

EDITORIAL

This is the seventh EADGENE Newsletter.

This time the host pathogen article this time highlights *E. coli* research within EADGENE. And Eva Perez Reinado tells about her work for the 'Genetic Markers in Domestic Animals' Groups.

A first impression of the sociological study into consumer perception of animal disease genomics is given. Hsiangsheng Nie is our 'In the picture guest'.

Angela van der Sanden

Host Pathogen interactions

In the EADGENE joint research programme several specific host (e.g. cow, pig)-pathogen relationships get special attention. In the former Newsletters the functional genomics of host pathogen interactions in common, Salmonella and Mastitis in particular were discussed. In this Newsletter *E. Coli* will be discussed.

Escherichia coli (*E. coli*) are one of the most common bacteria in the large intestine of warm-blooded animals. Although, in general *E. coli* are 'good' bacteria, with a positive and necessary function in the large intestine, some strains can cause a wide range of diseases, ranging from diarrhoea to extra intestinal infections such as septicaemia and urinary tract infection. Among them, Enterohaemorrhagic *E. coli* (EHEC) are zoonotic (can be transmitted to humans from animals) intestinal pathogens of global importance. EHEC are firmly associated with severe human illnesses like bloody diarrhoea and haemolytic uraemic syndrome, causing life threatening renal and neurological sequela (pathological condition resulting from a prior disease). EHEC rarely cause disease in animals, and ruminants are recognised as their main natural reservoir. Poorly cooked ground beef and unpasteurised milk have been the most frequent causes of infection, but also direct contact with ruminant faeces is a major risk of infection.

The *E. coli* working group tries to define the combination of virulence genes and the mechanisms that make an EHEC strain fully pathogenic. This will be essential to improve the efficacy of diagnostic tests for surveillance of animal reservoirs, the assessment of public health risks and for the development of novel vaccines or treatment for control of EHEC infections. Different strategies will be used for this research. Resources and expertise will be used to define genes contributing to virulence by hijacking the host cell signalling systems and/or genes that intermediate the colonisation of the intestines.

The working group will focus on the "type III secretion system", a sophisticated machinery (a kind of molecular syringe) used by the bacteria to inject proteins into the host cells. These proteins can then subvert, inhibit, or activate cellular processes to benefit the *E. coli* bacterium:

Furthermore, the emphasis of the group is placed upon the identification of new virulent determinants which could lead to the development of novel diagnostic methods and preventive strategies that would help monitor the flow of *E. coli* virulent genes in the food, animal reservoirs and the natural environment. Groups in several institutes (and laboratories) are working together, exchanging experimental data and resources.

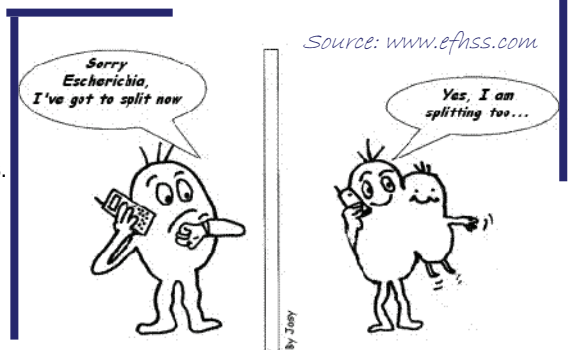
The E. coli's working group contribution to EADGENE's pathway to healthier animals and safer food!



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TYPICAL CELL PHONE CONVERSATION AMONG BACTERIA

With thanks to the Knowledge Management working group



Do's and Don'ts

Protocol Technology Transfer

Contents Do's and Don'ts

**Help by setting up cooperation's
between industries and research
institutes**

- Letter of Intent
- Consortium Agreement
- Publication Industrial Ownership
- Quick set up of a Contract
- Negotiation Collaborative Research Contract
- Intellectual Property Management

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[<<www.eadgene.info/iphelp.html>>](http://www.eadgene.info/iphelp.html)

Towards finding new candidate genes for improvement of swine immune response

By Eva Perez Reinado

The group named "Genetic Markers in Domestic Animals" belongs to the department of Genetics, located at the University of Córdoba (Spain). The main research work carried out is about the genetic base of the immune response in swine: *the characterisation of the genes that could be part of the immune response and the improvement of their immune response*, is the main objective.

Different strategies used to reach this:

• Genomics

MICROARRAYS. The genetic information present in its genome determines how the immune response of an organism will develop...A DNA microarray is a collection of microscopic DNA fragments. These spots show the expression profile, monitoring expression levels for thousands of genes simultaneously.

So with a porcine DNA microarray we can study which genes are implied in a certain phenotype...for example that we want to find genes implied in the response to a pathogen. We would hybridize DNA segments of individuals or cellular lines that have been in the presence of the pathogen, and compare them to the ones that haven't been in contact with it. The cells infected with the pathogen and the cells not infected will have the DNA segments labelled with different colours (fluorofores). In this way we will be able to find out which genes are more / less expressed in the infected individual...



• Proteomics:

Instead of looking for different expressions of genes, we can also compare protein expression profiles with **2D Bidimensional electrophoresis**. As in the DNA microarrays, we can compare the proteome map (map of proteins expressed by a cell) in two different situations to find proteins involved in the development of certain diseases...Now proteomes of macrophages infected with a pathogen are compared with the ones that are not infected, to find proteins involved in the inflammatory immune response.

A **Single Nucleotide Polymorphism**, or SNP (pronounced "snip"), is a small genetic change, or variation, that can occur within an individual's DNA sequence (relative order of nucleotide pairs..SNP variation occurs when a single nucleotide, such as a G, replaces one of the other three nucleotide letters—C, A, or T. An example of a SNP is the alteration of the DNA segment CGACT to CGAGT, where the fourth nucleotide "C" in the first snip-pet is replaced with a "G".

In our laboratory we have found SNPs (changes in the DNA sequence) in several genes involved in the immune response. Some genetic variants of the genes may confer a protective immune response against the pathogen which could be important for the development of the disease in pigs.

The discovery of new genes whose products are essential for the development of diseases and their characterisation is important since some of these gene variants may result in more resistant animals. When this strategy is used complementarily with other disease control strategies, genetic approaches will become a critical component of the sustainable control of animal disease and, hence, the provision of a safe, high quality and welfare-friendly food supply chain.

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Sociological Study of Animal Genomics and Key Findings

by Arouna Ouedraogo

Part of the EADGENE project consists of a sociological study into consumer perception of animal disease genomics. Animal disease genomics may seem to be a subject far removed from the general public – nevertheless it includes the area of food, animals, genes and health. These are all subjects of public interest. Values underlying this interest include perceptions of safety, trust, need, quality, health, animal welfare, experimentation, and care for a sustainable society and natural balance.

This article summarises the results of interviews with consumers in six study countries....a first impression can be given.

...Attitudes towards applied animal biotechnologies, including animal genomics, depend closely on the research goal..., the majority of the interviewees feel totally comfortable with using 'new genetic tools' on animals for medical purposes, but not in case of cosmetic purposes. The average person wonders whether research on animal genomics for food production purposes is necessary...feels uncomfortable about the idea of animals being used as 'surrogate humans' for medical purposes.

Public concerns regarding animal genomics are an integral part of widespread general "mistrust" regarding institutions being responsible for ensuring acceptable (safe, moral) applications of the new technologies. The terms "common interest" "transparency" in procedures, and "biodiversity", are frequently used in statements, and announcements of BSE and other crises.

Not all people react in the same way. Differences in attitude were recognised in this pilot study, and can be outlined as follows:

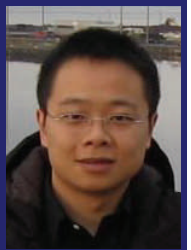
- Relative acceptability (vs. mistrust) of animal genomics within and across study countries is mostly related to the level of education (rather than social class), gender and age (31-45 vs. 18-30 and 45+).
- Variation in perception between study countries is mostly related to:
 - Power concerns in Farm Management: more extensive companies vs. local farms (France, Italy)
 - Animal Welfare Concerns: Animals mainly as production animals vs. Animals focussed on moral aspects (UK, NL, Norway, Spain)
 - Political and Ethical Concerns: Elite Animals vs. Right to Live for All (UK, France, Spain)

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In the picture:

Haisheng Nie

I am a second year PhD student in Animal Breeding and Genetics (ABG) group at Wageningen University and Research Centre (the Netherlands). I was born in 1981 in Beijing (China). I finished my MSc in animal science in Wageningen in 2005, and started as a PhD in Prof. Martien Groenen's group that same year.



My experience abroad began in August 2003 when I arrived in Wageningen for my two-year MSc study in animal science. My first scientific experience started with a seven-month thesis on Fine-mapping of a QTL region for Femur Head Necrosis in chicken with Dr. Richard Crooijmans in ABG group in Wageningen, followed by a project on Positional Cloning of the Congenital Muscular Dystonia Gene in Belgian Blue Cattle with Prof. Michel Georges in University of Liege (Belgium).

Within EADGENE, I am working on work package 5.1 structural genomics. My focus is on identification of the functional transcription factor binding sites in chicken promoters by sequence comparison and expression profiling, with special focus on the genes involved in host-pathogen interactions.

I live in Wageningen where I enjoy being in such a quiet small town with many friends around. My hobbies are jogging in the woods, music and I have also enjoyed the opportunity of traveling around Europe over the past three years. My wish for the future is to travel around the world!!