

# Symposium on Genomics and the Meat Industry

France, October 8-9, 2003

A Brief Review by Yuefu Liu, CCSI

A Symposium on Genomics and the Meat Industry was held in Paris, France on October 8 – 9, 2003. There were over 50 participants from 11 different countries who attended the meeting. The symposium was organized jointly by the International Meat Secretariat (IMS) and the French Meat and Livestock Association (INTERBEV).

The symposium organizers believed that the meat industry will be profoundly affected by genomics and genetic engineering in the short and medium term. The main objective of the symposium was to review and discuss the influences of new technologies including genetic engineering and genomics on the meat industry, and to discuss its relation with meat productivity, meat quality, food safety and animal health.

## World Meat Congress 2004

World Meat Congress 2004 will be held in Winnipeg, Canada on June 14-17, 2004. More information is available at <http://www.worldmeatcongress-canada.com> or through contact with Canada Pork International at [pomerleau@canadapork.com](mailto:pomerleau@canadapork.com).

There were nine invited speakers. The topics mainly covered three areas: (1) genetic engineering, (2) Contributions of genomics to meat animals and (3) Contribution of genomics to traceability.

### 1. Genetic engineering

Alan Archibald from Roslin Institute of the United Kingdom reviewed the techniques of genetic engineering. He discussed different techniques of gene transfer including DNA injection, sperm mediated gene transfer, virus vectors, and cellular vectors. In his presentation, Archibald concluded that

- Genetic engineering is costly,

- Its techniques are less efficient because of the low success rates, and
- It is facing the problem of public acceptance with GMO products, especially in Europe.

He suggested doing research on genetic engineering rather than application. He believed that it is likely to be sometime before genetic modification technologies see widespread use in farm animals. Genetic modification to eliminate livestock susceptibility to zoonotic disease might be acceptable to the public, but identifying appropriate target genes and carrying out the desired changes with minimal deleterious effect remains beyond our current capabilities.

Archibald pointed out that the farm animals selected by using the advancement of genomics studies, such as marker-assisted or gene-assisted selections, are not GMO's since all of the genes of the selected animals exist in nature.

Gerard Raphael Larrere from National Institute of Agricultural Research (INRA) in France discussed the ethical issue of genetic engineering.

**Genetic engineering** is the technique available to allow the insertion of genes into cells that do not possess those genes or to modify the expression of genes already existing.

A **GMO** (genetically modified organism) is an organism whose genome has been altered by the techniques of genetic engineering, so that its genome contains one or more genes that are not normally found in that organism.

## 2. Genomics contributions to meat animals

Genomics contribution to meat animals was a major topic in the symposium. Speakers generally very positively evaluated the new ways of breeding that genomics and molecular genetics have provided.

Andre Eggen from INRA, France reviewed the different techniques of molecular genetics and gene mapping methods as well as the strategies for identifying genes and economic trait loci (ETL). He concluded that very promising new tools and methodologies, based

on structural and functional genomics are now available for the study of the biology of a specific function or an organism in general. This set of tools will facilitate the identification of the genetic determinants of specific traits (ETL) and provide new ways and criteria for animal selections. He proposed a new concept of “genome breeding” that will make use of all information including those from structural and functional genomics.

Johan van Arandonk from Wageningen University and Gabriel Monin from INRA reported about the application of genomics in swine breeding.

Johan van Arandonk reviewed some of the already realized and potential opportunities of using genomics. The discovery of the Halothane gene has greatly helped the elimination of alleles with negative effect on meat quality. He also reviewed the RN gene causing red soft exudative pork, Calpastatin gene for meat tenderness, FABP genes for intramuscular fat and IGF2 gene for muscularity. He outlined how to combine genomic information and traditional breeding methods to improve pork quality. He emphasized the importance of the quality of phenotypic data in marker assisted selection and suggested collecting information of meat quality traits in a ‘slice’ of the production pyramid, all the way from the nuclear to hog production herds. Pigs and carcasses should be individually identified and followed in detail. The effects of markers and genes should be determined in crossbreds. He also talked about the major imprinted loci affecting body composition (IGF2) and believed that it has several implications for practical animal breeding because the IGF2 gene is imprinted in such a way that only alleles from the sire side are expressed while the alleles from the dam side are not expressed at this locus. The net result of gametic imprinting is a reduction of the expected phenotypic covariance between parents and offspring relative to that between sibs. Identification of imprinted loci opens new perspectives for crossbreeding, which is common practice in pig breeding. Imprinted genes could further accommodate differentiation between sow lines, which are required to have optimal body composition to support their reproductive performance, and boar lines, which ensure high-quality pork. Recently, a research project has started at Wageningen University in collaboration with two pig-breeding companies, where the opportunities are being investigated for exploiting the imprinting phenomenon in commercial pig populations.

Gabriel Monin’s presentation focused on the problems of technological and sensory quality encountered in pork production and processing, using examples taken from the French industry. He described how genomics allowed a clear improvement of the

technological quality of pork produced in France during recent years, by helping to reduce or eliminate the most striking defects (PSE and acid meats). He gave a list of foreseeable applications of genomics to adapt technological and sensory qualities to the requirements of the meat end-users, in order to better meet the growing market segmentation. This includes, for example, the FABP gene and 4 QTLs influencing intramuscular fat (Garnier 2003), the major gene for boar taint, and genes for meat tenderness, fatty acid compositions and stress reactivity.

Stephen Moore from the University of Alberta talked about the application of genomics technology in beef cattle breeding. He reviewed the major genes and QTLs mapped for beef cattle and emphasized the importance of 'direct QTLs', QTLs on markers or on candidate genes. He pointed out that the international effort in animal genomics has promised a better way to select animals based on predictive markers for many production and quality traits. However, approaches towards the application of the genomic technology are not universal across the different animal species, due in large part to the structures of the industries. The beef industry in particular is problematic, due to the lack of vertical integration and the diverse nature of the breeding sector. In order for genomics technologies to fully impact on the beef industry, a higher level of sophistication of the genetic tests will be needed. He also emphasized the importance of phenotypic records. He believed that the application of marker assisted selection will be best achieved in the context of traditional quantitative genetic analysis, already practiced in a wide section of the cattle breeding industry. Moore also thinks that nuclear transfer will be important technology for the meat industry since it can produce a lot of identical progeny.

Mohammad Koohmaraie from the Meat Animal Research Center of the USA also talked about application of genomics information to beef breeding. He suggested that patenting genes and QTLs is questionable. He pointed out that the developments of the patented gene tests were financed by public funds, and many patented genes are based on small sample sizes. He believed that gene patenting leads to negative influences on research. Once a gene is patented, no one wants to do any research again on that gene.

**Genome:** The entire DNA contained in an organism or a cell, including both the chromosomes in the nucleus and the DNA in mitochondria.

**Genomics:** A branch of biotechnology concerned with applying the techniques of genetics and molecular biology to discover genes, their chemical compositions and their position on chromosomes, or the complete genetic architecture of organisms, using high-speed methods, organizing the results into databases, and finding applications for them in biological, technological, agricultural or medical practices.

**Marker:** An identifiable location on a chromosome whose inheritance can be monitored. Markers can be expressed regions of DNA (genes) or some segment of DNA with unknown coding function but whose pattern of inheritance can be determined. Because DNA segments that lie near each other on a chromosome tend to be inherited together, markers are often used as indirect ways of tracking the genes controlling the trait in question.

**Candidate gene:** A gene located in a chromosome region expected to be involved in a biological function, whose protein product suggests that it could be the gene of the trait in question.

**QTL (Quantitative Trait Loci):** Sites in the genome containing genes controlling quantitative traits such as growth rate and body composition, many of which are of economic interest.

Alain Vignal from INRA of France talked about genomics studies and application to genetic improvement of chicken. Jean-Michel Elsen from National Institute of Agricultural Research in France illustrated how genomics information allows a fast livestock improvement by increasing selection precision and selection intensity, reducing generation interval, controlling genetic variation in the population, and optimizing breeding plans.

## **2. Genomics contributions to traceability**

Patrick Cunningham from Trinity College in Dublin, Ireland talked about the contribution of genomics to beef traceability. The meat traceability came along with the health threats from diseases such as BSE and Foot-and –Mouth disease. Consumers have been becoming more demanding regarding food safety. The traceability techniques became

important also because of the wide-scale mislabelling of meat products. In Ireland, consumers are being misled over the origin of the beef they are eating, according to the Irish Farmers' Association. The farmers union claims that following a DNA survey of beef in restaurants and shops, some of the beef labelled as Irish comes from Brazil or other South American countries. According to Cunningham, Japan passed compulsory traceability legislation for domestic beef cattle on February 25, 2003. The legislation also requires Japanese meat processors to take and store DNA samples of each animal at the time of slaughter. Random DNA tests at wholesale and retail will be introduced to ensure the integrity of the system.

Patrick Cunningham's research group developed a beef traceability system based on DNA tests. Four to six microsatellite markers are used for the traceability test. They also developed a DNA test for identify the beef imported from South America.

**Traceability** is the ability to trace and follow a food, feed, food producing animal or substance through all stages of production, processing and distribution.