes.

Research should be carried out throughout the network initiated by EAAP (Horse Commission) with the support of WBFSH and the European Commission throughout the FP7 – USA has already funded this research with 6.5 millions of dollars for mapping the genome. Several European Research teams are already International leader in the field ex. in Germany (Institute of Animal Breeding and Genetics, University of Hanover), in France (INRA – Department of Animal Genetics, Jouy en Josas), in UK (Animal Health Trust), which have been strongly involved in genome mapping with American labs. Other teams have already ever performed the first genetic indices for sport horses in the world using the animal model (BLUP): in France (INRA, Department of Animal Genetics, Jouy en Joas) and in Germany (University of Agriculture, Department of Animal Genetics, Göttingen). The relevance of this approach is well established. The questions which arise now are how to combine the new proposals, across the Countries and how to elaborate breeding value using several criteria.

The background of our proposals is scientifically well documented. The Horse Commission of EAAP has held those last years several sessions to elaborate new prospects (table 2). The new knowledge has been published in books, books of abstracts, Scientific Journals and Public Journals as well. New concepts, methods and tools have been subjected to debate with Equine Industry in each Country and in the scope of Seminars held by EAAP Horse Commission (table 3) and by WBFSH since 1998 (table 4). The Seminars organised by WBFSH were prepared by meetings of the working group Interstallion where scientists of EAAP Horse Commission and representatives of European Industry, namely Dutch-French-German and Nordic Countries, have extensively discussed the evolution. So far WBFSH and EAAP are well prepared to carry on the process, to design and manage the new prospect. But a strong development of Education in Equine Sciences in all the European Countries should be implemented to disseminate the new knowledge and a heavy transfer of technology to CEEC should be involved as well to promote the competitiveness of EU in the world as expected by the European Commission.

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World conference Rio Janeiro 1992.

Table 1
Research needs for the several years horizon
1.A – 5 years

Breeding & Genomics

Items	*Methods*	*Tools*
Identification = UELN	to be determined	Id
Parentage control	Blood typing	
Phenotype	Conventional	Judging
	Modern	Morphology 3D, Gait by accelerometry
New traits		
Health: OCD – Myopathy	Diagnosis	X Ray…., Scoring….
Behaviour = temperament	Model	Standard tests
Genome	Public databases	Genome assembly
Biodiversity	Estimation	Breeding schemes
Interactions with environmental factors		
Husbandry systems	Exp. Trials / survey	Measurement / evaluation
Riding systems	Evaluation	Judging
Nutrition	Exp. Trials / survey	Measurement / evaluation

Reproduction

Stallion physiology		
Sperm production and fertility: variability and prediction	Physiology, Cellular biology Modelization *In vivo, in vitro*	Laboratory evaluation
Inheritance of fertility & reproductive disorders	Molecular genetics	Selection scheme
Quality of preserved semen		
Chilled Frozen	Relationship between laboratory measurements and fertility	Quality threshold for exchange of semen in EEC
Mare and foal physiology		
Oestrus detection	Detection of pheromones	Diagnostic kit
Ovulation timing	Central, paracrine control	New treatments
Uterus pathology	Physiology	Evaluation, treatment
Pregnancy	Physiology, Metabolism	Soundness evaluation
Foetal-neonatal losses	Neonatal care hospital Epidemiology	Pregnancy and neonate monitoring Evidence of risk factors
Efficiency of freezing technique of embryos	Cryobiology Embryo quality	Applicable techniques
Interactions with environmental factors		
Nutrition of mares and stallions	Exp. Trials Physiology-Metabolism	Recommendations

Table 1
Research needs for the different years horizon
1. B – 15 years

Breeding & Genomics

Items	*Methods*	*Tools*
Identification of genes	QTL, micro arrays (SNP)	Bioinformatics
Fertility		
Growth	Measurement BW-BS	Scale-Photomorphotometry
Temperament	Model	Standard test
Performance	Gait-Jumping ability	Judging-video
Diseases		
Longevity	Model	
Main biological functions	Identification of bottlenecks	
And related to functional genes	in physiological and metabolic	
	pathways	
Muscle	Function genes involved and	
Bone	expression of genes	Bioinformatics
	(microarrays: EST)	
Nerve		
Breeding systems		
Including new traits		
Fertility	In vivo, in vitro	
Growth	Measurement BW-BS	Scale Photometry
Temperament	Model	Standard tests
Biomechanics	Evaluation gait...	Judging and video 3D

Reproduction

Fertility prediction of a stallion	In vitro: biology of spermatozoids	Lab tests for fertility evaluation
	and of seminal plasma	Therapy for some disorders
Mare and foal physiology		
Onset of seasonal cyclicity	Physiology	)New treatments
Superovulation	)	)
Pregnancy and neonatal periods	Physiology, metabolism, pathology	Assistance for premature or
	Neonatal care hospital: clinics	sick foals: diagnostic, treatment
	Epidemiology	Lab diagnostic
Assisted reproductive techniques	Mechanisms of fertilization	Evaluation of stallions
FIV, ICSI	Interaction sperm cells / oocytes	Preservation of genetic resources
	Oocyte quality	Management of valuable animals
Cloning	Physiology (cellular cycle	
	, embryo development, pregnancy)	
Selection of gametes or embryos		
Sexing spermatozoa	Physiology, cryobiology	Available semen
Selection of embryos	Molecular genotyping	Diagnostic kit
Efficiency of freezing technique of oocytes	Cryobiology	Applicable techniques
	Quality of oocyte	Assisted reproduction technologies

QT: Quantitative Trait Loci
SNP: Single Nucleotide Polymorphism
EST: Expressed Sequence Tag
BW: Body Weight
BS: Body Size

Table 2

EAAP Annual Meetings:
Main Sessions organised by Horse Commission

Year, Place, N°	***Themes***	***References***
2001 *Budapest (Hungary)* 52rd	Interstallion: European systems for testing and evaluating horses. EAAP, WBFSH-ICAR Joint Session Ch.: J. Philipsson (SW)	Books of abstracts EAAP
	Altenative usage and products of horses Ch: F. Habe (SLO)	Livest. Prod. Sci.
	The Lipizzan horse: Copernicus project Ch.: G. Brem (AUT)	EU Report Copernicus
	Horse production in Hungary Ch.: I. Bodo (Hun)	
2002 *Cairo (Egypt)* 53rd	Selection of Arabian & Anglo-arabian in different ecological zones Ch.: O. Nagel (GER)	Books of abstracts EAAP
	Adaptability of horses to stressful conditions Ch.: W. Martin-Rosset (FRA)	Lives. Prod. Sci. Sp Issue 92, vol. 2
	Horse production in Egypt Ch.:	
2003 *Rome (Italy)* 54th	Exercise physiology Ch.: E. Barrey (FRA)	Books of abstracts EAAP
	Welfare and behaviour Ch.: M. Kennedy (UK)	EAAP Publ. Sp. issue Livest. Prod. Sci.
	Horse production in Italy Ch.: M. Silvestrelli (IT)	Applied Animal Behaviour Sci.
2004 *Bled (Slovenia)* 55th	International genetic evaluation Ch.: E. Koenen (NL)	Book of abstracts EAAP
	Endangered horse breeds and genetic distance Ch.: I. Bodo (HUN)	EAAP, publ. n° 116
	Growth and bone disorders Ch.: Bergero (IT)	Livest. Prod. Sci.
	Evaluation and performances of horses Ch.: G. Fleurance (FRA)	
	Horse production in Slovenia Ch.: F. Habe (SLO)	
2005 *Uppsala (Sweden)* 56th	Systems identification in horses Ch.: X. Guibert (WBFSH)	Book of abstracts EAAP
	Performance and health in growing horses Ch.: G. Dalin (SW)	Equine Vet. J. Anim. Res.
	Horse production in Sweden Ch.: O. Karlander (SW)	

2006 *Antalya (Turkey)* 57th	Impact of reproduction technology on horse breeding programmes Ch: M. Saastamoinen (FIN)	Book of abstracts EAAP Livest. Prod. Sci. Gen. Sel. Evol.
	Breeding evaluation in horses Ch.: A. Ricard (FRA)	
	Effect of management and housing on welfare Ch. E. Sondergaard (DK)	Applied Animal Behaviour Sci. EAAP Publ. Sp. Issue
	Horse production in Turkey Ch.: M. Yener (TU)	
2007 *Dublin (Ireland)* 58th	Application of molecular genetics to breeding programmes in Horses Ch: G. Guerin (FRA)	Book of abstracts EAAP Animal Genetics Genet. Sel. Evol. Animal
	Breeding evaluation in horse Ch.: D. Lewzcuk (PL)	Equine Vet. J.
	Herd and Stable management: health and performance issues Ch: D. Burger (SE)	
	Horse production in Ireland Ch.: N. Finnerty (IRE)	

Table 3

Regular Meetings of Interstallion

Year	*Place*	*Country*
Regular Meetings of Interstallion		
October 1998	Zwolle	NL
April 1999	Paris	FRA
February 2001	Bremen	GER
March 2002	Herning	DK
August 2002	Montpellier	FRA
November 2002	Budapest	HUN
August 2003	Flyinge	SW
February 2004	Den Bosch	NL
June 2004	Paris	FRA
September 2005 (Worshop)	Warendorf	GER
July 2006	Verden	GER
February 2007-06-06	Lund	SW

Main Regular Topics

Breeding objectives
Testing methods and data availability
Genetics evaluation methods
Publication of indexes, then interpretation and use
Pilot project 1 breeding evaluation using young horse test
Pilot project 2 breeding evaluation using competition data
Status and use of International sport data from FEI
Interstallion web site

Participants

For Scientists

J. Philipsson, E. Koenen, E. Bruns, A. Ricard, B. Langlois, E. Thoren, C. Ruhlmann, L. Aldridge, T. Arnasson, K. Quinn.

For Industry

E. Fraehr, T. Niessen, I. Fredericson, L. Christmann, J. Jaitner, H. Van Tartwijk, K. Christiansen, M. Pierson.

Table 4
Seminars of WBFSH

Year	*Place*	*Themes*	*Chair - Speakers*
2004	Guadalajara	Size and Ability	J. Knapp (WBFSH)
	(Brasil)	Analysing Jumping ability	R. Van Weeren (NL)
		A 3- D Video morphometric measurement method : a new tool for	J. Knapp (WBFSH)
		breeding programm	N. Crevier-Denoix (FRA)
		New breeding techniques, possibilities and ethical aspects	K. Miesner (WBFSH)
		Sexing of semen	Dr. Rath (GER)
		Breeding with low doses of frozen semen	M. Vidament (FRA)
		Cloning	E. Palmer (FRA)
		Possibilites by DNA research and horse breeding	J. Knapp (WBFSH)
		Future role of DNA research in horse breeding	J. Leeb (GER)
		OCD mapping	G. Guérin (FRA)
2005	Brussels (BE)	Interstallion	J. Flanagan (WBFSH)
		Warendorf workshop	E. Koenen (Interstallion)
		Piot project 1on young horse test	E. Thoren (Interstallion)
		Piot project 2 on competitions results	C. Rhuhlmann (Interstallion)
		Data exchange WBFSH	H. Van Tartwijk (Interstallion)
		FEI/Studbook ranking	H. Van Tartwijk (Interstallion)
		Use the thoroughbred in the warmblood population	K. Miesner (WBFSH)
		For producing eventers	W.Micklem
		For Producing dressage and jumping horses	Bade (GER)
		Anglo-arab as an alternative to TB	L. Tavernier (FRA)
2006	Verden (GER)	Interstallion	K. Christiansen (WBFSH)
		General Information about Interstallion	J. Philipsson (Interstallion)
		Scale and base for publication of breed values	E. Koenen (Interstallion)
		Pilot project 1	E. Thoren Hellsten (SW)
		Pilot project 2	C. Ruhlmann (Interstallion)
		Workplan for 2007 & questions	J. Philipsson and the above
		Balance between inbreed and genetic progression in European breeding	J. Flanagan (WBFSH)
		Inbreed experience in Ireland	F. Kearney (IRE)
		How do AI and ET influence breeding ?	E. Bruns (Interstallion) & E. Koenen (Interstallion)
		Harmonization of EVA-tests	J. Knaap (WBFSH)
		Aetiology and epizootiology of eva	P. Thein (GER)
		Possibilities of prophylaxis and prevention	
		How to harmonize the test in all labs ?	A.E. Füssel (EU)
		Cloning	T. Nissen
		Ethical and legal aspects of cloning	P. Sandoee (DK)
		Position of EU Commission	A.E. Füssel (EU)
		Position of FEI	Representative from FEI
2007	(NL)	Supply and demand	
		Market	
		The sport horse in 2020	To be designed
		Vision 2020 seen from the studbooks	
		Ethics and Welfare	
		Horse welfare	
		Ethics in sport horse industry	To be designed
		Genetics and reproduction	
		Evaluation of temperament	
		Genetic trait of behaviour	To be designed
		Factors of experience	

Behaviour	To be designed

Table 5
Horses Expert Group

Name		*Country*	*Organization*	*Sector*		*Position*
Board						
Miesner	Klaus	Germany	FN-GER	Industry	kmiesner@fn-dokr.de	President
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Nissen	Thomas	Germany	Holsteiner SB	Industry	holsteiner@lkv-sh.de	Director
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	PHBA	Poland	Polish Horse Breeding Association= PHBA	Industry	Hodowla@pzhk.pl	
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Vidament	Marianne	France	INRA	Research	vidament@tours.inra.fr	Reproduction