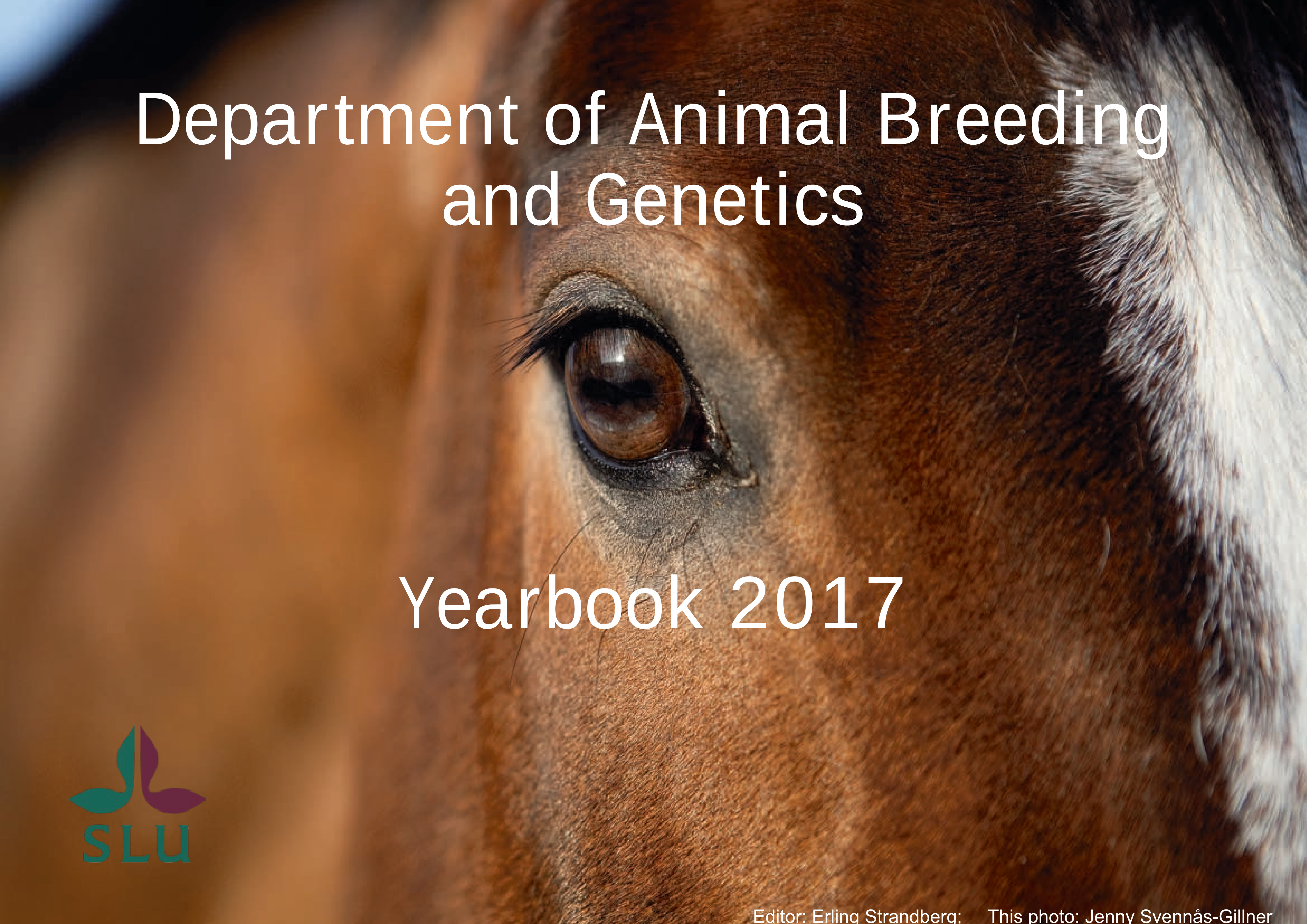
Department of Animal Breeding and Genetics

Yearbook 2017



Editor: Erling Strandberg;   This photo: Jenny Svennås-Gillner

About the department

- Our vision at the Department of Animal Breeding and Genetics is “Improved use of animal genetic resources”

- To achieve this vision we perform research and education within two areas of science: Molecular Genetics & Bioinformatics and Quantitative Genetics & Animal Breeding.

- The department comprises the Animal Genetics Laboratory which does parental testing as well as various molecular genetic tests of disease and coat colour genes.

- Furthermore, we host the SLU Biobank, the SLU Centre for Bioinformatics (SLUBI), and the Interbull Centre. SLU Biobank is SLU’s overall Biobank and acts as a resource for sample-related research. SLUBI is tasked to provide bioinformatics support across SLU by acting as a hub with dedicated bioinformaticians based at every faculty. The Interbull Centre is an internationally recognized institution; it provides genetic information services and applied research for improvement of livestock to a worldwide network. It is also the only European Union Reference Centre (EURC) in the field of animal breeding.

- We do fundamental research on molecular genetics, bioinformatics and systems biology, which later can be applied in breeding programs, e.g., disease gene tests and genetic evaluations. We do research on data from experiments at the Swedish Livestock Research Centre Lövsta, from own field studies in commercial farms and sometimes in natural populations. We also perform research on data from the industry, simulated data and data from the public domain.

- We are an international work place with PhD students and staff from more than 20 countries. Currently we have about 50 fulltime employees and about 20 PhD students.

- We believe that excellence in teaching is a core value of universities and we teach at both BSc and MSc levels in several programs at SLU: the Animal Science MSc program, two professional programs – Animal Science and Veterinary Medicine, the Ethology and Animal Welfare and the Equine Science BSc programs as well as the new BSc program Sport and Companion Animals.

- Some key figures:

  We have increased the number of peer-reviewed publications over the last three years, from around 55 in 2012-2014 to almost 70 in 2015-2017.

  On average we have had six PhD students defending their theses every year the last six years, in 2017 eight students became doctors.

- For more information about our department go to https://www.slu.se/en/departments/animalgenetics/

- The following pages will give some examples of our teaching and research projects that are ongoing or that have recently finished.

Important events 2017

- This was the first year in which we have had a shared leadership at the department. Officially Lotta Rydhmer is head of department and Dirk-Jan de Koning is deputy head. However, they share the leadership as much as possible.

- One of the great profiles in animal breeding and especially regarding international genetic evaluation of dairy cattle, Larry Schaeffer, became honorary doctor at SLU.

- Erik Bongcam-Rudloff became professor in bioinformatics.

Eight of our PhD students successfully defended their theses this year:

- Merina Shrestha: Genetics of equine insect bite hypersensitivity and genetic diversity in horses
- Amabel Tenghe: Milk progesterone measure to improve genomic selection for fertility in dairy cows

- Christina Rochus: Genetic diversity of domestic sheep. Examples from Swedish and French populations
- Kim Jäderkvist: Exploring the horse genome to elucidate the genetics of gaits and athletic performance
- Agnese Viluma: Applying massive parallel sequencing technologies to unravel the genomic complexity in domestic species
- Tomas Klingström: Data integration and handling. Building an informatics platform for research integrated biobanks
- Berihu Gebremedhin Welderufael: Genetc evaluation of susceptibility to and recoverability from mastitis in dairy cows

- All these PhD theses are publically available online: https://pub.epsilon.slu.se/

- Four of our professors turned 60 this year, Göran Andersson, Erik Bongcam-Rudloff, Hossein Jorjani (well, actually in 2018), and Erling Strandberg. To commemorate this we arranged a lunch-to-lunch seminar 30 November to 1 December with a large number of invited speakers, some of which are shown in the picture below.

- During the year we have done a substantial amount of teaching in a master program in Animal Production at the University of Rwanda

- Interbull Centre, which is a European Union Reference Centre responsible for the harmonisation and improvement of the methods of performance testing and genetic evaluation of cattle, became ISO 9001 certified during the year.

Some of our educational programs

Bachelor program: Sport and Companion Animals

This Bachelor program is for those who would like to work professionally with sport and companion animals, either in a company of their own or in one of the many companies working with animals.

The area of sport and companion animals is increasing and has a large economic turnover. The growing interest among owners and in the society as such, together with increasing focus within research, creates a promising future for this field of work. This also creates increased demands on knowledge and professionalism among those working in the area.

This program, which has animal science as scientific basis, gives good knowledge about our most common sport and companion animals, such as horses, dogs and cats. The program gives good knowledge about how animals function and their needs, their role in society and insight into business development within this area.

The sport and companion animal area is characterized by many small and medium-sized companies. However, also governmental organisations, NGOs, animal societies and feed companies are potential employers. Here are some examples of what the students may work with after graduation:

- consultation, advice to owners
- product development
- activities in connection with competitions
- breeding plans
- teaching
- animal protection and welfare
- journalism and communication.

Example of courses:

- Ethology and animal protection
- Animal biology: biochemistry, cellbiology, physiology
- Nutrition and feeding
- Animal breeding
- The biology and use of horses
- The biology and use of dogs and cats
- Entrepreneurship

The program is given in Swedish.

Photo Katja Nilsson

Some of our educational programs

Master program in Animal Science

Our domestic animals are of great importance to our society. Farm animals primarily supply us with food and clothing, while our sport and companion animals bring us other benefits.

Whatever we expect of our animals, it is important that they both function well and are in good health. We also have to consider the various needs of our society.

Through research, education and advisory work, animal scientists can improve the production and wellbeing of our animals. Animal science plays an increasing role internationally when it comes to improving and developing animal husbandry practices. The programme has a duration of 2 years and prepares the students for a number of careers. The interest in animals and their interactions with man and society has led to a strong job market for animal scientists. The education gives a degree of Master of Science with a major in Animal Science. As an animal scientist you can work nationally or internationally with research or product development, agricultural/animal advisory services and evaluation, but there are also exciting career opportunities in teaching, information and journalism.

By choosing courses and subject of the master thesis the student is able to create an individual profile for their studies within subdisciplines such as Ethology/Animal Welfare/Animal Environment, Nutrition/Production Biology or Genetics/Breeding. The programme ends with a Master degree project of 30 credits.

The programme gives a scientific basis enabling the student to identify, analyse and solve problems while taking the animals' and society's needs into consideration. Teachers within the programme are researchers from various disciplines and the students are kept in contact with current research. The courses include various teaching methods, e.g. lectures, laboratory work, seminars, study visits and shorter projects.

Example of courses for students interested in animal breeding and genetics (all are 15 ECTS):
- Animal science - a scientific approach
- Genome analysis
- Bioinformatics
- Animal genetics - health, behavior and welfare
- Designing breeding programs
- Research training and projects

For more information go to:
https://www.slu.se/en/education/programmes-courses/masters-programmes/animal-science/

Milking robots measure both udder shape and temperament of dairy cows

More and more cows are being milked in a milking robot (Automatic Milking Systems, AMS). Apart from making it possible to measure milkability objectively, it is also possible to get information about the udder shape and location and the cow's temperament.

When the robot is attempting to find the teats, it measures their position and height over the floor. These data can be used to calculate, e.g., udder depth (height) and teat placement.

We found that these measures were almost perfectly genetically correlated with similar measures from the type scoring (genetic correlation was 0.9) done by technicians.

The robot also records if there are problems when attaching the teat cups and if the cow kicks off the teat cups.

The number of milkings with teat cup attachment problems was strongly genetically correlated with temperament as reported by the farmer in connection with the type evaluation. The calmer cow (according to the farmer), the fewer problems with teat cup attachments. The genetic correation between these two measures were 0.71 for Swedish Red and weaker, 0.44, for Swedish Holstein.

In summary, this means that we can get udder conformation traits and temperament information on all cows milked in AMS, even if they are not part of the conformation (type) evaluation.

These result are expected to increase the accuracy in genetic/genomic evaluations and increase genetic improvement.

Researchers and financing:
This PhD project carried out by Caroline Carlström was partly financed by SLF, the Swedish farmers' foundation for agricultural research. Jan Philipsson and Erling Strandberg from the department also participated.

Scientific papers:

Carlström, C., Pettersson, G., Johansson, K., Strandberg, E., Stålhammar, H. & Philipsson, J. 2013. Feasibility of using automatic milking system data from commercial herds for genetic analysis of milkability. J. Dairy Sci. 96:5324-5332.

Carlström, C., Strandberg, E., Johansson, K., Pettersson, G., Stålhammar, H. & Philipsson, J. 2014. Genetic evaluation of in-line recorded milkability from milking parlors and automatic milking systems. J. Dairy Sci. 97(1):497-506

Carlström, C., G. Pettersson, E. Strandberg, K. Johansson, H. Stålhammar, and J. Philipsson. 2016. Genetic Associations of Teat Cup Attachment Failures, Incomplete Milkings and Handling Time in Automatic Milking Systems with Milkability, Temperament and Udder Conformation. Acta Agric. Scand. Section A Animal Sciences 66: 75-83

Carlström, C, E. Strandberg, K. Johansson, G. Pettersson, H. Stålhammar and J. Philipsson. 2016. Genetic associations of in-line recorded milkability traits and udder conformation with udder health. Acta Agric. Scand. Section A Animal Sciences 66:84-91

Some research projects

Genetic diversity in past and present Swedish sheep

We want to find out how much genetic variation there is in the Swedish breeds of sheep. We also want to compare sheep living today with sheep that lived in Sweden in the past.

Photo Anna Johansson

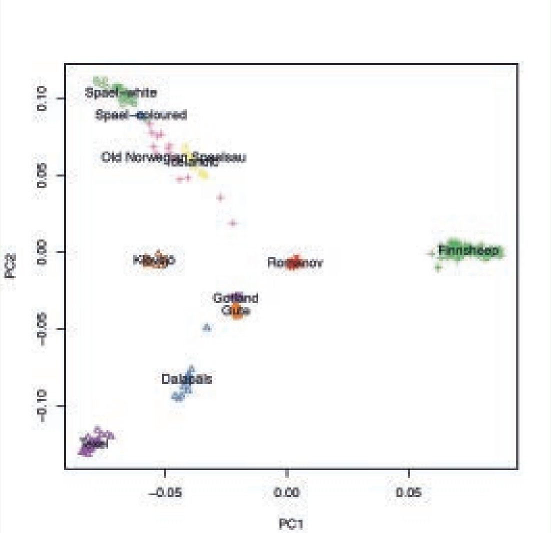
By studying the sheep DNA and pedigrees we can describe how much genetic variation that exists in different breeds of sheep in Sweden. We are also investigating which sheep breeds that are most closely related to each other and how closely related the Swedish breeds of sheep are with breeds of sheep in other countries.

We have collected samples from more than 1,000 sheep in Sweden. Some of the samples have already been investigated using different methods, but this is an ongoing project and more samples will be investigated in the future. We will also investigate DNA from ancient archaeological samples and compare sheep living today and ancient sheep.

The breed we so far have studied in most detail is the Gute sheep. We have shown that inbreeding is at a low and stable level and that the conservation programs seem to be successful.

Studies of endogenous retroviruses of the breeds Klövsjö sheep, Värmlands sheep, Swedish Finewool sheep, Gute sheep and Roslag sheep showed that they have characteristics of primitive breeds that came to Europe with the first wave of sheep migration.

We are currently analyzing data from a SNP chip (hundreds of thousands of sites in sheep DNA) to get more detailed results of sheep breed variety and origin.



Plot of the first two principal components based on allele frequencies from eight sheep breeds.

Scientific papers:

Mukiibi R, Rochus CM, Andersson G, Johansson AM. 2015. The use of endogenous retroviruses as markers to describe the genetic relationships among local Swedish sheep breeds. Animal Genetics 46(2):220-223

Rochus CM, Johansson AM. 2017. Estimation of genetic diversity in Gute sheep: pedigree and microsatellite analyses of an ancient Swedish breed. Hereditas 154:4

Rochus, CM. 2017. Genetic diversity of domestic sheep. PhD dissertation. https://pub.epsilon.slu.se/14322/

Genomic studies of horses lead the way to unravel genetic regulation of locomotion pattern and performance traits

The overall aim of this project is to get a better understanding of the genetics behind gaits and performance in the horse.

Locomotion in mammals relies on a central pattern-generating circuitry of spinal interneurons and motor neurons that coordinate the movement of the four limbs. We previously made a major discovery that a single base change causing a nonsense mutation in the DMRT3 gene and loss-of-function of the encoded truncated protein alters the pattern of locomotion in horses. The identification of the link between DMRT3 and locomotion pattern in horses revealed a new protein involved in the control of locomotion pattern and placed DMRT3 in a pivotal role in the configuration of the spinal circuits controlling stride in vertebrates. This locus was identified by a genome-wide association analysis (GWAS) that compared Icelandic horses with and without the ability to pace followed by whole-genome re-sequencing. The presence of the identified nonsense mutation is required to perform alternate gaits (gaits other than walk, trot and canter/gallop) and occurs at a high frequency in gaited horses and horses used for harness racing. These results clearly demonstrate how the study of unique phenotypes in domestic animals can lead to fundamental biological insights. As horses show a remarkable variation in the pattern of locomotion a whole new research field using the horse as a model to identify the underlying genes has emerged.

Photo Mirjam Horn. Horse: Thyrnir (genotype AA) Nordic champion 2016, Swedish champion 2014-2017. Rider: Thorvaldur Árnason (unknown genotype for DMRT3)

We described the effects of the DMRT3 nonsense mutation on harness racing performance in Swedish-Norwegian Coldblooded trotters and Finnhorses. Previous studies have demonstrated a major impact of the gene on harness racing performance results in Standardbreds where the vast majority of the horses are homozygous mutant (AA). While the gene clearly is important for harness racing performance in both Coldblooded trotters and Finnhorses, the most successful genotype differed between the two breeds. The AA Finnhorses were most successful on the racetrack, but had difficulties performing a good canter in riding. For Coldblooded trotters the CA horses were the better race horses overall, even though the AA horses performed well at young ages.

While previous studies have reported that homozygozity for the DMRT3 mutation is required for a horse to be able to pace, not all AA horses can pace. To understand more about the genetic regulation of pace we compared the genomes of AA Icelandic horses with and without the ability to pace. We performed a GWAS and identified a potential candidate region that contained the gene GRIN2B known to influence memory and learning ability.

Researchers and financing: This PhD project was carried out by Kim Fegraeus and funded by the Swedish Research Councils VR and Formas. Gabriella Lindgren, Brandon Velie, Leif Andersson, and Maria Rosengren from the department also participated in the project.

Scientific papers:

Andersson LS, et al. 2012. Mutations in DMRT3 affect locomotion in horses and spinal circuit function in mice. Nature. 488(7413):642-6.

Jäderkvist K, et al. 2015. Different DMRT3 genotypes are best adapted for harness racing and riding in Finnhorses. J Hered. 2015 Nov-Dec;106(6):734-40.

Jäderkvist Fegraeus K, et al. 2017. Lack of significant associations with early career performance suggest no link between the DMRT3 "Gait Keeper" mutation and precocity in Coldblooded trotters. PLoS One. ;12(5):e0177351.

Jäderkvist Fegraeus K, et al. 2017. To pace or not to pace: a pilot study of four- and five-gaited Icelandic horses homozygous for the DMRT3 'Gait Keeper' mutation. Anim Genet. 48(6):694-697.

Some research projects

Milk progesterone measures to improve selection for fertility in dairy cows

The overall objective of this project was to explore the use of milk progesterone records and genomic information to improve selection for fertility in dairy cows.

Improved reproductive performance has a substantial benefit for the overall profitability of dairy cattle farming by decreasing insemination and veterinary treatment costs, shortening calving intervals, and lowering the rate of involuntary culling. Unfortunately, the low heritability of classical fertility traits derived from calving and insemination data makes genetic improvement by traditional animal breeding slow. Therefore, there is an interest in finding novel measures of fertility that have a higher heritability or using genomic information to aid genetic selection for fertility.

In a first step, the use of in-line milk progesterone records from the Herd Navigator system (DeLaval) to define endocrine fertility traits was investigated, and genetic parameters estimated. Several defined endocrine fertility traits were heritable, and showed a reasonable repeatability. Also, the genetic correlation of milk production traits with endocrine fertility traits were considerably lower than the correlations of milk production with classical fertility traits.

In the next step 17 quantitative trait loci (QTL) associated with endocrine fertility traits, were identified on several chromosomes in a genome-wide association study with single nucleotide polymorphisms. Further, fine mapping of target regions on chromosomes 2 and 3, identified several associated variants and potential candidate genes underlying endocrine fertility traits.

The optimal use of endocrine fertility traits in genomic evaluations was investigated. We found that endocrine fertility traits have more predictive ability than classical fertility traits. The accuracy of genomic prediction was also substantially improved when endocrine and classical fertility traits were combined in multi-trait genomic prediction.

Results showed that for prediction of fertility, there is no benefit of investing in a cow training population when the breeding goal is based on classical fertility traits. However, when considering a more biological breeding goal for fertility like commencement of luteal activity, accuracy is substantially improved when endocrine traits are available from a limited number of farms.

Scientific papers:

Tenghe, A. M. M. 2017. Milk progesterone measures to improve genomic selection for fertility in dairy cows. PhD thesis: Sveriges lantbruksuniv., Acta Universitatis agriculturae Sueciae, 1652-6880 ; 2017:37; ISBN 978-91-576-8847-7. https://pub.epsilon.slu.se/14227/

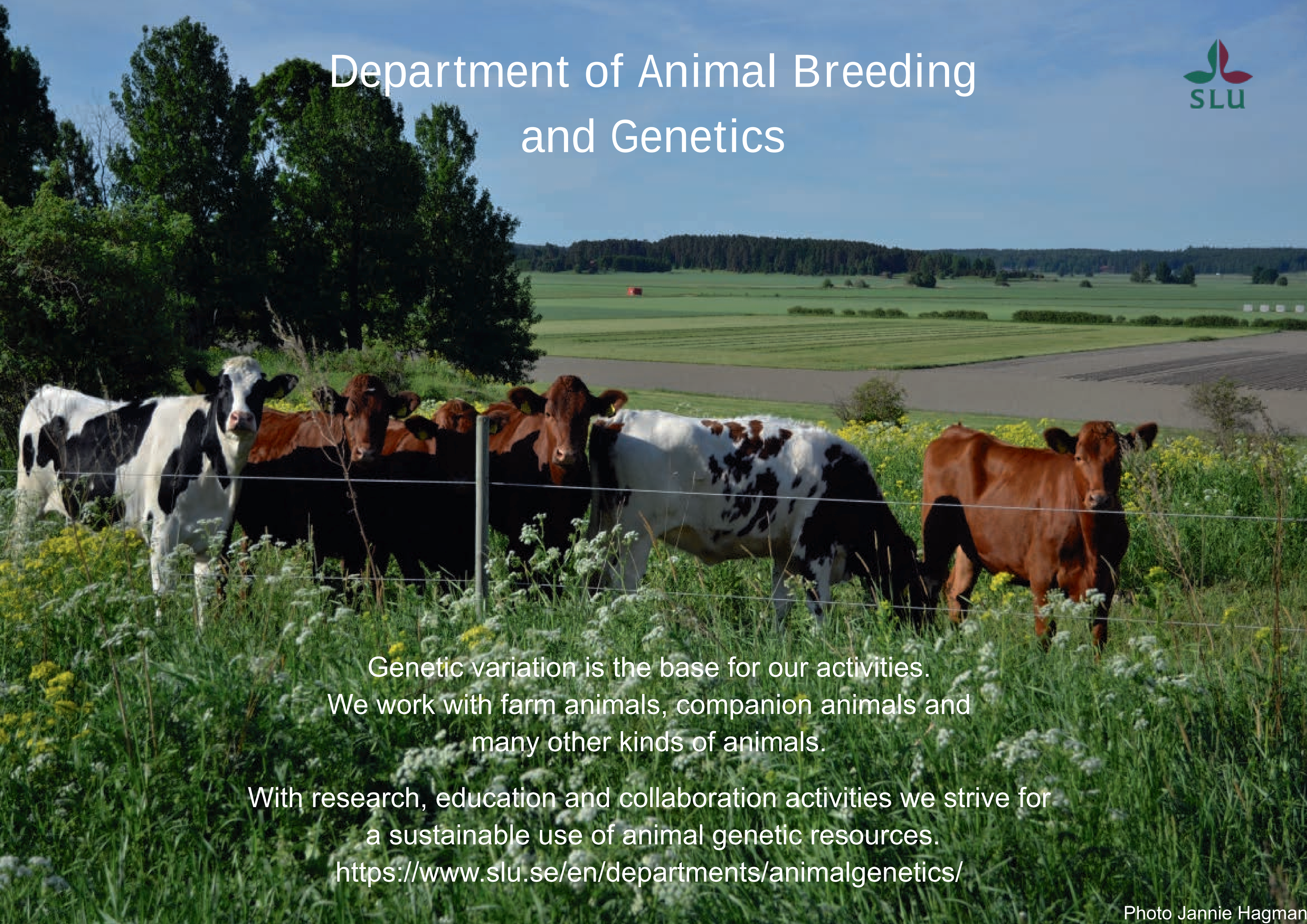
Tenghe, A. M. M., A. C. Bouwman, B. Berglund, E. Strandberg, J. Y. Blom, and R. F. Veerkamp. 2015. Estimating genetic parameters for fertility in dairy cows from in-line milk progesterone profiles. Journal of Dairy Science 98(8):5763-5773.

Tenghe, A. M. M., A. C. Bouwman, B. Berglund, E. Strandberg, D. J. de Koning, and R. F. Veerkamp. 2016. Genome-wide association study for endocrine fertility traits using single nucleotide polymorphism arrays and sequence variants in dairy cattle. Journal of Dairy Science 99(7):5470-5485.

Tenghe, A. M. M., B. Berglund, E. Wall, R. F. Veerkamp, and D. J. de Koning. 2016. Opportunities for genomic prediction for fertility using endocrine and classical fertility traits in dairy cattle1. Journal of Animal Science 94(9):3645-3654.

Tenghe, A. M. M., A. C. Bouwman, B. Berglund, D. J. de Koning, and R. F. Veerkamp. 2018. Improving accuracy of bulls' predicted genomic breeding values for fertility using daughters' milk progesterone profiles. Journal of Dairy Science. (in press)

Department of Animal Breeding and Genetics



Genetic variation is the base for our activities.
We work with farm animals, companion animals and
many other kinds of animals.

With research, education and collaboration activities we strive for
a sustainable use of animal genetic resources.
https://www.slu.se/en/departments/animalgenetics/

Photo Jannie Hagman