

EDITORIAL

This is the thirteenth EADGENE Newsletter.

We have articles about genomic selection and the EADGENE data comparison subproject is described.

Olivier Demeure is our "in the Picture" guest.

The date of the next EADGENE industry days is announced.

Angela van der Sanden & Marjolein Neuteboom

Genomic selection: revolution in animal breeding

By Mario Calus and Roel Veerkamp, ASG - Lelystad

Genomic selection is being branded one of the most significant developments in animal breeding since the introduction of BLUP to estimate breeding values. Nowadays up to 50,000 genetic markers are available for some species and can be measured for about €200,- per animal. The Netherlands are at the forefront of the introduction of genomic selection. The Animal Science Group (Wageningen and Lelystad) is closely involved in this development and its implementation, and is collaborating with the EADGENE Club of Interest members CRV and Hendrix Genetics.

An animal receives half of its genes from its father and half from its mother. An important question is which specific genes an animal receives from both parents. In traditional breeding practices, an animal's own performance, or that of close relatives, is used to estimate whether it predominantly received the "good" or "bad" genes of its parents. These performance tests are, however, in some cases expensive and time consuming. Genomic selection has the

potential to yield accurate breeding values for animals without the time delay and at considerable cost reduction for a breeding programme.

Genomic selection breeding values

Genomic selection uses a large number of markers, i.e. 50,000 markers, that are spread throughout the genome. In this way, the markers 'mark' the genes, without the genes themselves or their location on the genome being known. For each of the 50,000 markers a breeding value is estimated, and the sum of all marker effects is the genomic breeding value for an animal. A major challenge is the estimation of the breeding values for each marker. This is done by using what is termed a reference population. Generally this population consists of at least 1,000 animals, for which accurate breeding values are available (based on information from sibs or progeny) and for which all used markers are known. A statistical model is used to measure how these reliable breeding values can be 'divided up' in the effects of all markers.

Implications for breeding programmes

The most extreme application of genomic selection in animal breeding involves completely dispensing with progeny- or sib-testing and instead only testing animals for their markers. As a result of this, the best animals can be promoted to breeding animals on the basis of genomic selection, shortening the generation interval considerably.

Furthermore, genomic selection enables us to test progeny of a larger number of different animals relatively cheaply. The chance of identifying a new top breeding animal with an outcross pedigree thus increases. In conclusion, genomic selection has the potential to increase genetic advancement in breeding programs, to shorten the interval between generations, to reduce costs and to reduce inbreeding.



Hyperlinks

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(internal newsletter)



"YES, THERE ARE A FEW QUESTIONS ABOUT HIS PARENTAGE."

www.CartoonStock.com

EADGENE Industry Days*

3rd and 4th June 2009, Rome, Italy



The goal of the EADGENE Industry days is to further **encourage the integration of research and industry**. Now that we are near the end of the EADGENE project we will once more organise this special event, following on from the successful and well appreciated EADGENE Industry days of 2005, where a lot of fruitful **networking** took place.

The meeting will take place on the afternoon of 3rd June and the morning of 4th of June 2009, in the FAO building in Rome. During these days hot topics will be highlighted from both the industry and the research point of view. There will be plenty of opportunities to discuss and further brainstorm on these topics and there will be **extensive opportunities to network**.

Please mark these dates in you diary!

* the meeting will be organised satellite to the EFFAB annual meeting and the EFFAB-FAO biodiversity workshop (both members only)

EADGENE Data Comparison Project

Data comparison is one of the four subprojects of EADGENE's WP 10 (Technology Transfer). Phase 1 is completed and a summary is presented here.

Relevance to the goals of the European Union for animal disease control

The impact of epidemic livestock diseases can be devastating on farmers and the economy as a whole – in a specific country, a continent or even globally. The new Animal Health Strategy 2007-2013 for the European Union (EU) is striving for increased collaboration between EU member states to increase the prevention of animal health related problems before they happen and to be ready to manage outbreaks and crisis more effectively. The strategy builds on the current animal health legal framework in the EU and recognises the need for replacing the existing series of linked policy actions by a single regulatory framework with an incentive-orientated approach and an appropriate sharing of costs and responsibilities.

For plans to gradually develop an EU harmonised scheme, feasibility studies are necessary before concrete proposals can be made. Animal movement and health data is a key source of information in the effective management of disease prevention and outbreaks. The feasibility of harmonising the collection of animal health data within the EU is therefore of great interest.

The current project was a pilot study to provide an overview on animal health data recording in four EU member countries. This could help to assess the feasibility for harmonisation and increased collaboration in the collection of animal health data in the EU, which would be a major step in achieving the overall goal of the new EU animal health strategy. The methodology of this study in itself is a potential catalyst to increased sharing of relevant knowledge and collaboration between countries.

Methodology

The project was mainly concerned with gathering primary information on the national structures in animal health data collection for the Netherlands, France, UK and Denmark through an international team of researchers. This was achieved through interviews and discussions, held with representatives of government departments, government agencies, academics, animal scientists, veterinarians and industry organisations within each country. As the methodology was not only a process of gathering information, but also of building an extended network for the exchange of information on the research subject. The overview was supplemented with secondary information sourced through literature searches.

Main findings

1. The collection of animal health data within the four EU countries is strongly shaped by the national historical scale and organisation of animal production for each species, as well as by national and EU regulations, which to a large extent are being policed by official bodies.
2. Most of the currently existing data bases for animal health data have not been designed with the potential for exchange of data and accessibility for a variety of stakeholders in mind. However there are trends for more sophisticated integrated data bases with electronically data input, which are stronger in some countries than in others.
3. Generally animal health data collection policed through official bodies is more harmonised than that collected on a commercial level.
4. The availability of data collected to meet requirements of official bodies is limited. There is a lot of information potentially available from what is being collected through bodies such as animal breeding and milk recording companies. As a result of commercial competition, the latter pool of data is more difficult to access. Differences in accessibility exist between countries.
5. Animal health schemes and levy boards provide incentives for greater harmonisation and transparency of what is being collected on a commercial level on farms and in abattoirs.
6. The various stakeholders throughout the food chains in Europe are increasingly aware of the need for harmonised and accessible animal health data.

Conclusion

This pilot study gives an initial indication for potential opportunities and the feasibility of greater harmonisation and transparency in animal health data collection across EU countries. However, the main outcome is that more work is necessary to develop a feasible methodology to compare data across countries. Stakeholder groups, which have been found to be particularly proactive in collaboration within countries, such as commercial vets organised in this respect or organisations dealing with health monitoring, should be targeted to encourage cross-national collaboration/ networks in animal health data collection and assist the project team in championing cross country and cross sector learning and knowledge transfer.

More information about data comparison and the report are available at www.eadgene.info > Industry > Data Comparison Project.

In the picture:

Olivier Demeure

I am now a project scientist in the department of animal genetics, INRA institute, but it has been a long story.

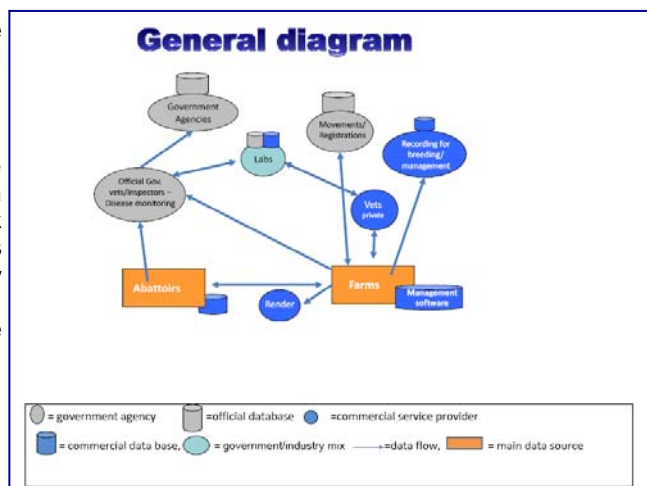


Everything started in November 1977 in Auray (Brittany, west of France). After graduating with a masters degree in 2000, focussing on meat quality with physiological approaches, I did a genetic PhD in Toulouse on refining localisation of QTL affecting growth and fatness in pigs. During this PhD, I spent 3 months in Urbana-Champaign (Illinois, USA) to learn about transcriptomes analyses. After three nice years in Toulouse, I did a post-doc in East Lansing (Michigan, USA), focussing on the lipid metabolism, mostly with biochemical and molecular approaches. Being almost able to speak English and having learned a lot from other research organisations, I went back to my sweet Brittany, in Rennes to work on... QTL affecting fatness in chicken (sounds like déjà vu, no?).

My project now is focussed on identifying QTL (testing additive effects or epistatic effects) and refining QTL positions (backcross design, identical by descent analyses...). This project is shared with other scientists and also includes use of transcriptomics data.

Within EADGENE, I am part of the workpackage 10 "technology transfer", managing a project with the aim of studying the extent of interaction (epistasis) between QTL affecting chicken coccidiosis sensibility.

In a parallel world, I am married and enjoy raising Laura (4) and Hugo (1) who give me a lot of joy, fun, short nights and grey hairs. Fortunately, I still have time to spend with my friends, I love playing soccer with them. I also like travelling, comic strips (French and Belgium ones), rock bands (those from Great Britain are the best), and filling EADGENE time sheets.



This "General diagram" is a description of animal health data recording systems. Specific diagrams were made per specie per country.