



European Animal Disease Genomics Network of Excellence

Network News N°15, December 2009

Editors' Introduction

In this final edition of EADGENE's Network News we have increased the size of the newsletter so that we can highlight the achievements of the EADGENE project over the last five years. We have twelve articles from our workpackage leaders, detailing the success stories from our Integrating, Research and Spreading of Excellence activities.

Many of you were able to join us in October, for the fifth and final EADGENE conference in the stunning venue of the Museum National d'Histoire Naturelle in Paris. For those of you who could not make it to the meeting we have included a two-page report and some photos from the meeting.

Finally, from the EADGENE Communication Team, we wish you a very Merry Christmas and all the best for 2010.

Celebrating EADGENE' achievements over the last 5 years



By Marie-Hélène Pinard van der Laan

It is with great pride, but also with a hint of "nostalgie", that I introduce this final edition of Network News.

Great pride for all that has been accomplished thanks to your hard work, commitment and, above all, faith in this adventure that was called the "Network of Excellence". Five years ago, many were sceptical about NoE: What was the meaning of integration? Could you really carry out research in a NoE? Fortunately, some of us were enthusiastic enough about this idea to get it started. Gradually, ongoing

collaborations have been strengthened, new collaborations have been facilitated, exchanges of people and resources have been taken place, people have got to know each other and we have had the pleasure of meeting at our workshops, partner meetings, yearly EADGENE days...and a real network arose!

The "success stories" presented in this newsletter provide true evidence of the significant outputs and impacts of the EADGENE NoE; which would not have happened otherwise...and many additional successes we didn't even think about when we started!

You may be amazed by the diversity and the quality of achievements, covering wide-ranging aspects and also having managed to pinpoint specific research issues. You will read about integrating resources, developing and sharing up-to-date technologies and tools, successful collaborative research outputs on host-pathogen interactions in several models, bridging the gaps between research and industry, increasing exchanges of ideas and knowledge through mobility, workshops and meetings, while challenging ourselves with ethical concerns.

Of course I'm a little bit nostalgic because this is the last Network News and we have had our last EADGENE days conference. But fortunately the Network we have built together, each bringing a personal contribution, can continue and keep its identity. All EADGENE partners have agreed to follow up the Network in a durable way by creating a "European Research Group" (ERG). So this will be another new adventure, which will allow us to further develop our capabilities using our acquired knowledge, resources and experiences. We are also actively preparing a Coordination and Support Action (CSA) for EADGENE with a deadline in January. So, no time to be nostalgic – instead we can look at the future of "Animal Genomics and Animal Health" research together!

I will again express my sincere thanks to all of you who have made this Network a success and wish to continue. And my special thanks to the Communication Team for all their support.

And I wish you a very Merry Christmas and a Happy New Year!

Marie-Hélène

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Sharing resources and facilities in the “virtual lab” (WP1.1)

Ingrid Olsaker, Norwegian School of Veterinary Science, Norway

One of the primary objectives of the EADGENE Network was to coordinate and facilitate access and sharing of biological resources and advanced technological facilities through a “virtual laboratory”. To achieve this the partners have established **databases of available resources and facilities**, a model **Material Transfer Agreement** to regulate IPR issues, and a list of elements to consider for **contracts between a visitor and a hosting facility**. It was also important to agree on common sets of rules regarding experimental procedures such as Good Laboratory Practices (**GLP**), Standard Operating Procedures (**SOP**) and Quality Assurance/Quality Control (**QA/QC**).



In order to produce comparable results within the Network it was highly desirable for EADGENE partners to conduct their experiments using microarrays from the same sources. Therefore, EADGENE has invested in chicken, pig and bovine oligo microarrays which are now produced within partner institutes and distributed to partners on request:

- ◆ **Chicken oligo array:** ARK Genomics, The Roslin Institute and R(D)SVS, University of Edinburgh (UEDIN), UK and CRB-Gadie, INRA Jouy-en-Josas, France
- ◆ **Bovine oligo array:** ARK Genomics, The Roslin Institute and R(D)SVS, University of Edinburgh, UK
- ◆ **Pig oligo array:** University of Aarhus, Denmark (AU) and CRB-Gadie, INRA Jouy-en-Josas, France

The value of these tools has been further increased by the continually improved annotations of these microarrays by the bioinformatics group of WP1.3 (see article on next page). We have also identified sources of microarrays for salmonids, *E. coli* and Salmonella. The EADGENE coordinator, INRA, has established high-quality collections of microbes and

bacterial pathogens. The partners also have collections of clones from genomic and cDNA libraries of various sources and individuals, and samples from animal selection lines. All these collections are available to EADGENE partners.

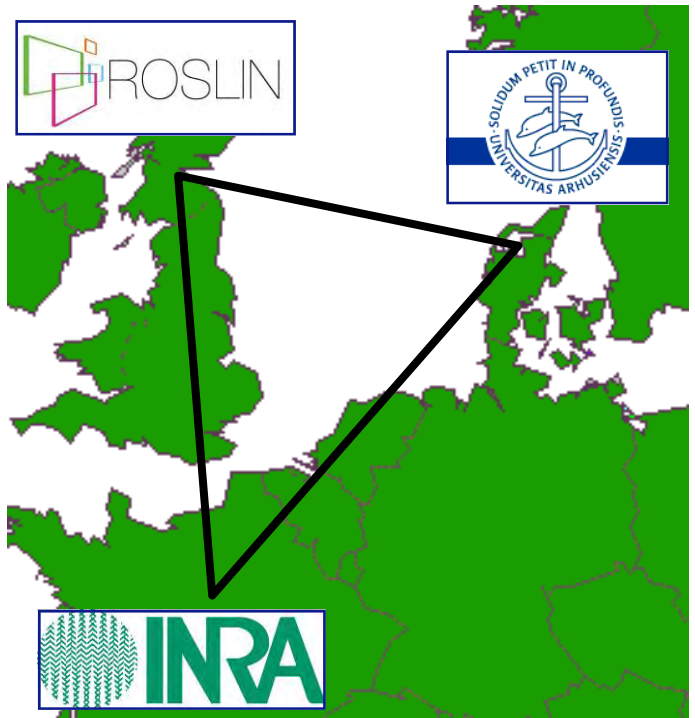
Three partners (INRA, UEDIN, AU) have conducted a microarray quality control (QC) study of the reproducibility of transcriptomic profiling experimental results between their laboratories. The fundamental idea of the QC experiment was to repeat the same experiment in three different laboratories using identical microarrays and aliquots of the same RNA samples. The experiments were conducted using laboratory-specific protocols for labelling, hybridisation, washing and scanning, which all differed between the laboratories.

Personnel were also exchanged between the three laboratories of this “**technological triangle**” in order to share experiences, ideas, methods etc. and thereby further stimulate the interactions between the institutions.

The resulting gene lists produced by the three laboratories have shown that results from DNA microarrays are reproducible, affected gene-sets are very reproducible, but that affected genes are less reproducible. This work will be published in the near future.

Our interactions on transcriptomics technology will continue and are moving into the area of high throughput sequencing.

EADGENE members have been involved in the creation of a network of European animal facilities concerned with animal models of infection, which obtained a grant from the Capacities-infrastructure European programme. NADIR (Network for animal diseases/infectiology research infrastructures initiative) has 15 partners from within and outside EADGENE. In November 2009 the NADIR network opened a call for transnational access project proposals (see http://www.nadir-project.eu/nadir_project).



EADGENE Technological Triangle

Providing up-to-date bioinformatics tools for biologists (WP1.3)

Christophe Klopp, INRA, France

Up-to-date bioinformatics tools are critical in all studies including genomic data types. Genome sequences, cDNA resources, and micro-array expression studies all involve the generation of thousands if not millions of data points. It is essential that these data are handled correctly and made available to the wider scientific community in a user-friendly format, conducive to furthering the understanding of the biological systems being investigated.

The EADGENE network has provided biologists with easy access to common genomic tools - most importantly oligo-arrays for three species: chickens; cattle; and pigs (see article on previous page). One of the major contributions from EADGENE's bioinformatics group has been the **production of up-to-date annotation files**, allowing the extraction of biological knowledge from the microarray experiment results.

Annotation is the process of giving a recognisable gene id (or label) which will identify the gene which is targeted by a given probe on the microarray. Genomic information is continually evolving as new genome assembly versions are published, new gene build versions are issued, etc. In addition, annotation information is continually being updated as new information on gene ontologies, orthologous genes, biological pathways, etc. becomes available to the scientific community.

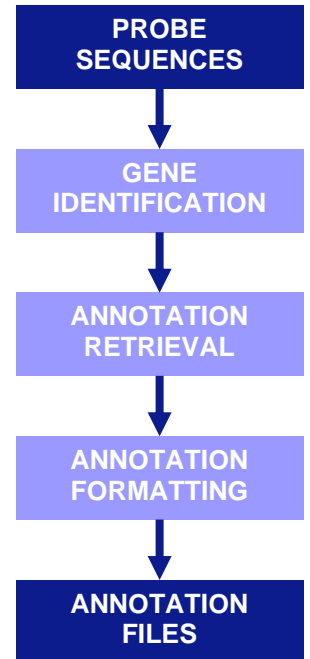
As part of the EADGENE project, several national groups from across Europe have shared their knowledge on microarray annotation during annual work package meetings, short-term stays (funded by EADGENE) and at a microarray annotation workshop.

The **Microarray Annotation Workshop** was held in conjunction with the EADGENE and SABRE Post-analyses Workshop in November 2008. The aims of the workshop were: (i) to present the different annotation strategies and tools; and (ii) to compare the resulting annotations of a common set of oligos which were distributed to participants prior to the meeting. The results gave the biologists a good insight into these oligo-sets, by analysing the specificity of each probe versus the corresponding transcriptome and genome. Another result was the highlighting of possible oligo design caveats like retained introns or transcriptome fragment banks artefacts.

Since early 2008, biologists have been able to download chicken, pig and bovine **annotation files from the EADGENE website**. The file data and formats have been adapted to the users' needs according to feedback received. We have also provided a kind of "identity card" of the oligo-sets with these annotation files, which is intended to help the biologists choose between oligo-sets when they start a new experiment. This two page description gives information about the size of the set, the number of oligos which have been annotated, and how precisely they match the corresponding genes. It also indicates how many of the genes have human or mouse orthologues, the IDs of which are commonly used to retrieve data from biological network software like Ingenuity Pathway Analysis Software or Genomatics.

Further information: The results of these oligo annotation pipelines were published in BMC Proceedings 2009, 3(Suppl 4).

- ◆ Comparison of three microarray probe annotation pipelines: differences in strategies and their effect on downstream analysis. P.B.T. Neerincx, P. Casel, D. Prickett, H. Nie, M. Watson, J.A.M. Leunissen, M.A.M. Groenen, C. Klopp. BMC Proceedings 2009, 3(Suppl 4):S1
- ◆ IMAD: flexible annotation of microarray sequences. D. Prickett, M. Watson. BMC Proceedings 2009, 3(Suppl 4):S2
- ◆ sigReannot: an oligo-set re-annotation pipeline based on similarities with the Ensembl transcripts and Unigene clusters. P. Casel, F. Moreews, S. Lagarrigue, C. Klopp. BMC Proceedings 2009, 3(Suppl 4):S3
- ◆ OligoRAP – an Oligo Re-Annotation Pipeline to improve annotation and estimate target specificity. P.B.T. Neerincx, H. Rauwerda, H. Nie, M. AM Groenen, T.M. Breit, J.A.M. Leunissen. BMC Proceedings 2009, 3(Suppl 4):S4



Re-annotation pipeline



Participants in the Annotation and Post-analyses Workshop, November 2008

Sharing European expertise in analytical methods and tools (WP1.4)

Dirk-Jan de Koning, The Roslin Institute and R(D)SVS, University of Edinburgh, UK

Throughout the last five years, EADGENE's Analytical Tools group has shared expertise from throughout the Network to provide practical solutions and guidance for analysis of animal disease genomics data. The work of this group has been very much demand-led: at the start of the project, in 2005, a survey of members was used to establish the priority areas to be addressed over subsequent years. New topics have since been added as the technologies and the analysis methods have evolved.

The provision of a **training course** for research scientists who wished to increase their understanding of the **design and statistical analysis of microarray experiments** was quickly identified as a priority and the creation of this course was one of the first major achievements of the group. Microarrays have a number of set stages: experimental design, image analysis, removal of outlier slides, normalisation, statistical analysis of gene expression, and interpretation and reporting of results. A 3-day course was designed to address each of these issues, and provide the students with approaches and strategies to cope with each stage. The course was first held in Edinburgh in 2005, and has since been repeated by ARK-Genomics in 2006 and 2008 with EADGENE support, and will continue in the future.



An EADGENE workshop dedicated to the **analysis of microarray data** was held in November 2006. Real and simulated microarray data had been distributed prior to the workshop, and participants analysed the data using their preferred methodologies. The real data came from an EADGENE mastitis working group study looking at gene expression changes following artificial infection with two different strains of mastitis causing bacteria, and included several time-points, resulting in a true analytical challenge (48 microarrays). Participants were expected to deliver a list of differentially expressed genes. The workshop participants reported on a good mix of analyses using web based tools (GEPAS, Orange), commercial packages (GeneSpring), standard statistical software (SAS) and open source software like R for which microarray tools are available that can be customised by the users (Limma, Bioconductor etc). Reassuringly, the simulated data showed that despite very different approaches nearly all groups correctly identified their best 250 genes as differentially expressed. The mastitis working group were very interested in the results from the real data and four EADGENE papers were published as a result of this workshop (Genet. Sel. Evol. 39 (2007) 621-683).

A joint EADGENE and SABRE **working group on post-analyses of microarray data** was set up to follow on from the success of the microarray data analysis workshop. During a 3-day workshop in November 2008 we discussed five aspects of post-analyses of microarray data: 1) re-annotation of the probe set on DNA microarrays, 2) pathway analyses to identify significantly affected biological processes from microarray results, 3) reverse engineering of regulatory networks from microarray results, 4) the integration of gene expression studies with QTL detection studies and 5) the prediction of phenotypic outcomes using gene expression results. Fifteen EADGENE papers were published in BMC Proceedings 3 (2009) Suppl. 4 as a direct result of this work.

An EADGENE **workshop on bioinformatics and data handling methods for next-generation sequencing data** was held in October 2009. The focus of the workshop was the scientists' experiences of a variety of bioinformatics and data handling methods for next-generation sequencing data. These new generation sequencing technologies, where a single machine can rapidly sequence several genomes, have greatly increased the amount of data to be handled by bioinformatics, and this presents scientists with fresh challenges.

In order to **cross-foster expertise**, a workshop entitled "From Infection to Inference: Interpreting Animal Health and Disease Data" was held in June 2007 to facilitate the dialogue between disease experts and specialists in data. Animal disease data presents many challenges, so specialists with expertise in both animal health and data analysis are needed to design experiments and interpret the data, and to translate the results to industry. Three contrasting disease categories (mastitis, gut health e.g. *E. coli* or Salmonella infections, and nematodes) were each overviewed by disease experts who described the nature of the traits resulting from the disease, and then addressed by statistical specialists who highlighted the issues arising from the particular disease trait data and presented potential state-of-the-art solutions.

During the cross-fostering workshop there were expressions of interest in holding similar, more disease specific workshops on a similar theme in the future, therefore a workshop on the **design, collection and analysis of field disease data** will be held during early 2010, with the objective of developing a blueprint for the design and analysis of disease genetic studies using field data.

The successes of this group can be attributed to the willing cooperation and active participation of the various researchers from our EADGENE partner institutes, and the willingness of research groups to share their data and results. In particular, the publication of 19 scientific papers provides a concrete and long-lasting output from this group and is a good example of the collaborative work that can take place within a Network of Excellence.

Host and pathogens response to Salmonella infection (WP7)

Annemarie Rebel, Animal Sciences Group, Wageningen UR, The Netherlands

The host response to a Salmonella infection can differ between lines of animals. These differences in susceptibility can be due to differences in the invasion of the Salmonella in the gut or differences in the clearance of the Salmonella from the animal. Differences in susceptibility can also be linked to differences in gut and systemic response. In addition to differences in animal responses to the same Salmonella infection, differences in host response also exist when different species of Salmonella are the source of infection.

To obtain a better understanding of the host response and relative susceptibility to Salmonella infection we can investigate differences and similarities in gene expression between different animal species, or different lines within an animal species, after infection by a given Salmonella strain. Conversely, host responses to different Salmonella mutants should also be considered.

Initially we have focussed on the gut response; later the systemic response can also be investigated. We should then be able to conclude to what extent variations in invasion or clearance explain differences in susceptibility to Salmonella. Genes involved in the response to Salmonellosis in different species (pigs and poultry) could also be identified. Using different Salmonella strains we could identify differences in the host-pathogen dialog.

We have had several meetings of the EADGENE Salmonella Working Group (INRA, Institute for Animal Health, Parco Tecnologico Padano, ASG-Lelystad, University of Cordoba, The Roslin Institute and R(D)SVS, University of Edinburgh) over the last five years, in which we have discussed our results and made a project outline. For some of the partners there has been a close relationship between EADGENE and SABRE results.

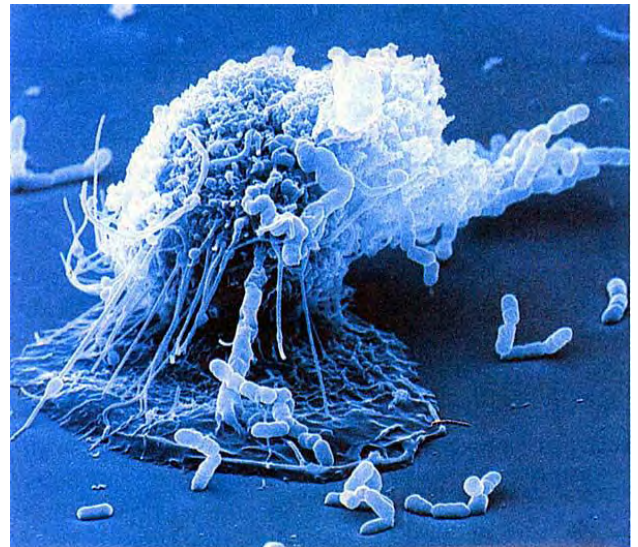


Photo: *Salmonella typhimurium*
Source: Rocky Mountain Laboratories, NIAID, NIH

In order to take into account the different infection models being studied and out-read parameters, an inventory was made of the tools being used. There was an exchange of Salmonella strains, PCR primers and protocols to isolate Salmonella RNA and protocols to culture pig intestinal cells, which took place in order to overcome major differences between institutes. The use of different lines and species of animals and the use of different Salmonella species was encouraged so that we could obtain more information about host response to Salmonella infection.

Host response upon a Salmonella infection: All partners have studied the host response upon infection with Salmonella; some have used *in vitro* models and some have used *in vivo* models. In addition, different strains of Salmonella were used. All partners have shared their "top 5" induced genes after Salmonella infection and the lists have been combined to depict genes that were found to be regulated in the different infection models within different species (chickens, cattle and pigs). TLR4 was often found to be induced in the different models, therefore we wrote an additional proposal to focus on the TLR4 response after Salmonella infection and in the Salmonella carrier state.

Salmonella response after interaction with a host: One partner worked on the Salmonella response in an *in vitro* model. We had discussed how to investigate the induction of the top induced Salmonella genes in the material that we had collected in *in vivo* experiments, but this was not possible due to problems with isolating bacterial RNA out the already collected *in vivo* samples. The time points of the *in vivo* experiments had been chosen so that the host response was optimal, but the bacterial amount was not optimal for the isolation of enough RNA.

Identification of specific cells which react after infection: Various partners worked towards the identification of specific cells which react after infection. Some obtained cells, such as neutrophils, from animals and measured the response after an *in vitro* infection with Salmonella. The response was measured in different ways. Some partners used q-PCR, others used microarrays and others used protein analyses. All these results were coupled back to the host response upon a Salmonella infection. Other partners investigated which cells responded after Salmonella infection with in situ hybridization of genes that were regulated according to microarray analyses in parts of the intestine of *in vivo* infected animals.

Combining results of different infection models, species, and salmonella strains: The results on the host side have been combined and an additional proposal has been written based on these results. It was not possible to combine the Salmonella response results as these were only obtained by one partner. Different salmonella strains were used in an *in vitro* model of HD-11 cells of chicken origin and the results from the various partners working on this will be combined in the near future.

Genomics of pathogen-salmonid interactions (WP7)

Bjørn Høyheim, Norwegian School of Veterinary Science, Norway

The EADGENE **fish pathogen working group** has been working on the genomics of pathogen/salmonid interactions and genetic resistance of the host. The group consists of partners from 6 different institutions from 5 countries and has been active since 2007. The working group brings together scientists in the fields of genomics and immunology from both the pathogen and the host side.

The group has focused on salmonids (**Atlantic salmon and rainbow trout**) and on two viruses: **Infectious Salmon Anaemia virus (ISAV)** and **Infectious Pancreatic Necrosis Virus (IPNV)**, but partners have also been working on **viral haemorrhagic septicaemia virus (VHSV)** and the bacterial pathogen ***Aeromonas salmonicida*** in rainbow trout.



Trout (Photo courtesy of INRA)

Salmonids were chosen because they are of high commercial value in Europe and therefore the impact of viral diseases represents a major economic cost. In addition, both salmon and trout are among the fish species that have been used most extensively for genome studies. Much of what is done on the genomic side can easily be used in both species because of the large degree of genetic similarity between them, i.e. genetic markers and microarray chips developed for one species can often be used on the other.

On the pathogen side, Infectious Salmon Anaemia Virus (ISAV) and Infectious Pancreatic Necrosis Virus (IPNV) were chosen since they both represent a major economic cost and because there are good challenge models for both viruses. The natural disease caused by ISAV is only found in Atlantic salmon (*Salmo salar*) and not in closely related species. However, results from one of the project teams show that rainbow trout are susceptible to ISAV through different routes of infection.

In order to investigate the host response to ISAV and IPNV, we focused on performing genome scans of Atlantic salmon challenged with IPNV, and performed transcriptome analysis on both Atlantic salmon (AS) and rainbow trout (RT) challenged with ISAV (AS and RT) and IPNV (AS).

- ◆ Two **genome scans of Atlantic salmon challenged with IPNV** were performed. This identified the position of the QTLs both in seawater (post-smolt) and the freshwater/fry (pre-smolt) stage of the lifecycle. The most **significant QTL was found in the same region on LG 21** in both instances, and **explains the majority of the genetic variation in resistance to IPN**.
- ◆ Several **transcriptome studies** have been carried out to identify candidate genes. Both differential expression and microarray experiments have been completed on salmon challenged with ISAV, resulting in identification of a set of genes that are differentially transcribed after infection. This includes immune-related genes as well as other genes and also a set of transcripts that has no known counterpart in the available protein databases. Although the high number of the genes found provided novel information and new insights, the unknown transcripts/genes that were revealed to be differentially regulated might play crucial roles in infection and immunity, and work aimed at uncovering their roles are the focus of further studies. At present transcriptome studies involving Atlantic salmon challenged with IPNV and rainbow trout challenged with ISAV are underway.
- ◆ At the same time the **genome of ISAV has been entirely sequenced**, and reverse genetics of ISAV after infection of rainbow trout has been completed. This opens up the possibility of a more detailed study of the host/pathogen interaction during infection.

In addition, transcriptome analysis was performed to enrich the available repertoire of VHSV induced genes. Results so far have shown that **gene expression profiles differ between the resistant and the susceptible trout families**. The profiles show differences in both the timing and quantity of up- and down regulation of genes.

The modulation of the cell response to the pathogen was also investigated by analysing Toll-like receptor (TLR) signalling cascades and complexity by PAMP from different pathogens as well as subversion of immune response by ISAV. The focus was on the TLR signalling cascade that is relevant for the expression of immune genes. Therefore, we have isolated and characterised three key factors of innate immunity from rainbow trout. These include MyD88 as an adaptor protein interacting directly with TLRs, Tollip as a regulator of TLR signalling, and serum amyloid A as an effector molecule that is induced by the activated Toll-like receptor signalling cascade. Our current sequence analyses reveal that these factors share a remarkable high degree of structural conservation with their mammalian orthologs suggesting that innate immune defence mechanisms are conserved over a period of more than 450M years, when piscine and mammalian lineage separated.

Comparative transcriptomic studies of mastitis in cattle, sheep and goats (WP7)

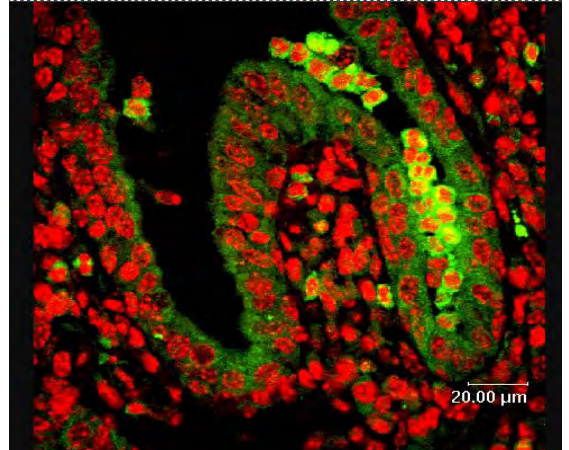
Hans-Martin Seyfert, RIBFA, Germany

The **EADGENE mastitis working group** has brought together the research activities and results from institutes located in seven European countries, working on **mastitis in cattle, goats and sheep**. Immune defence in the udder is organ specific, but is also modulated by the species of the host. The mastitis working group characterises the genetic basis of host specific properties of udder defence, using both *in vivo* and *in vitro* techniques.

Whole genome covering transcriptome profilings were conducted to identify key genes in udder and immune cells counteracting the attack of three pathogens: ***Escherichia coli*, *Staphylococcus aureus* or *Streptococcus uberis***. Experimental infections of cow udders, and also of immune cells from cows, were conducted with these three pathogens. All groups applied as common strategy to experimentally infect healthy animals with well characterised asseverated pathogens. This ensured controlled experimental settings.

The contribution of milk cells to counteract *S. aureus* infections of goat udders was also recorded. Selection lines with differing genetic predisposition for suffering from mastitis were established in sheep and the selection line specific response of their milk cells towards an *S. aureus* challenge has been recorded.

The data are exploited in different ways. A large data set from transcriptome profiling of infection related modulation of gene expression in the udder of the cow was used to evaluate the power and robustness of different biostatistical tools in EADGENE's Microarray Data Analysis Workshop (Nov 2006). Guidelines for proper data handling emerged as a result and were documented in several publications. Based on these experiences the data are currently being exploited for gene mining in different ways. Biostatistical and bioinformatical tools are being used to identify host genes contributing to the pathogen-specific, and eventually udder or cell type specific immune response. The data have also been used for hypothesis driven analysis into organ specific immune mechanisms and their pathogen-specific modulation.



Section through an udder quarter sampled 24h after infection with *E. coli*. Green fluorescence indicates expression of the bactericidal b-defensin peptide LAP. Arrows indicate Neutrophile Granulocytes having been recruited into the alveoli of the milk parenchyma as a consequence of infection. Nuclei are stained in red.

Analysis of the mastitis data carried out by the "Operational Genomics" working group is reported on the next page.

Table 1: Summary of the mastitis working group experiments

Infected for:	<0h	0h	1h	2h	3h	6h	8h	12h	24h	36h	48h	72h	Meta-analysis
Expt 1	<i>E. coli in vivo in cattle</i>												
						E,O		O	L,O				✓
	<i>S. aureus 24h in vivo in cattle</i>												
Expt 1						O		O	E,O				✓
	<i>S. aureus 72h in vivo in cattle</i>												
Expt 2								E,O				L,O	✓
	<i>S. uberis in vivo in cattle</i>												
Expt 3				E,O		L,O							✓
	<i>S. aureus in macrophages in vitro in cattle</i>												
Expt 4								E,O	O			L,O	✓
	<i>S. aureus in vivo in goats</i>												
Expt 5					E,O		I,O						✓
	<i>S. aureus in dendritic cells in vitro in sheep</i>												
Expt 6													
	<i>E. coli in vitro in primary Mammary Epithelial Cells (MEC) in cattle</i>												
Expt 7													
	<i>S. aureus in vitro in primary Mammary Epithelial Cells (MEC) in cattle</i>												
Expt 8													
	<i>S. aureus virulence factors in vitro in primary Mammary Epithelial Cells (MEC) in cattle</i>												

E = Early time response (no signs of mastitis), L = Late time response (clear signs of mastitis), O = Used in "overall" meta-analysis, Green = data

Meta-analysis of EADGENE's mastitis results (WP8)

Elisabetta Giuffra, Parco Tecnologico Padano

One way to integrate results obtained from **different groups under different experimental conditions** is to adopt a **meta-analysis** approach, with the goal of identifying commonalities between data sets which would not be evident by single analyses (e.g. genes commonly induced by a pathological state). This is possible thanks to the higher statistical power and diminution of false positives which are obtained when data sets are integrated by meta-analysis.

Data from the various mastitis experiments were collected, combined and re-analysed in the same way taking into account the contrasting experimental designs and sizes, host species and tissues, pathogens, arrays and time points (see table 1 on previous page). Pointillist (Hwang et al. 2005 Proc. Natl. Acad. Sci. 102, 17302-7 and 17296-301) was chosen as meta-analysis tool in order to deal effectively with the high heterogeneity of the final dataset.

The **11 gene lists obtained** (see below) were analysed by IPA (Ingenuity Package Analysis) to infer which genes and gene pathways were modulated in different mastitis biological systems:

1. Bovine specific response
2. Goat specific response
3. Sheep specific response
4. General, overall response (bovine, goat and sheep)
5. Early time response (bovine, goat and sheep)
6. Late time response (bovine, goat and sheep)
7. Early time specific (early but not late, bovine, goat and sheep)
8. Late time specific (late but not early, bovine, goat and sheep)
9. General, overall in vitro response (bovine macrophages and sheep dendritic cells (DC))
10. Late time in vitro response (bovine macrophages and sheep DC)
11. Early time in vitro response (bovine macrophages and sheep DC)

Overall, meta-analysis was able to cope very efficiently with data heterogeneity and allowed us to identify important features. Some **key results** are provided below (Genini et al. in preparation):

- ◆ Despite the small number of genes (7221) common between the different types of arrays used, the **immune response** (e.g. acute phase response signalling and antigen presentation pathways) was the most significant commonality emerging from the global dataset (list 4). The same picture was obtained from the meta-analysis of the bovine specific response (list 1), which was based on a higher number of genes (19452).
- ◆ The visualisation of fold change directions of the individual genes (magSigPro R package and Path Designer softwares) showed that **the pattern of up-or down-regulation is generally uniform across experiments** (e.g. bovine *in vivo* experiments: see figure 1).
- ◆ The meta-analysis highlighted **pathogen specific response signatures** for *E. coli*, *S. aureus* and *S. uberis*, e.g. the magnitude of inflammation induced by the *E. coli* challenge is stronger than the one induced by *S. aureus*.

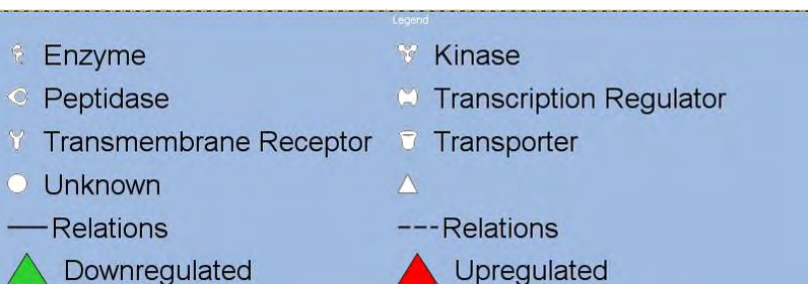
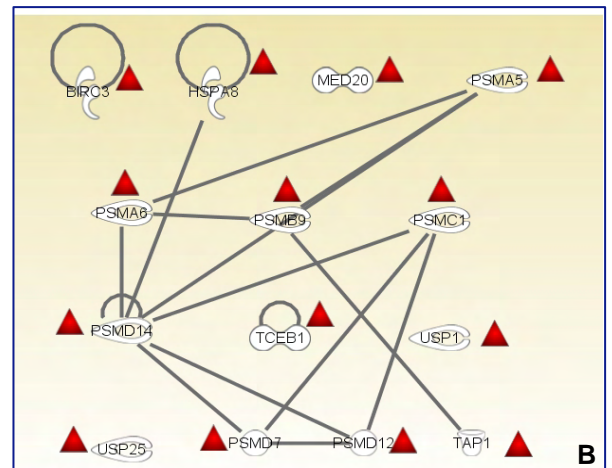
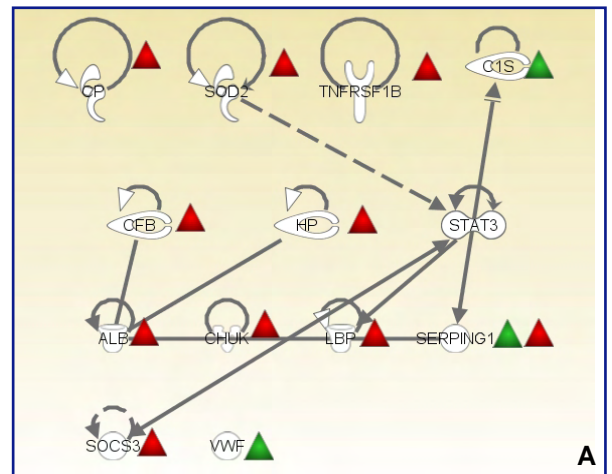


Figure 1: Direction of change of the genes belonging to two canonical pathways inferred by meta-analysis of the bovine microarray datasets. **A:** Acute phase response, **B:** protein ubiquitination

Technology transfer: From the laboratory to industry application (WP10)

Marjolein Neuteboom, EADGENE Technology EFFAB, The Netherlands

Since the start of the EADGENE project in 2004, many activities have been undertaken to bring research and industry closer together:

- ◆ **Club of Interest:** A club of interested industries has been formed around EADGENE and has provided the basis for the technology implementation related activities. Their particularities have been mapped by extensive enquiries, as well as their needs, possible animal populations and other material of interest.
- ◆ **Knowledge Management and Technology Transfer Industry Expert Groups:** During the first 18 months of the project two working groups of industry experts developed technology transfer guidelines and advised on contracts for industry–research cooperation in animal genomics. They also developed the concept of the industry days.
- ◆ **Industry Days:** Successful “Industry Days” conferences were organised in the UK in 2005 and (together with SABRE) in Rome in 2009. They consisted of industry/research presentations, highlighting results and outlooks of interest for industry.
- ◆ **Technology Transfer visits and industry participation in EADGENE working group meetings:** The EFFAB Technology Transfer Facilitators (TTFs) have visited companies across Europe setting up links between the EADGENE research partners and industry, mapping the needs within animal health genomics, and identifying gaps in order to enhance animal health implementation. Numerous industry-research co-operations have been initiated through these visits; the visits were especially important for linking partners across countries, across species, or between fields of business/research that had not been linked before. TTFs are independent experts, able to make links between groups independently, not marketing one research organisation, nor one country, nor one industry.

Based on the results of these enquiries, the expert groups, and the TTF visits, three large projects were formulated: Poultry Project; Data Comparison; and Ontology.

- ◆ **Technology Transfer Poultry project:** In this project researchers are in direct contact with the breeding industry in order to work towards applicable results. The research proposals were optimised with input from industry, the industry participants are regularly updated with progress and results, and they can give their input to the project. The researchers use commercial lines, bringing the research closer to industry practice. There have been very positive discussions about the continuation of this project in the future, as both industry and research see this as a win-win situation. This project provides necessary research for industry and provides the scientists with the commercial lines needed to continue their work. A follow up project between research and an animal breeder is being initiated. Please see the article of the next page for further information.
- ◆ **Animal Health Data Comparison across countries:** Genomics needs phenotypic data, but animal health data is scattered through Europe over a broad range of companies and institutes. Sensitivities and issues over ownership of the data make it especially difficult to bring these data together on a large scale. In the first phase of this project we mapped the existing data systems within countries (UK, FR, NL, DK) and the overview can be found on the EADGENE website (www.eadgene.info > Industry > Data Comparison). The second phase brought stakeholders together at two workshops in order to define a way forward. The conclusion from the first workshop was that there should be different pathways per species and therefore working groups were set up per species. There is a lot of interest from different parties, including DG Sanco, Copa-Cogeca, OIE, European Pig Producers, ICAR, to work towards a more comparable animal health data system in Europe. The first project proposals from the working groups are now in preparation and a final report will be published in the beginning of 2010 and will be available from the webpage mentioned above, along with presentations and summaries.
- ◆ **Ontology project:** A worldwide ontology for genetics and genomics is currently being set-up and it is important for industry to add their traits in this process to link research terms and definitions to their work. The process of collecting traits and definitions will be a time consuming exercise, with many repetitions and the risk of errors, so it was decided that we would focus on the development of a tool which would allow the adding of traits in a very structured manner and take away the need to add similar traits for every species. This tool is almost finished and the traits already collected will be entered. A follow up project proposal is now underway.
- ◆ **Phenotypic database:** The phenotypic database was developed to provide a virtual place where industry can indicate what material they wish to bring into pre-competitive scientific research. It is one of the outputs based on the inquiry amongst the Club of Interest in year 1. This database will provide researchers with a unique opportunity to search for possible partners from industry, and provides lots of benefits for both parties in terms of connections and collaborations. There is now a new version under development which will make it even more easy to find the right information and this tool will soon be integrated in the EADGENE website.

Poultry disease resistance projects for industry (WP10)

Olivier Demeure and Fanny Calenge, INRA

Technology transfer between science and industry is a particular priority for EADGENE. The technology transfer poultry project is guided by a working group with equal numbers of representatives from science and industry. The project aims to: 1) investigate epistasis effects on resistance to disease traits in chicken; and 2) search for SNP markers associated with resistance to Salmonella.

Experiment 1: Epistasis effects on resistance to disease traits in chicken

For the first part of the project, MarkerSet (Demeure and Lecerf, 2008), a tool created for SNP selection based on their informativity and location was used to select 1536 SNP covering the genome. 2380 animals with phenotypes for disease, composition or quality traits have been genotyped. The first QTL analyses are underway using the QTLMAP software which has been adapted to handle large number of markers. Different methods for epistasis analysis will be tested to estimate its impact on these traits. Results will then be transferred to a high quality, slow growing commercial line targeting the previously detected regions by genotyping 1000 animals (10 families) for 384 SNP.

Experiment 2: SNP markers associated with resistance to Salmonella

For the second part of the project, 1536 SNP were chosen. 194 of them had been formerly identified within the three QTL regions (GGA1, GGA2, GGA5) known for their effect on resistance to Salmonella carrier-state. Indeed GGA1 has been confirmed in these commercial lines at the younger age, GGA2 has been confirmed in the F2 cross between the inbred N and 6 lines (Calenge et al., 2009) and it has been shown that GGA5 is close to Sal1. The other 1342 SNPs were chosen for their informativity giving a good coverage of the rest of the genome.

This SNP set has been used to genotype 650 animals measured for resistance to Salmonella carrier-state, either at a younger age (at 1 week of age, to mimic infection of broilers) or at the adult age (at the peak of lay when hens may lay contaminated eggs which are the main source of human toxo-infections). Consideration of both traits is of importance since they appear to be negatively and moderately genetically correlated (Beaumont et al., 2009). A statistical evaluation of each SNP effect on carrier state and of each animal's genetic value is underway.

For **further information** please visit www.eadgene.info > Industry



Laying hen
Photo: Roslin Institute & R(D)SVS of University of Edinburgh



Pathogens interact with host cell
Photo: University of Otago microbiology.otago.ac.nz

Facilitating the exchange of ideas and expertise (WP3)

Hans-Martin Seyfert, RIBFA, Germany

A key method of increasing cooperation between institutes is to facilitate **short-term stays** (up to 3 months) of scientists at other organisations, allowing the face-to-face exchange of ideas and technical expertise, and fostering long-term research collaborations.

EADGENE has developed an easy-to-follow scheme to file applications - a “**Mobility Centre**” on the EADGENE web-site. All applications are independently evaluated by three reviewers and the financial support is awarded to successful applicants as a stipend.

The EADGENE short-term stay (STS) funding instrument has been highly successful in enabling motivated researchers to visit other organisations within the 15 EADGENE partner institutes, and also other institutes, including some in the USA, Japan and Australia. Twelve of the 15 EADGENE members and 13 non-members, including Eastern European Countries, have sent or received visiting scientists. These visits include exchanges of senior scientific staff, as well as post-docs and students.

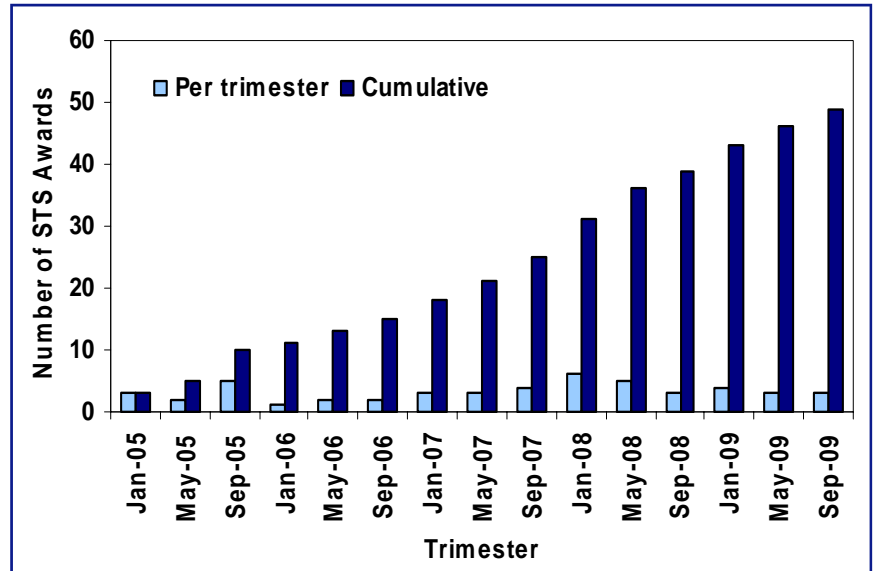
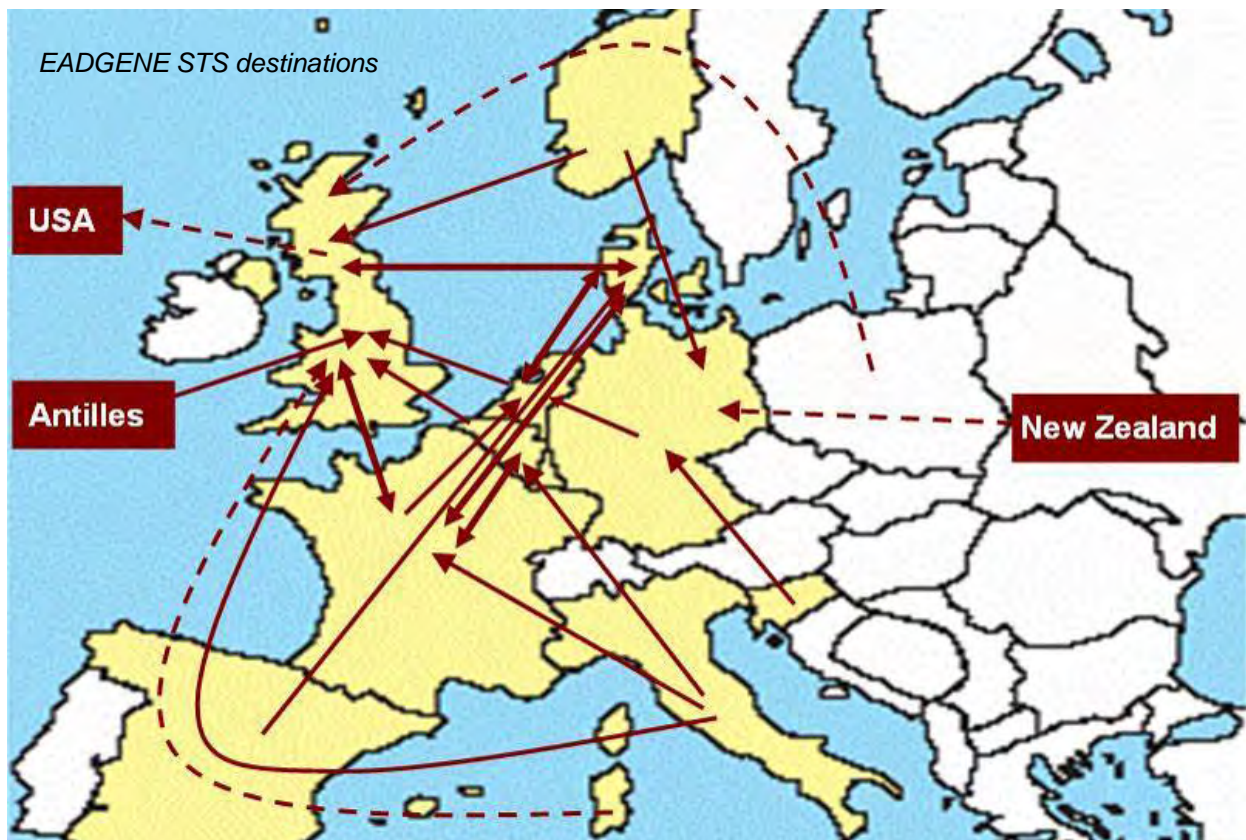


Figure 2. Number of STS Awards

The STS programme has been a continual success throughout the project. To date there have been **49 STS visits** funded with a total of **120,184€** (see figure2).

Recipients of EADGENE short-term stay funding write short reports upon completion of their visits and these are added to the EADGENE website (www.eadgene.info > Training & Careers > Short-term Stay Results & Reports). The results of STS visits have also been featured at EADGENE’s annual conferences in 2006, 2007, 2008 and 2009.



Increasing skills through training (WP9)

Diego Llanes, University of Cordoba, Spain

Laboratories involved in the EADGENE Network have extensive experience in organising scientific training at a number of levels, ranging from the individual training of students and visiting workers, through organised workshops, to specific training modules focussed on particular scientific topics. Over the last five years EADGENE has been involved in **developing and funding new courses and promoting and sponsoring existing courses**, including:

- ◆ **European Institute for Statistical Genetics** (Sept 2009, Sept 2007)
- ◆ **QTL-MAS Workshops** (Apr 2009, May 2008)
- ◆ **Study of Resistance Mechanisms in Animal Infectious Diseases** (Mar 2009, Nov 2006)
- ◆ **Cytoscape Software** (Nov 2008)
- ◆ **Microarray Data Analysis & Meta-Analysis** (Oct 2008, May 2006, Dec 2005)
- ◆ **miRNAs Workshop** (May 2008)
- ◆ **New Insights into Mixed Model Methodology with Applications to Genomics & Biostatistics** (May 2007)
- ◆ **Microarray Course** (Nov 2006)
- ◆ **cDNA Microarrays: Experimental Procedures and Data Analysis** (Oct 2005)
- ◆ **Genomics for Beginners** (Oct 2005)



Practical session at the EADGENE Microarray Data Analysis and Meta-Analysis Course

Educational materials such as bibliographies and protocols from courses are available from the **training pages of the EADGENE website** (<http://www.eadgene.info> > Training and Careers). These pages have become a place where scientific and industrial staff can find information about relevant courses and workshops held around the world on topics related to animal genomics and health. A list of some upcoming short courses is given on the last page of this newsletter, and a more comprehensive list of courses in 2010 is given on the website. We have also advertised the online course "Principles of Genetic Improvement" which has been developed from a module in the University of Edinburgh's MSc in Quantitative Genetics and Genome Analysis.

In addition to short courses and workshops, we have promoted longer-term courses, such as the 2-year European Master in Animal Breeding and Genetics (EM-ABG), under the Erasmus Mundus Programme. This course is co-ordinated by an EADGENE Partner, Wageningen University, and involves five other universities from across Europe.

Over the last five years the EADGENE Network has been involved in various training proposals with the aim of creating a stable framework for animal genomics and health education activities. We were involved in the initial proposal for an Erasmus Mundus Master on animal genomics that finally was carried out by another group of educational institutions, including EADGENE members, and in an Initial Training Network (ITN) proposal on animal health and genomics which unfortunately was not funded.



We have been successful in creating a **Collaborative Group on Animal Genomics Training within Veterinary Faculties** from members of the EADGENE Network: University of Cordoba, Norwegian School of Veterinary Science, University of Liège, Ecole Vétérinaire de Toulouse and University of Ljubljana. This group will offer a framework for training in animal genomics and health as part of the veterinary studies under the Erasmus programme. The aim is to establish a shared resource for training in the field of genomics for host-pathogen interactions, which could later possibly be expanded by making course materials available to animal science and agriculture courses at other institutions.

Training activities will continue to have an important place in the future activities of EADGENE, in the European Research Group (ERG) and in the proposed Coordination and Support Action (CSA). If we obtain CSA funding we will have the opportunity to stabilise and increase our training capacity in the field of animal genomics and health.

Ethical deliberation within EADGENE

C. Gamborg, K. Klint Jensen, G. Meyer, P. Sandøe, Danish Centre for Bioethics and Risk Assessment, University of Copenhagen

The identification of **ethical challenges, relevant to research in the field of animal disease genomics**, has been the task of a separate work package (WP 12.1), which has also been responsible for inspiring and supporting reflection and deliberation on such challenges within the network. Regardless of the approach – and very different methods have been used – key ethical challenges have consistently been identified as relating to vested interests, to communication with the public at large, and to the question of how to combine the use of animals with care and concern for animals in their own right.

Interviews and workshops: The initial approach consisted of an analysis of basic EADGENE documents. The second approach used a series of interviews with individual EADGENE researchers as the point of departure for suggesting a set of principles for ethical deliberation within the network and in public: moderation, openness, animal welfare as a research purpose and a goal in its own right, and continuous reflection on responsibilities. The third approach consisted of a series of workshops, involving network participants in discussions structured by the **ethical matrix** – a conceptual tool for supporting discussions on ethics and technology. Used as a framework for reflection, the ethical matrix is aimed at furthering exchanges between different points of view and at forcing participants to explicit ethical reasoning. Six workshops were arranged, including four regional workshops, using local cases as their starting point, and one external stakeholder workshop (organised in cooperation with Kate Millar, University of Nottingham).

Demands from the workshops have resulted in the production of a set of internal research guidelines for experiments on animals, and an on-line manual for ethical reflection. The 13 reports from the work package include a report on perceptions among external stakeholders, and an implementation strategy regarding ethical and societal issues. Finally, a paper reporting the workshops will soon be submitted to an international journal.

Interest group	Respect for		
	WELL-BEING	AUTONOMY	JUSTICE
PRODUCERS/INDUSTRY			
CONSUMERS/CITIZENS			
SCIENTISTS			
ANIMALS IN RESEARCH			
PRODUCTION ANIMALS			
ENVIRONMENT			

Ethical Matrix modified for EADGENE

Three major issues: The first major area of concern – **how to cope with vested interests and conflicts of interest** – has been discussed in relation to the growing prominence of intellectual property rights in the field of biotechnology. This is an area of outspoken disagreement both in society at large and among scientists in general, EADGENE participants included. In practice, a dilemma is often experienced between a general principle of openness and demands for confidentiality when a process of patenting is ongoing. Discussions have been hampered by a lack of established routines for coping with social interests within, and not just outside, the world of scientific research.

Exchanges within the network on the second issue, concerning **relations with the public at large**, have consistently been characterised by ambiguity. Basically, arguments have been put from two different positions. In one position, arguments are based on the assumption that the main purpose of communication is to gain trust, educate and convince the public at large about the rightful aims of the research project. The internal sphere of science is taken to be clearly separated from the external, public sphere. Another position, which has been much less explicit and clear-cut in interviews and at workshops, tends to combine internal reflection and discussions on the mores and means of the research with a broader societal discussion.

The challenge of **combining the use of animals with concern and care for animals** in their own right is the third major ethical issue that has remained on lists of ethical challenges throughout the project. In the initial reports, concerns regarding production animals were in focus, and it was suggested that the relationship between the economic interests of breeders and farmers, on the one hand, and the welfare of production animals, on the other, should be presented as issues for reflection within the network. At the internal workshops, attention was given to the conditions of the research animals. However, there was also concern about the risk that breeding for more robust animals might not materialise in better conditions for future production animals. At the external stakeholders' workshop, this concern reappeared as an ethical issue.

Lessons learned: Ethical challenges may be acted upon in a variety of ways and at different levels. At one level, internal reflection and exchanges may be stimulated. At another level, internal policies, rules and routines may be altered. And at yet another level, problems that seem to go beyond the scope of an individual project may be taken to the public sphere/and or to public authorities. The practical impact in the case of EADGENE has so far remained largely at the first level.

Discussions at the workshops and feedback forms completed by participants indicate that **the goal of raising awareness with respect to ethical challenges has been reached**. Thus, the ethical matrix may serve to structure discussions, but care should be taken to use it only as a starting point and an initial frame for discussions, not as an end in itself. The direct link to the actual research projects of the participants – as distinct from general ethics teaching – is important to make ethical reflection seem relevant to the researchers. At the same time, however, the challenge of meeting society at large in an informed and value based dialogue remains. It remains a challenge to consider how reflection and deliberation on ethical issues may and should affect the actual policies and management of research projects.

Communicating EADGENE's results to the wider scientific community

Caroline Channing, The Roslin Institute and R(D)SVS, University of Edinburgh

The communication of EADGENE's results to the general public, scientific groups and industrial communities is an essential output of the project.

Website: The EADGENE website (www.eadgene.info) provides information for the general public, industry and scientists on EADGENE's research, news, events, training courses, career opportunities and other information relevant to the EADGENE project. The website also provides access to the secure Intranet area for EADGENE's partners.

Newsletters: The two EADGENE newsletters, "EADGENE News" for the general public and industry, and "Network News" for the EADGENE Partners, are published three times a year, with 15 editions of each to date. All the back issues of these newsletters are available for download from the EADGENE website (www.eadgene.info > News & Publications).



Promotional materials and communication tools: The Communication Team has provided EADGENE's scientists with promotional materials (e.g. posters and leaflets), tools (e.g. online meeting tools, templates) and guidance, to encourage the open flow of communication and help them to promote the achievements of the EADGENE Network.

Scientific Publications: Peer-reviewed scientific papers provide a concrete and lasting output from any scientific project. EADGENE has not only funded the research reported in these papers, but has also helped bring scientists together in working groups which have produced multi-partner papers, and has paid for publications to be made open-access for everyone through online journals. A list of EADGENE publications can be found on the EADGENE website (www.eadgene.info > News & Publications).

Conferences, workshops, and meetings: EADGENE has held annual conferences in Partner countries every year since the start of the project:

- ◆ Brussels 2005: "EADGENE – its possibilities and its possible applications"
- ◆ Oslo 2006: "EADGENE Days 2006"
- ◆ Utrecht 2007: "Genomics for Animal Health"
- ◆ Edinburgh 2008: "Animal Disease Genomics: Opportunities and Applications"
- ◆ Paris 2009: "Genomics for Animal Health: Outlook for the Future"

These annual EADGENE Days conferences have been very popular and have helped increase the knowledge, understanding and recognition of EADGENE among relevant scientific and industrial communities through the presentation of EADGENE's research results. The communication of the results presented at these conferences continues through the conference pages on the EADGENE website (www.eadgene.info > Events). EADGENE has also organised numerous workshops on topics such as analytical tools, specific diseases (mastitis, *E. coli*, Salmonella, fish pathogens), and ethics, and has organised satellite workshops and sessions at major international conferences (e.g. the EAAP conferences).



Photos: Delegates at the EADGENE Days 2009

EADGENE days 2009: "Genomics for Animal Health: Outlook for the Future"

The fifth and final EADGENE conference on "**Genomics for Animal Health: Outlook for the Future**", took place on 12th-15th October 2009 at the **Museum National d'Histoire Naturelle** in Paris. Over 170 delegates attended the meeting, which also included two open satellite workshops, with 51 organisations represented, from 17 countries and 5 continents (Europe, North America, South America, Australia and Asia).



Marie-Hélène Pinard van der Laan opening the conference

The 4-day event started on Monday 12th October with a workshop on **Bioinformatics and Data Handling for Next Generation Sequencing**. This workshop focussed on the scientists' experiences of a variety of bioinformatics and data handling methods for next-generation sequencing (NGS) data, with various EADGENE partners presenting the results of their NGS research. These NGS technologies, where a single machine can rapidly sequence several genomes, have greatly increased the amount of data to be handled by bioinformatics, and this presents scientists with fresh challenges.

The main conference sessions took place on Tuesday 13th and Wednesday 14th October. The EADGENE Co-ordinator, Marie-Hélène Pinard van der Laan (INRA), opened the conference by reflecting on the previous EADGENE conferences and emphasising the relevance of our venue to genomics research during Darwin's anniversary year, celebrating the 200th anniversary of Charles Darwin's birth and the 150th anniversary of his famous book "On the Origin of Species".

Session 1, on "**Technologies and Approaches**," opened with a keynote presentation on next generation sequencing technologies and bacterial genomics by Nick Thomson of the Wellcome Trust Sanger Institute. Nick gave an overview of the technologies and then went on to discuss how NGS methods have been used to reveal the evolution and diversification of the salmonellae, from the common ancestor millions of years ago to the many types we see today. This was followed by a second keynote presentation by Michel Georges (ULg), on the effect of the CLPG mutation on the microRNA catalogue of skeletal muscle using high throughput sequencing.

Johann Detilleux (ULg) gave an overview of genetic-epidemiological models, and emphasised the need to be careful when moving from genetic associations to genetic causation. The "Phenotype Gap" was tackled by Liz Glass (UEDIN): with recent advances in sequencing technologies there are increasing amounts of genotype information available to us, but to discover genetic markers or polymorphisms that control variation in a trait, you need two linked features - the phenotype and the genotype.

Florence Jaffrezic (INRA) presented some gene network results from the EADGENE and SABRE workshop on the post-analyses of microarray data. There are specific advantages of network inference from microarray data: they are based on gene expression measurements; there is no need for annotations; and they can allow us to discover new relationships between genes not known in already existing databases. However, there is a need for biological validation of these new links.

Jakob Hedegaard (AU) described the EADGENE "technological triangle" experiment, where three Partner laboratories have conducted a microarray quality control experiment which is repeated at each of the three laboratories using their specific equipment and protocols. The experiment indicates that the results from DNA microarrays are reproducible, that affected gene-sets are very reproducible, but affected genes are less reproducible. Henri Woelders (ASG) concluded the first session with a lecture on systems biology in animal sciences.

Session 2 focussed on the "**Research Results**." In his keynote presentation, Dan Bradley (Trinity College Dublin) gave a fascinating overview of population genetics and disease genetics, using the domestication of cattle across the world as an example.

The next talk highlighted a research result which has already been implemented by a breeding company: the identification of a major QTL for resistance against IPN in Salmon. This research, presented by Thomas Moen of AquaGen, was in agreement with work by EADGENE's fish pathogen working group (Houston et al. 2008).

The following presentations gave very specific examples of EADGENE research results: Rachel Rupp (INRA) described gene expression profiling in divergent lines of sheep for enhanced insight into genetic resistance to mastitis; and in two related presentations Olivier Demeure and Fanny Calenge (INRA) updated delegates on the progress of EADGENE's technology transfer poultry projects.



Jakob Hedegaard presenting the Technological Triangle

EADGENE days 2009 (continued)

Ethical consideration and awareness has been emphasised throughout the EADGENE project, so Karsten Klint Jensen (CeBRA) described an ethical deliberation tool which has been used with some success during our ethical workshops.

The highlighting of results of EADGENE funded short-term stays has become a regular feature of EADGENE conferences, particularly as it often gives our younger scientists the chance to present their results. This year Cristina Arce-Jimenez (UCO) presented her work on NLRs in porcine macrophages and dendritic cells and Joseph Powell (UEDIN) talked about association mapping models. This session ended with a series of 5 minute short communications, which allowed those people who would normally submit a poster to give a quick overview of their work.

The conference cocktail session was held in the stunning venue of the **Galerie de l'évolution**. Delegates were able to explore the exhibits in the Galerie, which was closed to the public, before enjoying drinks and canapés on the balcony over-looking the promenade or "caravane" of preserved mammals.

The next day started with the "**Focus on Pathogens**" in session 3. Our original keynote speaker, Rino Rappuoli (Novartis), was at the last minute unfortunately unable to join us due to an emergency meeting at the Italian Ministry of Health. However, he kindly arranged for his colleague, Vega Masignani, to replace him and she gave an extremely interesting lecture on pathogen genomics, including examples from various pathogens such as *Neisseria meningitidis*, and *Streptococcus pneumoniae*. She concluded that "Genome-based approaches have proved successful for the identification of novel candidates for the development of vaccines against important human pathogens."

Mark Stevens (IAH) focussed on Salmonella & *E. Coli*, both of which are pathogens of particular interest to EADGENE's working groups, and John Fazackerley (UEDIN) talked about emerging and re-emerging viruses, highlighting the threats from rodent-borne and vector-borne infections.

Espen Rimsted (NSVS) described the results coming out of EADGENE's fish pathogen working group, who have projects focusing on salmonids (Atlantic salmon and rainbow trout) and on the viruses Infectious Salmon Anaemia Virus (ISAV), Infectious Pancreatic Necrosis Virus (IPNV), and Salmonid Alphavirus (SAV).

The role of TLR4 in resistance to Salmonella infection and carrier state was discussed in Philippe Velge's (INRA) talk. He concluded that TLR4 could be a good marker of selection to improve animal resistance to Salmonella in hens but that TLR4 gene expression is not always correlated with resistance to Salmonella carrier state in chicks and piglets.

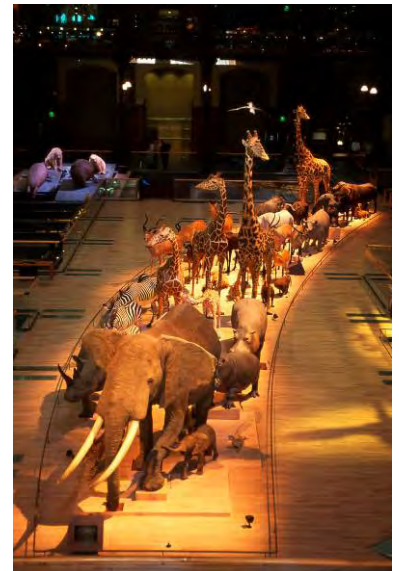
Hilde Smith (ASG) discussed genome based approaches to identify virulence factors and vaccine candidates, using the particular example of her work with *Streptococcus suis*. Finally, Wolfram Petzl (LMU Munich) described the development of in vivo mastitis models, giving the example of an EADGENE study where "cross-talk" between udder sections was detected, and emphasising the importance of taking these kinds of effects into account when developing such models.

The final session of the main conference, on "**Breeding to Improve Animal Health**", took a different format from the previous three sessions. Three speakers gave presentations on the scientific view of genomic selection (Theo Meuwissen, Institute for Animal and Aquacultural Sciences, Norway), the industry view of genomic selection in cattle (Sander de Roos, CRV), and the industry view of genomic selection in chickens (Albert Paszek, Cobb). This was followed by a roundtable discussion during which the audience was free to pose questions to the panel which was composed of the three speakers, plus Didier Boichard (INRA) and Alan Archibald (UEDIN).

The closing speech was given by Muriel Mambrini, head of INRA Jouy-en-Josas, who emphasised the various achievements of the EADGENE Network over the previous 5 years, and thanked the Coordinator, Marie-Helene Pinard van der Laan and the other members of the Network for their hard work towards making the project a success.

The main conference officially ended on the 14th October 2009, but in actuality the conference continued on the next day with the satellite workshop on Mastitis. This workshop was divided into two sessions: Biology of Mastitis, and Meta-analysis. After a series of presentations the speakers from both sessions participated in an open discussion session.

For **further information** please visit the EADGENE website at www.eadgene.info > Events > EADGENE Days 2009, where most of the presentations are now available for download.



The "Caravane" in the Galerie de l'évolution.

Photo: MNHN service audiovisuel



"Breeding to Improve Animal Health" discussion panel



European Animal Disease Genomics Network of Excellence

Network News N°15, December 2009

Upcoming Events

Plant and Animal Genome (PAG) XVIII

9-13 Jan 2010, San Diego, USA

<http://www.intl-pag.org>

5th International Cattle Breeders Round Table 2010

11-13 Jan 2010, Sandbjerg, Denmark

Email: ksm@agrsci.dk

5th IDF International Mastitis Conference 2010

21 - 24 Mar 2010, Christchurch, NZ

www.idfmastitis2010.com

14th QTL-MAS workshop

17 - 18 May 2010, Poznan, Poland

<http://jay.au.poznan.pl/qtlmas2010>

International Symposium on Animal Genomics for Animal Health (AGAH)

31 May-2 Jun 2010, Paris, France

<https://colloque.inra.fr/agah2010>

Poultry Science Association

11-15 Jul 2010, Denver, USA

<http://www.adsa.asas.org/meetings/2010>

International Society for Animal Genetics Conference 2010 (ISAG)

26-30 Jul 2010, Edinburgh, UK

www.isag2010.org

9th World Congress on Genetics Applied to Livestock Production

1-6 August 2010, Leipzig, Germany

www.wcgalp2010.org

EAAP 2010

23-27 Aug 2010, Crete, Greece

<http://www.eaap2010.org>

Contact Us

Network News is the EADGENE
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Management Communications

Following on the 6-month extension which was granted by the EC, the EADGENE Network of Excellence will officially end on 28th February 2010, and we will then be required to submit our final reports to the EC.

All EADGENE partners have agreed to follow up the Network in a durable way by creating a "European Research Group" (ERG), and the proposal document for the ERG is currently being finalised and will very soon be ready for signing by the partners.

The next deadline will be the submission of our Coordination and Support Action (CSA) proposal for EADGENE, with a deadline in January.

Upcoming Training Courses

10th International Long-Oligonucleotide Microarray Workshop

3-8 Jan 2010, University of Arizona, Tucson, Arizona

Please contact David Galbraith (galbraith@arizona.edu) or Georgina Lambert (georgina@cals.arizona.edu)

Genomic Evaluation: Short Course

11-15 Jan 2010, Colorado State University, Fort Collins, Colorado, USA

Please contact Dr. Denny Crews (Denny.Crews@ColoState.edu) or Dr. Mark Enns (Mark.Enns@ColoState.edu).

2010 Armidale Animal Breeding Summer Course

27 Jan - 5 Feb 2010, University of New England, Armidale, NSW Australia

<http://www.personal.une.edu.au/~jvanderw/aabc.htm>

11th Fish Immunology Workshop

11-15 April 2010, Wageningen University, The Netherlands.

The objective of the present workshop is to provide participants with advanced knowledge, both theoretical and practical, on the immune system of fish and shellfish.

http://www.cbi.wur.nl/UK/fish_workshop/

Working with the Human Genome Sequence Workshop

10-12 May 2010, Wellcome Trust Genome Campus, Hinxton, Cambridge, UK

This workshop provides an intensive introduction to bioinformatics tools freely available on the internet, focusing primarily on the Human Genome data.

<http://www.wellcome.ac.uk/Education-resources/Courses-and-conferences/Advanced-Courses/Workshops/WTX034160.htm>

Molecular Basis of Bacterial Infection: Basic and Applied Research Approaches

9-15 May 2010, Wellcome Trust Genome Campus, Hinxton, Cambridge

<http://www.wellcome.ac.uk/Education-resources/Courses-and-conferences/Advanced-Courses/Courses/WTX026211.htm>

Next Generation Sequencing

18-24 Jul 2010, Wellcome Trust Genome Campus, Hinxton, Cambridge, UK

<http://www.wellcome.ac.uk/Education-resources/Courses-and-conferences/Advanced-Courses/Courses/WTX056918.htm>

Design and Analysis of Genetic-based Association Studies

23-27 August 2010, Wellcome Trust Genome Campus, Hinxton, Cambridge

<http://www.wellcome.ac.uk/Education-resources/Courses-and-conferences/Advanced-Courses/Courses/WTD038867.htm>

