NEWSLETTER

EADGENE

European Animal Disease Genomics Network of Excellence for Animal Health and Food

February 2006

EDITORIAL

This is the fifth EADGENE Newsletter.

In this Newsletter you can find the follow up to the Host Pathogen Interaction column. This time it is focusing on Salmonella.

A short overview of the EADGENE Microarray course is given.

Jacques Mainil is this time our 'In the picture guest'. And Matthias Kaiser has written a very interesting article about ethics in Aquaculture.

Furthermore, attention is brought to bear on the Sheep genome sequence.

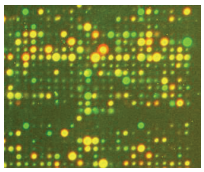
Angela van der Sanden

Host Pathogen interactions Salmonella

In the EADGENE joint research programme several specific host (e.g. cow, pig)-pathogen relationships get special attention. In Newsletter four (November 2005) the functional genomics of host pathogen interactions in common were discussed by Mari Smits. Functional genomics is the analysis of the function of genes of an animal. One of the goals of the joint research groups is to identify the genes of the pathogens that are involved in host-pathogen interactions, in this Newsletter Salmonella will be discussed by Annemarie Rebel.

Upon an infection, Salmonella can induce various pathological changes and clinical signs of disease in animal hosts. The molecular aspects of the host response upon a salmonella infection are, however, relatively unknown. Many different factors determine the type, the specificity and efficiency of such a host response. Examples of these factors are: genetic background of the individual host; breed; age; health status; salmonella strain and subtypes; environmental factors; etc. In the joint salmonella research project we will compare the host (e.g. chicken, pig, cattle) responses at the molecular level in different models of salmonella infections. From this we will extract the common response parameters of a salmonella-induced host response. Initially, we will concentrate on host responses within one animal species and later on we will also compare the responses of different animal species, for example pigs vs. chicken.

We will perform this by generating a list of genes that are up- or down-regulated* upon an infection with salmonella in each animal model operative in the participating institutes. We will exchange information on gene sequences (order of bases in a gene which determines which protein a gene will produce), in order to evaluate the behaviour of genes..



Method to identify host response genes: micro-array analysis. Red or green is induced, while yellow is differentially regulated.

Hyperlinks

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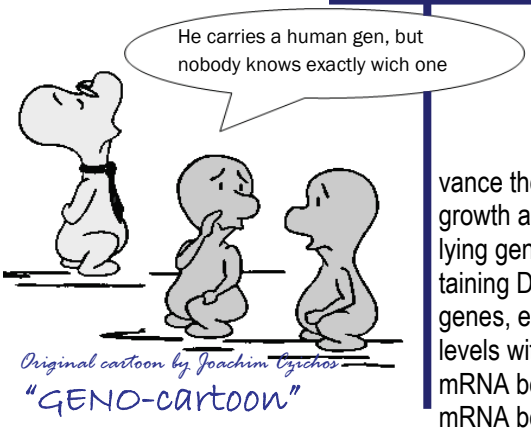
- ORGANISATION
- INFORMATION
- PARTNERS

*The switching on/off of a particular gene leading to a positive/ negative regulatory effect on certain physiological processes.

Read more: www.eadgene.info/newsletter.html



EADGENE Microarray Courses

by C Channing

Micro arrays allow scientists quickly and efficiently to analyse the expression of thousands of genes in a single experiment. Scientists can use this powerful technology to advance the understanding of fundamental aspects of growth and development as well as to explore the underlying genetic causes of many diseases. Each array, containing DNA probes that represent (tens of) thousands of genes, enables scientists to determine the expression levels within a sample by measuring the amount of mRNA bound to each site on the array. With the aid of a computer, the relative amount of mRNA bound to the spots on the micro array is precisely measured, generating a profile of gene expression in the cell. In order to make this information meaningful and useful, it is important that scientists and bio-infomaticians are provided with up-to-date training in the computer-based techniques for handling micro array data.

EADGENE scientists have recently been involved in the organisation of two micro array training courses. This course was designed to give both hands-on experience of different techniques in the laboratory and to improve understanding of some of the statistical procedures used for analyzing the data from these experiments. A second course, which concentrated on the statistical aspects of micro array design...

Read more: www.eadgene.info/newsletter.html

In the EADGENE project special attention is paid to ethics. The project involves a comparison of consumer concerns about animal genomics. Aquaculture is one of the animal species represented by EADGENE as well. In the following article Matthias Kaiser*, an ethicist specialised in aquaculture, discusses these subjects.

*The National Committee for Research Ethics in Science and Technology (NENT), Oslo

Aquaculture and ethics: the need for value debate

Aquaculture relates to the fishing industry roughly the same way as agriculture relates to hunting. Surely this is a positive feature of aquaculture. Furthermore, it is beyond doubt that aquaculture production is in principle better adapted to the demands of modern markets than the traditional fishing industry. It provides for a much more stable and targeted delivery of food products. Yet, looking on the downside, while agriculture has slowly developed over the last millennia, aquaculture has developed very rapidly in the last decades. The great boost in aquaculture happened during the last 5 or 6 decades. Thus, while agriculture had history on its side to develop at least some forms of rudimentary ethical standards for animal husbandry, aquaculture is still in its infancy.

…So what is so ethically critical in aquaculture? First, there is obviously the issue of food safety and other consumer worries. ….Obviously there are also other issues that are related to consumer worries and how they are met by industry, such as e.g. traceability, labelling and certification practices. This is what could be called the sustainability issues of aquaculture…..
What are we to think about production fish being caught along the shores of, say, Chile, being processed somewhere in Europe, then being fed to aquaculture salmon in, say, Norway, for this fish then being finally flown to, say, Japan where consumers can enjoy high quality and high price products? Can the energy use along the way be considered to be sustainable in the long run? ... From an ethical point of view, if the "system" is wrong, then all those who "follow" the system take on co-responsibility.

Aquaculture sometimes makes the claim that fishing down and farming up the food chain must be the only sustainable and reasonable way to go. Among others they cite arguments that the feed conversion rate in salmon is so much better than in other animals. Furthermore, we get much more edible energy out of 10 kg of capelin if used as feed for farmed salmon (~28 MJ), than if eaten by cod that then is caught by fishing boats and sold on the markets (~3 MJ)…. who can define for us what is at stake here? Is it an issue of salmon or cod or pork on our dishes? Or is it an issue of the management of natural resources? Or even wider issues, such as the growing world population or finding adaptive technologies?

….The whole point of my communication is to show how ethical issues are at the basis of many of our current food debates; and how aquaculture in particular is in need of opening up to a broad public debate. And to be honest and self-reflexive: in this respect not only our aquaculturists and scientists need to engage much more, but my fellow social scientists and philosophers need to realize that they, too, have a job to do.

Read whole article: www.eadgene.info/newsletter.html

In the picture

Jacques Mainil was born in August 1957 in Namur (Belgium); however he spent most of his life in Brussels. In 1981 he graduated as a “Docteur en Médecine Vétérinaire” (DVM) at the University of Liège and started working as an assistant in the Bacteriology laboratory. In 1983 he obtained a postgraduate degree in Molecular Biology at the University of Brussels and his PhD degree in January 1988 at the University of Liège. In 1993 he was promoted to professor and head of the Bacteriology laboratory. He also obtained another PhD degree that year. Meanwhile he spent one sabbatical year at the National Animal Disease Center, Ames, Iowa (USA) and a second one at the Veterinary School of the University of Glasgow, Scotland.

Nowadays he supervises research projects and PhD students. He lectures veterinary students on pathogen bacteria and bacterial diseases of domestic animals, and he deals with the administration of the bacteriology laboratory.

The overall purpose of his research work and projects is understanding the molecular mechanisms involved in bacterial virulence, thus to identify the basis of the host specificity of bacterial pathogens, to develop specific identification assays and to study the molecular epidemiology of bacterial pathogens. The main bacterial target species is *E. coli*, with its various groups of pathogen strains for different animal species and for humans. Other pathogens studied include *C. perfringens* (which causes an acute poisoning condition) , *M. bovis* (linked to respiratory conditions) , and *S. aureus* (which causes mastitis) in cattle .
He participated in the FP4 and FP5 EU projects. Within EADGENE his purpose is to interpret the exchange of pathogen bacteria in the target host species for the eukaryotic and animal geneticists.

Nowadays he and his wife Christiane live in Villers-le-Temple close to Liège. They have two children: François (22) and Florence (19). Although Jacques has taken part many different kind of sports, nowadays he and Christiane enjoy hill walking (especially in the Scottish Munros) and practise aikido.

His only wish for the future is to keep physically fit for another fifty years (at least !).

Sheep genome sequence

by C Channing and C Warkup

An international consortium of scientists, including EADGENE members, has moved one step closer to producing the full genome sequence of the sheep. The “virtual” sheep genome sequence is an assembly of small fragments of the genome that has been aligned to the bovine (cattle), human and dog genomes as templates. Only the ends of these fragments have been sequenced, but a high proportion of them find a closely matching sequence in the other mammalian species sequenced. This alignment of fragments is an important first step to sequencing the whole sheep genome when this becomes affordable. Until the full sheep genome is available, the close similarity between cattle and sheep, together with this 'virtual' genome will help sheep researchers study sheep genes. The genome sequences of cattle and sheep will be essential tools for researchers working to improve health and disease management in farm animals. For example, a better knowledge of the cattle and sheep genomes may eventually lead to breeding solutions to control disease problems such as mastitis.