

Feed-a-Gene



Book of abstracts

69th **EAAP Annual meeting**,
Feed-a-Gene/SAPHIR joint session,
30 August 2018, Dubrovnik,
Croatia

14th **International Symposium
Digestive Physiology of Pigs**,
21-24 August 2018, Brisbane,
Australia

15th **European Poultry
Conference**, 17-21 September
2018, Dubrovnik, Croatia

The Feed-a-Gene Consortium

- › Institut national de la recherche agronomique (INRA)
- › Wageningen UR Livestock Research (WUR)
- › Newcastle University (UNEW)
- › Universitat de Lleida (UdL)
- › Institut de Recerca i Tecnologia Agroalimentàries (IRTA)
- › Kaposvár University (KU)
- › Aarhus University (AU)
- › China Agricultural University (CAU)
- › Topigs Norsvin
- › Cobb Europe
- › Hamlet Protein
- › Bühler
- › DuPont Industrial Biosciences
- › Exafan
- › Claitec
- › INCO
- › Gran Suino italiano
- › Association de coordination technique agricole (ACTA)
- › IFIP institut du porc
- › ITAVI
- › Terres Inovia
- › Association française de zootechnie (AFZ)
- › INRA Transfert (IT)



Feed-a-Gene



Adapting the **feed**, the **animal** and the **feeding techniques** to improve the efficiency and sustainability of monogastric livestock production systems

The Feed-a-Gene project (2015-2020) aims to better adapt different components of monogastric livestock production systems (i.e., pigs, poultry and rabbits) to improve the overall efficiency and to reduce the environmental impact. This involves the development of new and alternative feed resources and feed technologies, the identification and selection of robust animals that are better adapted to fluctuating conditions, and the development of feeding techniques that allow optimizing the potential of the feed and the animal. The project was awarded a grant from the European Commission (Grant agreement No 633531) under the EU Framework Programme for Research and Innovation Horizon 2020. The project will:

- ▶ Develop new and alternative feeds and feed technologies to make better use of local feed resources, green biomass and by-products of the food and biofuel industry
- ▶ Develop methods for the real-time characterization of the nutritional value of feeds to better use and adapt diets to animal requirements
- ▶ Develop new traits of feed efficiency and robustness allowing identification of individual variability to select animals that are more adapted to changes in feed and environmental conditions
- ▶ Develop biological models of livestock functioning to better understand and predict nutrient and energy utilisation of animals along their productive trajectory
- ▶ Develop new management systems for precision feeding and precision farming combining data and knowledge from the feed, the animal, and the environment using innovative monitoring systems, feeders, and decision support tools
- ▶ Evaluate the overall sustainability of new management systems developed by the project
- ▶ Demonstrate innovative technologies in collaboration with partners from the feed industry, breeding companies, equipment manufacturers, and farmers' organizations to promote the practical implementation of project results
- ▶ Disseminate new technologies that will increase animal production efficiency, whilst maintaining product quality and animal welfare, and will enhance EU food security, to relevant stakeholders

To register on the stakeholder platform, click on:
www.feed-a-gene.eu/user/register

Abstracts

Communications presented at the Feed-a-Gene/SAPHIR joint session at EAAP 2018.....5

Multidisciplinary approaches to livestock production	7
Twists and turns of interdisciplinary work in research projects: which conditions and achievements?	7
Detection and characterization of the response of growing pigs to perturbations by using feed intake.....	9
Layers response to suboptimal diet through phenotypic and transcriptomic changes in four tissues.....	11
What potential of genome-wide integrative approaches to predict vaccine responses?	12
Immune responses after administration of innovative <i>Mycoplasma hyopneumoniae</i> bacterins in pigs	13
Effect of heat stress on fecal microbiota composition in swine (preliminary results).....	14
The socio-economic evaluation of vaccines in livestock systems.....	16
Innovations for sustainable animal nutrition.....	17
Expectations of poultry breeding industry from research projects	18
The importance of research for developing standards to control animal diseases: the role of the OIE.....	20
Effects of protein restriction on rumen metagenome and metabolic profile in Holstein calves	21
Genetic and environmental influence on colostrum quality and absorption in Swedish dairy cattle	22
A systems genetics approach reveals potential regulators of feed efficiency in pigs.....	23
Why farmers adopt environmental practices? The case of French dairy farms	24

Feed-a-Gene communications presented in other EAAP sessions, DPP and EPC 28

The influence of faeces drying method on nutrient digestibility of growing pigs.....	29
Rapeseed meal and enzyme supplementation on growth performance and nutrient digestibility in pigs.....	30
Effect of novel soya bean meal processing technologies on broiler performance and digestibility.....	32
Genome-wide association study of post-weaning growth in rabbits.....	33
Operational measures of efficiency: make them measureable on large scale.....	35
Effects of birth weight on nitrogen digestion and utilization in grower pigs.....	36
Plasma metabolites related to nitrogen efficiency in low and high birthweight pigs.....	38
Precision feeding of lactating sows: development of a decision support tool to handle variability	39
Precision feeding with a decision support tool dealing with daily and individual pigs' body weight	41
Genetic bases of individual performance variation in pigs	43
Structured antedependence model for longitudinal analysis of social effects on ADG in rabbits	45
Effect of gut microbiota on production traits, interaction with genetics.....	47

Except when noted otherwise, the research presented in this booklet has received funding from the European Union's Horizon 2020 Programme under grant agreements No 633531 (Feed-a-Gene) and No 633184 (SAPHIR).



Communications presented at the Feed-a-Gene/SAPHIR joint session at EAAP 2018

30 August 2018, Dubrovnik, Croatia

Multidisciplinary approaches for improving sustainable livestock production: research needs, opportunities and difficulties

Livestock production is an essential component of a sustainable food supply. The dimensions of sustainability in combination with the complexity of biology call for multidisciplinary approaches to assess the functioning of (components of) livestock production systems. The communications presented in this joint Feed-a-Gene/SAPHIR session have a multidisciplinary approach (e.g., nutrition and genetics, genetics and immune control of infectious diseases, integrated health/management strategies and economics) and arise from multidisciplinary projects such as Feed-a-Gene and SAPHIR.

Feed-a-Gene



SAPHIR is a Horizon 2020 project running from 1 March 2015 to 28 February 2019. SAPHIR's ambition is to tackle current vaccine weaknesses and provide effective vaccine-based strategies. It aims to show the potency of promising vaccines against frequently occurring pathogens and to design innovative vaccine strategies, resulting in an increased viability, sustainability and profitability of food animal production systems and an improved animal welfare.

- ▶ Scientific objectives: to unravel mechanisms of immune protection, induce rapid and long-lasting immunity, develop safe vaccines and predict epidemiological consequences of vaccination.
- ▶ Technical objectives: to generate models and assays for the development of vaccines, investigate a variety of vaccines and delivery systems, and bring promising vaccines to demonstration.
- ▶ Socio-economic objectives: to explore the economic impact of the SAPHIR diseases and predict the socio-economic benefits of using the designated vaccination strategies.

Learn more about SAPHIR at www.h2020-saphir.eu



Jaap van Milgen

Feed-a-Gene Project coordinator

Contact: jaap.vanmilgen@inra.fr

Jaap van Milgen is currently head of the INRA-Agrocampus Pegase research unit in Rennes (Brittany, France). Pegase's mission is to "identify the biological basis and conceive levers by which animal production will contribute efficiently and responsibly to a sustainable development". Jaap van Milgen obtained an MSc degree from Wageningen University and a PhD degree from the University of Illinois. He joined INRA as a post-doctoral researcher in 1992 after which he obtained a permanent position to work on the nutrition modelling of growth in pigs. He developed the growing pig module of the InraPorc® model and software tool and he also developed an extensive experimental research program of energy and amino acid nutrition. Jaap van Milgen is coordinator of the Feed-a-Gene project and contributes to WP3 on the modelling of biological functions with emphasis on feed use mechanisms.



Marie-Hélène Pinard-van der Laan

SAPHIR Deputy-coordinator

Contact: marie-helene.pinard@inra.fr

Marie-Hélène Pinard-van der Laan is senior scientist at the INRA GABI (Animal Genetics & Integrative Biology) research unit in Jouy-en-Josas (Paris area, France). She obtained a French Agronomic Engineer degree and a PhD degree from the Wageningen University in 1992. Then she joined INRA where she continued to develop national and European projects focused on animal disease genomics with a special interest in host-pathogen interactions in poultry. Her research interests are 1- to decipher the genetics of the host response to a pathogen, but also, 2- to study and exploit the individual genetic variability of the host response to vaccines, and ultimately 3- to identify genetic- and bio-markers of immunocompetence which can be predictive of a better response of the host to pathogen and vaccine. Marie-Hélène Pinard-van der Laan is deputy-coordinator of the SAPHIR project and contributes to WP13 on the analysis of the individual variability of immunocompetence and the search for markers predictive of vaccine responses.



Multidisciplinary approaches to livestock production

Feed-a-Gene / SAPHIR

**J. van Milgen¹, M.H. Pinard-van der Laan²,
E. Schwartz³, Ç. Kaya⁴, V. Heuzé⁵**

1 INRA-Agrocampus Ouest, UMR Pegase, Le Clos, 35042 Rennes, France, 2 INRA, UMR GABI, Domaine de Vilvert, 78352 Jouy-en-Josas, France, 3 INRA, UR VIM, Domaine de Vilvert, 78352 Jouy-en-Josas, France, 4 EFFAB, Dreijenlaan 2, 6703 HA Wageningen, The Netherlands, 5 Association Française de Zootechnie, 16, rue Claude Bernard, 75231 Paris, France

Contact: jaap.vanmilgen@inra.fr

Livestock production is an essential component of a sustainable food supply. The dimensions of sustainability combined with the complexity of biology call for multidisciplinary approaches to assess the functioning of (components of) livestock production systems. Horizon 2020 projects such as Saphir and Feed-a-Gene are funded by the European Commission and have a multidisciplinary approach towards livestock production (e.g., nutrition and genetics, genetics and health, novel management strategies and socio-economic aspects). The objective of this session is to address and discuss the challenges and opportunities in multidisciplinary research in livestock production. As there is no "one-size-fits-all" solution, how can different actors and stakeholders make collectively best use of (disciplinary) knowledge and levers to make livestock production more sustainable?

Twists and turns of interdisciplinary work in research projects: which conditions and achievements?

M. Cerf

INRA, UMR LISIS, BP1 Bâtiment EGER, 78850 Thiverval-Grignon, France

Contact: marianne.cerf@inra.fr

The emphasis on interdisciplinary research is far from new: promoting it was at the core of the DGRST French research plan in the 70's and of the Hawkesbury University experience in Australia. It resulted in the emergence of the INRA SAD division in the 80's. Today, many funding agencies ask for interdisciplinary work teams. Well recognized journals such as *Science* give room to interdisciplinary results. Doctoral schools value interdisciplinary training even if this remains controversial regarding recruitment standards. More epistemological reflexion is available to address the foundations of interdisciplinary scientific work. Anyway, practising interdisciplinary work and managing interdisciplinary projects remain a big challenge. There is no clear-cut recommendations or on-the shelf tools which can be transferred to newcomers. Many researchers who joined interdisciplinary projects find it difficult, disappointing. They acknowledge that the project is more a collection of disciplines working on separate tasks with loose coordination in terms of renewed understanding of the issue addressed in the project. Why is it so?

I will rest on my experience at the interface between agronomic and social sciences to address the dynamic of interdisciplinary work

in practice. I will put emphasis on various dynamic patterns and stress the need for intermediary objects, shared learning and reflexivity along the interdisciplinary journey. I will illustrate that fruitful interdisciplinary work takes place at the border of the disciplines but often questions core assumptions underlying its main stream. Therefore, taking part to interdisciplinary work puts the participants in a risky position in their own community as the legitimacy of their work becomes discussed. To escape this uncomfortable position, researchers often trigger a debate on the balance between excellence

and relevance of the scientific work. I will then conclude by focusing on the management of interdisciplinary projects. I will argue that people involved in the management of interdisciplinary work act as brokers. As for any brokering work this implies to have the ability and the curiosity to navigate between different points of view on a reality and to support the cross fertilization between these points of view.

Marianne Cerf

Senior researcher at INRA in the LISIS Research Unit, Marianne Cerf was trained as an agronomist (MS degree) and an ergonomist (PhD in cognitive ergonomics). She carried most of her research at the interface between agronomic sciences and social and human sciences to analyse and support farmers' decision making, advisory work, or the design of decision support tools for farmers and advisers. Within transdisciplinary projects, she develops design methods with a human centred focus by considering that design and use are two faces of the same coin. Since 2008, she participates to a network of practitioners developed at the interface between INRA and agricultural R&D and advisory boards to contribute to the design and evaluation of innovative and sustainable cropping systems.

In close relation with participants of this network or with various farmers' associations, she studies the processes of change which farmers and advisers experienced and the new skills they develop when they respectively carry on or support a transition towards agro-ecology. In such processes, she pays attention to knowledge and innovation brokering activities and tools which support collectives and individuals in their transition. Since 2017, she manages the Initiative for Design in Agri-food Systems (IDEAS), which is a network of scholars based in Ile-de-France and involved in developing radical, distributed and open design methods to contribute to innovation processes within agri-food systems in transition towards more sustainability.



Detection and characterization of the response of growing pigs to perturbations by using feed intake

Feed-a-Gene

H. Nguyen Ba¹, M. Taghipoor², J. van Milgen¹

1 INRA, Pegase, 35590 Saint-Gilles, France,
2 INRA, MoSAR, 75231, Paris, France

Contact: hieu.nguyen-ba@inra.fr

Improving robustness for farm animals is seen as a new breeding target. However, robustness is a complex trait and not measurable directly. On the other hand, it can be characterized by examining the animal's response to environmental perturbations. Although the origin of environmental perturbations may not be known, the effect of a perturbation on the animal can be observed, for example through changes in voluntary feed intake. Perturbations such as heat stress and sanitary challenges typically have a negative and transitory effect on the voluntary

feed intake. We developed a generic model and data analysis procedure to detect these perturbations, and subsequently characterize the feed intake response of growing pigs in terms of resistance and resilience as elements of robustness when faced with perturbations. We hypothesize that there is a target trajectory curve of cumulative feed intake, which is the amount of feed that a pig desires to eat when it is not facing any perturbation. Deviations from this target trajectory curve are considered as a period of perturbation, which can be characterized by its duration and magnitude. It is also hypothesized that, following a perturbation, animals strive to regain the target trajectory curve. A model based on differential equations was developed to characterize the animal's response to perturbations. In the model, a single perturbation can be characterized by four parameters. The start and end times of the perturbation are defined by the perturbing factor (e.g. a period of heat stress) while the last two parameters describe the resistance and resilience potential of the animal to that perturbing factors. One parameter describes the immediate reduction in daily feed

Figure 1. Target trajectory curve (TTC) estimated from the data of cumulative feed intake (CFI) by eliminating feed intake data in periods during which the pig may have been perturbed. There are two periods CFI were deviated from the TTC. Only the second period is considered as a perturbation because of its duration and magnitude.

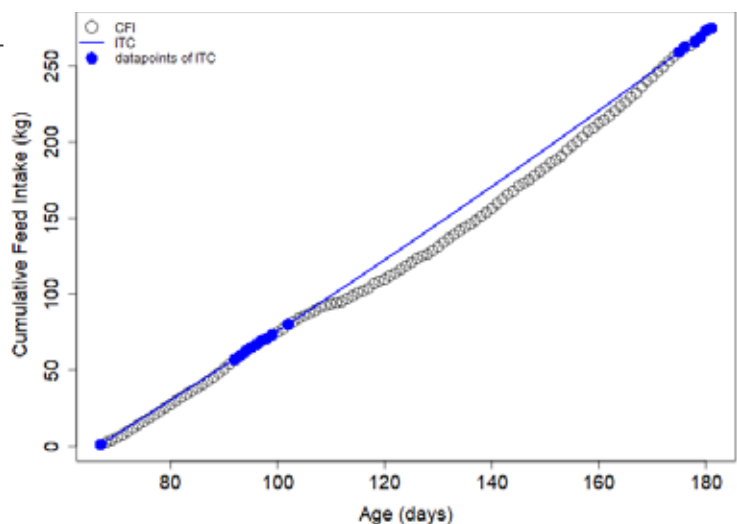
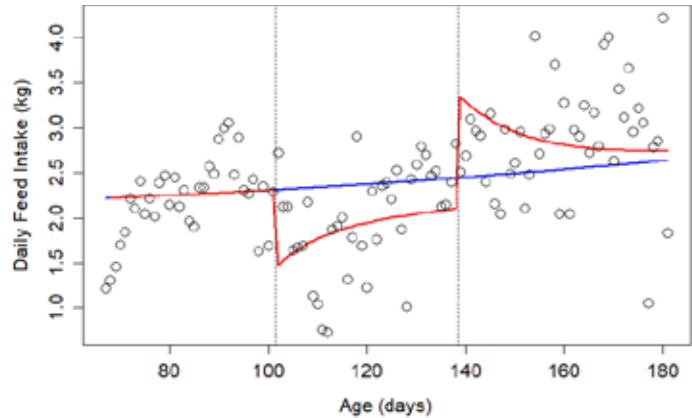


Figure 2. Simulation modeling's response of pig to the perturbation in term of daily feed intake (DFI). Blue curve indicates the TTC. Red curve indicates simulation the model. Points are observation of DFI.



intake at the start of the perturbation (i.e., a “resistance” trait) while another describes the capacity of the animal to adapt to the perturbation through compensatory feed intake to rejoin the target trajectory curve (i.e., a “resilience” trait). The model has been employed successfully to identify the target trajectory curve of cumulative feed intake

in growing pigs and to quantify the animal's response to a perturbation by using feed intake as the response criterion. Further developments include the analysis of individual feed intake curves of group-housed pigs that can be exposed to the same environmental perturbing factors to quantify and to compare different pigs.

Table 1. Four estimated parameters of the model characterizing the pig's response to a perturbation

Start (day)	End (day)	Impact of perturbation (%)	Compensatory capacity (%)
101.5	138.6	37.4	3.6

Hieu Nguyen Ba

Hieu Nguyen Ba is a junior researcher from Vietnam. He has a Master degree obtained at Wageningen University in the Netherlands in 2016 and currently is a PhD student at INRA-Agrocampus Ouest research unit PEGASE in Rennes, France. The main interest of his study focuses on understanding and improving physiological and behavioural adaptation of pigs and poultry. Since 2016, he has been involved in the Feed-a-Gene project and his objective is to develop a mathematical model which can automatically detect and characterize the response of growing pigs to environmental perturbations in terms of resistance and resilience by using voluntary feed intake. The model's parameters can then be used as genetic selection criteria for more robust animals.



Layers response to suboptimal diet through phenotypic and transcriptomic changes in four tissues

Feed-a-Gene

F. Jehl¹, M. Brenet¹, A. Rau², C. Désert¹, M. Boutin¹, S. Leroux³, D. Esquerré⁴, C. Klopp⁵, D. Gourichon⁶, A. Collin⁷, F. Pitel³, T. Zerjal², S. Lagarrigue¹

1 *Pegase INRA-Agrocampus Ouest, Rennes, France*, 2 *GABI INRA, Jouy-en-Josas, France*, 3 *Genphyse INRA, Castanet Tolosan, France*, 4 *Genotoul INRA, Castanet Tolosan, France*, 5 *Sigenae INRA, Toulouse, France*, 6 *PEAT INRA, Nouzilly, France*, 7 *BOA INRA - Université de Tours, Nouzilly, France*

Contact: frederic.jehl@inra.fr

Poultry meat and eggs are major sources of nutrients in human alimentation. The long production career of laying hens expose them to biotic or abiotic stressors, lowering their production. Understanding the mechanisms of stress adaptation is crucial for selecting robust animals and meeting the needs of a growing human population. In this study, financed by the French ChickStress and the European Feed-a-Gene programs, we compared the effects of a 15%-energy-reduced diet (feed stress, FS) vs. a commercial diet (control, CT) on phenotypic traits and adipose, blood, hypothalamus and liver transcriptomes in two feed-efficiency-diverging lines. Phenotypic traits showed differences between lines or diets, but no line \times diet interactions. In the FS group, feed intake (FI) increased and hens had lower body- and abdominal adipose weight, compared to CT group. We found no differences in egg production or quality. At the transcriptomic level, 16461 genes were expressed in one or more tissues,

41% of which were shared among tissues. We found differentially expressed genes between lines or diet in all tissues, and almost no line \times diet interactions. Focusing on diet, we found that adipose and liver transcriptomes were unaffected. In blood, pathways linked to amino-acids, monosaccharides, and steroid metabolisms were affected, while in the hypothalamus, changes were observed in fatty acids metabolism and endocannabinoid signaling. Given the similarities in egg production, the FS animals seem to have adapted to the stress by increasing their FI and mobilizing their adipose reserves. Increase in FI did not appear to affect liver's metabolism, and the mobilization of adipose reserves was apparently not driven at the transcriptomic level. In blood, the pathways linked to metabolic processes suggest a metabolic role for this tissue in chicken, whose erythrocytes are nucleated and contain mitochondria. FI increase might be linked with the hypothalamic pathway of endocannabinoid signaling, which are lipid-based neurotransmitters notably involved in the regulation of appetite.

Frédéric Jehl

Frédéric Jehl is a 1st year PhD student in genetics and genomics at INRA, France. He has a master's degree as well as an Engineer's degree in agronomy obtained at Agrocampus Ouest (Rennes, France) in 2017. His PhD subject consists in the study of the genetic component of feed efficiency and adaptation in laying hens, using RNA-seq data.



What potential of genome-wide integrative approaches to predict vaccine responses?

SAPHIR

F. Blanc¹, T. Maroille¹, M.H. Pinard-van der Laan¹, G. Lemonnier¹, J.J. Leplat¹, E. Bouguyon², Y. Billon³, J.P. Bidanel¹, B. Bed'hom¹, J. Estellé¹, S. Kim⁴, L. Vervelde⁴, D. Blake⁵, C. Rogel-Gaillard¹

¹ GABI, INRA, AgroParisTech, 78350 Jouy-en-Josas, France, ² VIM, INRA, 78350 Jouy-en-Josas, France, ³ GenESI, INRA, 17700 Surgères, France, ⁴ The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Midlothian, United Kingdom, ⁵ Department of Pathobiology and Population Sciences, Royal Veterinary College, University of London, Hatfield, United Kingdom

Contact: claire.rogel-gaillard@inra.fr

The impact of host genetic variations in shaping innate and adaptive immune responses is an emerging lever to consider in new vacci-

nation strategies. Merging genetic and genomic data to identify prospective biomarkers that could predict individual's immune capacity and response to vaccines is a challenging question addressed by the H2020-funded SAPHIR project, both in chickens and in pigs. Large White pigs (48 families) were vaccinated against *Mycoplasma hyopneumoniae* (M. hyo, 182 piglets) or Influenza A Virus (IAV, 98 piglets) at weaning (around 28 days of age) with a booster vaccination three weeks later. The humoral vaccine response was measured by following the dynamics of seric M. hyo- or IAV-specific IgG every week during five weeks post-vaccination, and before slaughtering at 21 weeks of age. For chickens, vaccine responses were measured on vaccinated commercial broilers (Cobb 500) and on a subset of animals challenged with *Eimeria maxima* (from 96 to 36 chickens). Animal responses were evaluated by the measure of serum levels of IL-10 with an in-house developed ELISA system, body weight gain, lesion scores, and parasite load. For each species design, blood was sampled before vaccina-

Claire Rogel-Gaillard

Claire Rogel-Gaillard is a senior scientist at INRA where she heads the Laboratory of Animal Genetics and Integrative Biology (Jouy-en-Josas, France). She is director of Sciences Animales Paris-Saclay. She obtained a PhD on human papillomaviruses at the Pasteur Institute. She participated in the international sequencing projects of the pig and rabbit reference genomes, co-coordinated the annotation of the pig immunome and co-authored the first reference gene catalogue of the pig gut microbiome. She is involved in the committee for pig MHC nomenclature. Her current research activities focus on the characterization of individual variability of immune capacity, mainly in pigs. She runs integrative projects on large-scale animal cohorts that combine phenotyping

of immune and production traits, genetics, functional genomics and metagenomics, in a perspective of data integration and modelling. In SAPHIR she leads the WP13 with the aim to identify genetic markers and blood biomarkers that predict vaccine efficiency in pigs (vaccine against *Mycoplasma hyopneumoniae*, porcine flu, PRRSV) and in chickens (vaccine against *Eimeria maxima*).



tion on the vaccine day for high-density SNP genotyping and RNAseq analysis. We have identified significant associations between gene expression in blood before vaccination and vaccine responses in pigs or body weight as a measure related to the vaccine follow-up in chickens. Thus, we provide a proof of concept that blood could be used as a relevant source of biomarkers predictive of vaccine responses. We will further discuss the potential of integrating multi-level genomic and phenotypic data to better understand individual vaccine responses and identify levers of action.

Immune responses after administration of innovative *Mycoplasma hyopneumoniae* bacterins in pigs

SAPHIR

D. Maes¹, A. Matthijs¹, G. Auray², C. Barnier-Quer³, F. Boyen¹, I. Arsenakis¹, A. Michiels¹, F. Haesebrouck¹, A. Summerfield²

1 Ghent Univ., Salisburylaan 133, 9820 Merelbeke, Belgium, 2 Institute of Virology and Immunology, Sensemattstr. 293, 3147 Mittelhäusern, Switzerland, 3 Univ. Lausanne, Chemin des Boveresses 155, 1066 Epalinges, Switzerland

Contact: dominiek.maes@ugent.be

Vaccination against *M. hyopneumoniae* is widely used, but available vaccines provide only partial protection. This study aimed to screen innovative bacterins based on a highly virulent *M. hyopneumoniae* field strain for their ability to induce potent immune responses. Nine groups, each consisting of 6 *M. hyopneumoniae*-free piglets, were primo- (D0; 39 days of age) and booster (D14)

Dominiek Maes

Dominiek Maes is full professor and head of the Unit of Porcine Health Management at the Faculty of Veterinary Medicine at Ghent University Belgium. He is a specialist of the European College of Porcine Health Management. His main research areas include infectious diseases in pigs, reproduction and production and prudent antimicrobial use. His research group has performed many studies on *Mycoplasma hyopneumoniae*, with emphasis on the pathogenesis and transmission of the pathogen, interaction with the animal host, and

control measures, including vaccination. He is chair of the porcine section of the International Research Programme on Comparative Mycoplasmaology (IRPCM), standing committee of the International Organization of Mycoplasmaology (IOM).

Dominiek Maes

has published over 280 papers in peer-reviewed international scientific journals. Within the SAPHIR project, he is responsible for the workpackage focusing on developing innovative vaccines against *M. hyopneumoniae* in pigs.



vaccinated with 7 different experimental bacterins, a commercial bacterin as a positive control or PBS as a negative control. The experimental bacterin was formulated either with dmLT (group A), DDA:TDB liposomes (B), DPPC:DC-Chol liposomes+C-di.AMP (C), DPPC:DC-Chol liposomes+CpG ODN, resiquimod and Pam3Cys-SK4 (TLR ligands; D), PL-GA:CTAB microparticles+TLR ligands (E), O/W emulsion+TLR ligands (F) and DOPC:Chol liposomes+TLR4 agonist and QS-21 (G). The specific immune response was assessed by the levels of specific antibodies in serum and in bronchoalveolar lavage fluid (BALF), and by T-cell specific responses measuring TNF, IFN- γ and IL-17 in CD4 T cells. On D28, 6/6 pigs from groups B, C, D, F, G and the commercial vaccine group, and 2/6 pigs from group E were seropositive. Group B, C and the commercial vaccine group had significantly higher OD-values for IgG in serum than group A and the negative control group, and the OD-value from group E was significantly lower compared to group C and the commercial vaccine group ($P \leq 0.05$). Serum IgA ELISA results did not differ over time or among groups. In group F, 1/6 pigs tested positive for *M. hyopneumoniae* specific IgA in BALF on D28. At D14, there was an upregulation of both TNF and IFN- γ double positive as well as IL-17+ CD4 T cells in the commercial vaccine and F groups. At D28, a strong TNF and IFN- γ response was observed in CD4 T cells from groups B and F, while a significant IL-17 response was seen in cells from the group E compared to the negative control group. Formulation B, E and F seem to be promising *M. hyopneumoniae* vaccine candidates.

Effect of heat stress on fecal microbiota composition in swine (preliminary results)

M. Le Sciellour¹, I. Hochu², O. Zemb², J. Riquet², H. Gilbert², M. Giorgi³, Y. Billon⁴, J.-L. Gourdine⁵, D. Renaudeau¹

Feed-a-Gene

¹ PEGASE, INRA, Agrocampus-Ouest, 35042 Rennes, France, ² GenPhySE, Université de Toulouse, INRA, INPT, INP-ENVT, 31320 Castanet Tolosan, France, ³ PTEA, INRA, 97170 Petit-Bourg, France, ⁴ GenESI, INRA, 17700 Surgères, France, ⁵ URZ, INRA, 97170 Petit-Bourg, France

Contact: mathilde.lesciellour@inra.fr

Gut microbiota plays a central role in health and nutrient digestion and would help the host for better coping with environmental perturbations. In tropical conditions or in temperate countries during summer, elevated ambient temperatures can cause economic losses to the pig industry. During heat stress (HS), the reduction in voluntary feed intake is the main adaptation response for reducing heat production. This lower feed intake has subsequent negative effects on pig performance. The main purpose of this study was to investigate the relationships between HS and gut microbiota composition. A better understanding of the microbiota response to HS could allow the selection for animals well adapted to HS. Genetically related pigs were raised under temperate or tropical farm conditions with mean thermal humidity indexes respectively 23 and 25.5 from 11 to 23 weeks of age. In temperate conditions, pigs were submitted to a 3-week HS challenge at 30°C. Fecal samples were collected in all pigs at 23 weeks of age in both environ-



Credit: Hamlet Protein

ments (n=1200 samples) and at 26 weeks of age in the temperate environment (n=600). Therefore, it was possible to compare microbiota from pigs raised in a temperate environment, a tropical climate, and exposed to HS. Microbiota extracted from pigs under temperate and tropical climate had different compositions whereas pigs exposed to heat challenge or raised in tropical conditions

tended to share a common microbiota. HS challenge drastically modified gut microbiota and the groups before and after the challenge could be predicted in a multilevel sparse partial least square discriminant analysis with 30 OTUs and a mean classification error rate of 14%. Our experiment suggests that microbiota can be used as biomarkers of HS exposition. This study is part of the Feed-a-Gene Project funded by the European Union's H2020 Program (grant 633531), and of the PigHeat project funded by the French National Agency of Research (ANR-12-ADAP-0015).

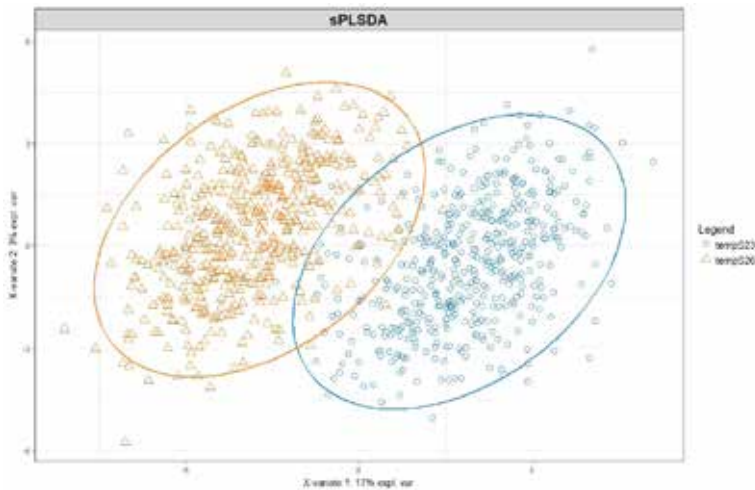


Figure 1. Score plot of two-component sPLS-DA model showing feces sample clustering according to the heat stress challenge in temperate climate with percentage of variance captured for each principal component (Δ : before heat stress, \circ : after heat stress). According to the cross-validation permutation test, the misclassification error rate was 10%.

Mathilde Le Sciellour

Mathilde Le Sciellour is a PhD student working on microbiota and feed efficiency in pigs at INRA UMR PEGASE, France. She obtained a Master degree in agriculture at the Ecole Supérieure d'Agriculture of Angers in 2013. Before she started her PhD at INRA, she has been working as a junior researcher for the pig genetic company Nucleus. Since 2016, she has been involved in the Feed-a-Gene project and aims at describing the relationships between feed efficiency and microbiota. Fecal microbiota will be used as a predictor of the performance of growing-finishing pigs across various environmental and dietary conditions in order to improve the selection for feed efficiency and other performance traits.



The socio-economic evaluation of vaccines in livestock systems

SAPHIR

C. Bellet, J. Rushton

Institute of Infection and Global Health / University of Liverpool, IC2 Building, 146 Brownlow Hill, L3 5RF, Liverpool, United Kingdom

Contact: camille.bellet@liverpool.ac.uk

Socio-economic evaluations provide a foundation to define resource allocation priorities and disease management strategies, which in turn help to tailor interventions to the specific context of a livestock system. This presentation examines how socio-economic evaluations of vaccines are performed in animal health research in relation to three European cases of respiratory and digestive diseases in cattle, pig and poultry. It explores their limitations and the potential

of transdisciplinary approaches to support more robust evaluations of livestock vaccination interventions. Vaccines not only help to protect against acute diseases but also against chronic diseases that may not hit the headlines, but which are important for livestock businesses and society. Vaccines also benefit unvaccinated animals, their owners and consumers by decreasing disease transmission, which in turn reduces the risk of epizootics and the pressure generated by these epizootics on health care providers and market economy. In addition, vaccines impact on drug use reducing selection pressure for drug resistance, and improving drug efficacy in humans. However, for vaccines to generate these benefits, the associated vaccination strategies need to protect critical proportions of animals on a given time scale. These strategies depend on vaccine quality, availability, accessibility and acceptability to farmers, their animal health advisors, and increasingly consumers. The growing complexity of vaccines, vaccine delivery and their relationship to long and diverse food systems

Camille Bellet

Since 2017, Camille Bellet is a postdoctoral researcher at the Institute of Infection and Global Health at the University of Liverpool, United Kingdom. She has a background in veterinary sciences (DVM, 2010), public health (MPH, 2010) and epidemiology (PhD, 2017) and is currently specialising in social sciences, in particular economics and the sociology of science and technology. As part of her current research and since her involvement in the H2020 SAPHIR project, she has been interested in understanding the different articulations that exist between animal health sciences and the development of new technologies such as veterinary vaccines. By exploring this issue and restoring a plurality of meanings to animal health contexts from which complexity is frequently eliminated, richer conceptions of veterinary vaccine development can be fostered and help to build a sustainable common future.



demand interdisciplinary and integrative approaches that address human, animal and ecosystem dimensions. Yet current socio-economic evaluations of livestock vaccines remain mostly limited to one of the many dimensions of a disease problem such as the reduction of disease incidence. The presentation concludes that there is a need to unpack the dynamics of farm practices and the food system to understand how these shape animal health management and vaccine intervention. This requires a transdisciplinary approach with a depth of different forms of expertise and data sources in order to achieve informed evaluations on the trade-offs of vaccine intervention.

Innovations for sustainable animal nutrition

Feed-a-Gene

L.A. den Hartog^{1,2}, F. Brinke²

1 Wageningen University, Animal Nutrition Group, P.O. Box 338, 6700 AH, Wageningen, the Netherlands, 2 Trouw Nutrition, Research and Development, P.O. Box 299, 3800 AG, Amersfoort, the Netherlands

Contact: leo.den.hartog@trouwnutrition.com

The overall increase (2010-2050) in animal and aqua protein production expectation is 60% ranging from 38% for pork to 104% for poultry (IFIF, 2017). But there is also a significant number of challenges facing the animal and allied industries with respect to sustainable global production of meat, fish,

dairy and eggs where market demands and consumer needs will put more constraints on our production systems and methods (Alders, 2016). For an optimal utilization of earth's surface for producing food, 35% - 40% of the recommended daily protein consumption of adults should come from animal protein (van Zanten, 2016). In addition, the average worldwide productivity of farm animals is 30-40% below their genetic potential because of suboptimal conditions and health status. These challenges are dynamic and diverse solutions and opportunities will require development of appropriate technology and using and advancing our knowledge base. Advances in animal nutrition will contribute to meet these challenges. Environmental and nutritional influences during early life have a profound and long-lasting effect on performance and health. The rapid development of antimicrobial resistance urges the need for effective strategies to reduce antibiotic use

The importance of precision feeding



Genetics

New opportunities in the production of animal feeds, crops and livestock.

Feed

More accurate analysis of feedstuff nutritional content and greater understanding of market pricing.

Animal

Better understanding of digestive processes and exact nutritional requirements.

End product

High efficiencies in terms of getting to market, but with no compromise on quality.

Consumer

Critical and demanding in terms of quality, choice, value, safety and sustainability.

in animal production. A drastic reduction of antibiotic use can be achieved by moving to a new farming model based on an integrated and multi-stakeholder collaboration that integrates feed, farm and health management. Targeted feed additive strategies can be applied to control microbial quality of feed and water and support gut health. Precision nutrition methods and tools, such as dynamic feed evaluation and animal models, can be implemented to economically optimize the feed program and reduce emissions into the environment. Sustainable feed supply meeting market demands is feasible and will require a multidisciplinary approach of all stakeholders in the value chain.

Leo den Hartog

Leo den Hartog is director of R&D at Trouw Nutrition (a Nutreco company) and part-time professor in Sustainable Animal Nutrition in Production Chains at Wageningen University. It was from this same university that den Hartog graduated in Animal Sciences and where he obtained his PhD. Den Hartog's extensive experience in animal production is reflected in over 450 scientific and applied articles and seven books as author or co-author. To date, he has given more than 600 lectures in over 35 different countries. Since

the start in 2015, den Hartog has been involved in the Feed-a-Gene project and he is chairman of the Stakeholder Advisory Board.



Expectations of poultry breeding industry from research projects

J.A.M. van Arendonk

Hendrix Genetics, PO Box 114, 5830 AC Boxmeer, The Netherlands

Contact:

johan.van.arendonk@hendrix-genetics.com

Animal genetics has played a key role in improving the sustainability of animal production and needs to continue to do so in the future. Within Hendrix Genetics, we have established a sustainability program comprising of three building blocks: animals, people and planet. Animal welfare, biosecurity and genetic resources are the key priorities within the building block animals. Ensuring animals are treated with care and respect and are kept under the highest standards of welfare is essential. We ensure that taking good care of animals is embedded in our company culture. As global suppliers of breeding stock, we have a responsibility for ensuring biosecurity and animal health. In addition, we also have an obligation to protect our genetic resources. People make our business, that's why we strive to enhance the quality of life for consumers, customers and colleagues. Consumers in different countries across the world vary but purchasing with sustainability in mind has increased overall during the last years. For enhancing colleague's quality of life employee engagement, equal opportunity, expertise, community support and health and safety are vital elements. Minimizing the environmental impact of livestock through improving input efficiency and helping to reduce the use of antibiotics are key parts of the building block planet.

By responding to the needs of our partners in the protein value chain, we are continuously exploring new opportunities for improving sustainability. In addition, the company is investing in minimizing its own ecological footprint to preserve and improve the environment that its activities impact. Responding to the needs of our partners implies that we are continuously exploring innovations in the domain of measuring health, welfare and productivity of animals. These innovations need to be based not only on a solid understanding of the underlying biology but also an overall view on the issue at stake. Developing a solid understanding is an important but not the only driver to be involved in a research project. Equally important drivers for par-



Credit: Cobb

ticipation in a research project are creating awareness in the scientific community for the issues involved in improving sustainability and training a new generation of researchers. Solving sustainability issues often requires collaboration in multidisciplinary teams. Industry participation in research projects is expected to speed-up innovations and contribute to training of new talents that are focussed on generating solutions. Collaboration is therefore crucial for realizing improvement of sustainability.

Johan van Arendonk

Dr. Johan A.M. van Arendonk is Chief Innovation & Technology Officer at Hendrix Genetics (Boxmeer, Netherlands-EU), a global multi-species animal breeding, genetics and technology company. Hendrix Genetics has breeding programs in turkeys, layers, guinea fowl, swine, salmon, trout and shrimp with operations in 24 countries. Johan contributes to strengthening the research and product development activities in these species. Prior to joining Hendrix Genetics, he was full professor and dean of sciences at Wageningen University. His research focussed on quantitative genetics and the impact on novel technologies on breeding schemes. Over time, he changed from doing research himself to coaching people involved in research and training. He played an active role in coaching a new generation of scientists by supervising over 90 PhD candidates. Dr van Arendonk obtained his PhD in Animal Breeding in 1985 at Wageningen University. He is author of over 300 publications in international refereed scientific journals: details can be found at <http://www.researcherid.com/rid/E-2536-2011>. Johan grew up on a dairy farm in Bavel, a small village in the South of The Netherlands where its interest in livestock improvement started.



The importance of research for developing standards to control animal diseases: the role of the OIE

S. Messori, E. Erlacher-Vindel

*World Organisation for Animal Health (OIE),
Science and New Technologies Department,
12 rue de Prony, 75017 Paris, France*

Contact: s.messori@oie.int

The World Organisation for Animal Health (OIE), is the intergovernmental organisation responsible for improving animal health and welfare worldwide. The OIE was established in 1924, and it has today 181 Member Countries. Recognised as reference by the World Trade Organization, the OIE develops standards designed to prevent and control animal diseases including zoonoses, to ensure sanitary safety of world trade. The Sixth Strategic Plan of the OIE for the period 2016-2020 outlines the need for continued development of standards and guidelines based on science for the management, control and/

or eradication of disease, including zoonoses, taking into account economic, social and environmental factors. Scientific research is key to find effective ways to prevent, control, and eradicate pathogens posing threats to both animal and human health. National and international research collaborations are fundamental for ensuring the timely delivery of needed disease control tools, greatly contributing to protect animal health. The OIE is actively supporting research collaboration and coordination through its participation in the STAR-IDAZ International Research Consortium on Animal Health (IRC), a global forum of public and private R&D programme owners/managers. The aim of the STAR-IDAZ IRC is to improve the control tools for a list of priority diseases/issues through the delivery of candidate vaccines, diagnostics, therapeutics, procedures, and key scientific information/tools to support risk analysis and disease control. Through its involvement in the STAR-IDAZ IRC, the OIE supports the implementation of research projects on topics of high interest for advancing animal health at global level.

Stefano Messori

Stefano Messori graduated in veterinary medicine at the University of Parma (Italy). He holds a PhD in animal science obtained at the University of Bologna (Italy) and has been recognised as European Veterinary Specialist on Animal Welfare Science, Ethics and Law. During his career, he undertook research on animal nutrition (especially focusing on piglet weaning), animal health and welfare. Since 2016 he is Chargé de mission at the World Organisation for Animal Health (OIE). There, he oversees the Scientific Secretariat for the STAR-IDAZ IRC (<http://www.star-idaz.net/>), a major international collaboration initiative to coordinate research on animal health at global level. In his current function, he directs research gap analyses and advise on the realignment of research programmes, as to foster the development of new and improved animal health strategies and tools for prevention, diagnosis, treatment, control, and eradication of priority animal diseases, including zoonoses.



Effects of protein restriction on rumen metagenome and metabolic profile in Holstein calves

S. Costa, J. Balcells, G. De La Fuente, J. Mora, J. Álvarez-Rodríguez, D. Villalba

University of Lleida, Animal Science, Rovira Roure 178, 25198, Spain

Contact: scosta@ca.udl.cat

The aim of this work was to study the impact of a crude protein (CP) restriction on productive performance, metagenomics and metabolic profile in growing (120 to 270 days of age) Holstein calves intensively reared. Forty calves were assigned to two dietary treatments: CP in the concentrate was formulated either based on the levels used commercially (CTR: 12% CP on an as-fed basis) or reducing them (LP: 10% CP on an as-fed basis). Concentrate was supplemented with barley straw and both were supplied *ad libitum*. Live weight (LW) and concentrate intake were registered automatically. Ten animals

per treatment (220 kg of LW and 155 days of age) were sampled to determine nitrogen balance, rumen metagenome, and urinary/plasma metabolic profiles. Nitrogen balance was estimated by difference between intake and excretion (urinary plus faecal excretions). Rumen bacterial and archaeal community composition was analysed by taxonomic profiling of 16S ribosomal RNA variable regions. Urine and plasma samples were analysed by liquid chromatography coupled to mass spectrometry. The results showed that, at the beginning of the growing phase, CP restriction reduced average daily gain in LP animals (1.65 ± 0.04 vs. 1.77 ± 0.04 kg/d, for LP and CTR respectively, $P=0.044$). Nitrogen excretion (65.9 ± 5.3 vs. 81.7 ± 5.3 g/d, for LP and CTR respectively, $P=0.049$) and retention (30.2 ± 4.2 vs. 48.7 ± 4.2 g/d, for LP and CTR respectively, $P=0.006$) were lower in LP animals than in CTR animals. Only 69% of detected operational taxonomic units were common between both treatments and protein restriction raised richness levels in rumen microbiota (129.9 ± 7.8 vs. 101.4 ± 7.8 OTUs/animal, for LP and CTR respectively, $P=0.019$). Dietary

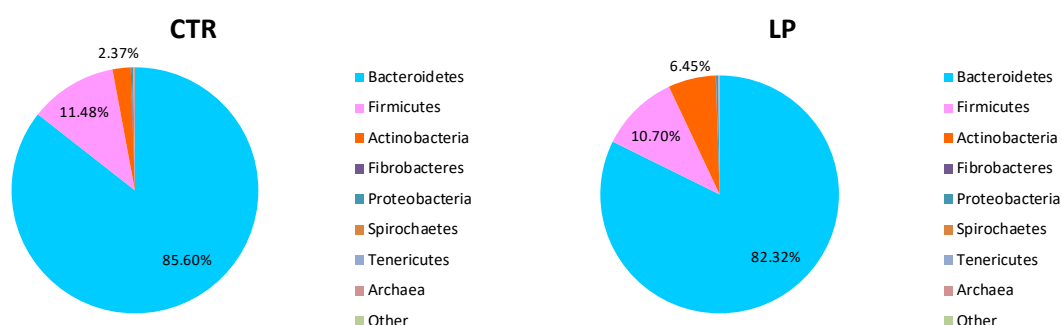


Figure 1. Rumen bacterial and archaeal composition at phylum level. Obtained in growing Holstein calves (221 kg of body weight and 155 days of age) receiving two different diets: commercial concentrate (12% crude protein on an as-fed basis) plus barley straw (CTR) or low protein concentrate (10% crude protein on an as-fed basis) plus barley straw (LP).

CP restriction led to an increase in *Actinobacteria* phylum (Figure 1), mainly integrated by *Bifidobacterium* genera which is capable of fermenting starch. CP restriction induced the appearance of new discriminant metabolites, being this effect clearer in urine than plasma samples. Research funded by INIA-RTA-14-038-C02.

Sandra Costa

Sandra Costa is a PhD student in the Department of Animal Science at University of Lleida, Spain. She has a degree in Animal Science (University of Lleida) and a MSc diploma in Animal Nutrition (University of Zaragoza). During this past year, her topic has focused on the relationship between protein supply and digestion, rumen microbiota and metabolic profile in young animals. Regarding the

Feed-a-Gene project, she has been optimizing the urine and plasma sampling method and analytical procedure to improve precision in downstream metabolome studies, in both pigs and beef cattle.



Genetic and environmental influence on colostrum quality and absorption in Swedish dairy cattle

J.M. Cordero-Solorzano^{1,2}, J.J. Wensman³, M. Tråvén³, A. Larsson³, T. De Haan³, D.J. De Koning¹

1 Swedish University of Agricultural Sciences, Department of Animal Breeding and Genetics, Box 7023, 750 07 Uppsala, Sweden,
2 Animal Health Service of Costa Rica (SENASA), Box 3-3006, 40104 Heredia, Costa Rica,
3 Swedish University of Agricultural Sciences, Department of Clinical Sciences, Box 7054, 750 07 Uppsala, Sweden

Contact: juan.cordero@slu.se

Colostrum with sufficient IgG content is essential for the newborn calf, as it requires this passive immunity to survive until weaning. Previous studies have shown a high variation in the amount of colostrum antibodies in dairy cows, with a large proportion having low antibody levels. Failure of passive transfer (FPT) occurs when a calf does not absorb enough antibodies (<10 g/l of IgG in serum) from the colostrum. Some calves absorb antibodies very effectively while others do not. This difference in uptake cannot be explained solely by the time, amount and quality of the colostrum given. The purpose of this study is to identify genetic and environmental factors that can explain this difference in the effectiveness of antibody uptake in calves and variation in colostrum quality in cows. Three experimental farms were included in the study. Colostrum samples from 1311 cows calving from January 2015 to April 2017 were collected and analyzed by Brix refractometer to estimate antibody concentration. For two of the farms, serum from 785

calves was collected at 2 to 7 days after birth and analyzed by total IgG ELISA. Brix values ranged from 6.5 to 38.9%, and calves serum IgG from 1.1 to 91.6 g/l. Preliminary results using a linear mixed model show an effect of breed on colostrum quality with Holstein cows displaying significantly higher values than Swedish Red ($p = 5 \times 10^{-12}$). This was also true for samples with shorter calving to colostrum sampling times ($p = 2 \times 10^{-16}$). Genetic parameters will be estimated for colostrum Brix values, serum total IgG and Apparent Efficiency of Absorption (AEA). Early estimates of Herd-Year-Season explain 2.5 to 16% of the variation observed.

Juan Cordero-Solorzano

Juan Cordero-Solorzano is a doctoral student from Costa Rica in a joint PhD programme between the Swedish University of Agricultural Sciences (SLU) and Wageningen University. He started this position in 2015 within the framework of Erasmus Mundus European Graduate School in Animal Breeding and Genetics (EGS-ABG). His current work focuses on the genetic association between antibody levels in colostrum of dairy cattle and its effects on calf health by combining serological diagnostics with genetic analyses. He is also looking into Natural Antibodies (NABs) and their potential as predictors of health traits in dairy cows.



A systems genetics approach reveals potential regulators of feed efficiency in pigs

Y. Ramayo-Caldas^{1,2}, M. Ballester¹, J.P. Sánchez¹, R. González-Prendes^{2,3}, M. Amills^{2,3}, R. Quintanilla¹

1 IRTA, Animal Breeding and Genetics Program, Torre Marimon, 08140, Caldes de Montbui, Spain, 2 Universitat Autònoma de Barcelona, Facultat de Veterinària, UAB, 08193, Bellaterra, Spain, 3 Centre of Research in Agricultural Genomics, Universitat Autònoma de Barcelona, 08193, Bellaterra, Spain

Contact: yulixaxis.ramayo@irta.cat

Feed efficiency (FE) has a major impact on the economic sustainability of pig production. In this study, we used the Association Weight Matrix (AWM) approach to identify interacting genes and pathways associated with FE in pigs. Eleven traits related to FE, growth and fat deposition in 352 Duroc pigs were considered, including body weight gain (ADG), feed intake (ADFI), residual feed intake (RFI), and food conversion ratio (FCR). Initially, a genome-wide association analysis was performed on the 11 traits using ~31K SNPs. The additive effects of the significant SNPs located within or ≤ 10 kb from the nearest annotated gene (Sscrofa11.1 assembly) were used to build the AWM matrix relating genes effects to phenotypes. Pairwise correlations across AWM rows were used to predict gene-gene interactions. The resulting co-association gene network was formed by 704 genes (47 were Transcription Factors (TF)) connected by 35,819 edges. To identify putative regulators, we explored combinations of TF that spanned most of the network topology with minimum redundancy. Among them, it is worth noting that LHX4, POU2AF1 and TCF7L2 were co-associated with 397

genes. SNPs in these genes explained 51%, 48%, 46%, 35% of the phenotypic variance for RFI, ADFI, FCR and ADG, respectively. The functional annotation of these 397 genes showed that immune response is among the most overrepresented biological processes. In addition, social behaviour, circadian entrainment, and regulation of cell growth processes were also identified as overrepresented. According to the literature, TCF7L2 has been associated with eating behaviour,

FCR, and RFI in pigs. LHX4 is involved in the control of differentiation and development of the pituitary gland, whereas POU2AF1 is essential for the response of B-cells to antigens. We hypothesize these TF mediate a highly inter-connected regulatory cascade that seems pivotal for FE in pigs.

Why farmers adopt environmental practices? The case of French dairy farms

T.T.S. Siqueira^{1,2}, D. Galliano², G. Nguyen²

1 Université de Toulouse - Ecole d'Ingénieurs de PURPAN, 75 Voie du TOEC, 31400, France, 2 Institut National de la Recherche Agronomique, 75 Voie du TOEC, 31400, France

Contact: tiago.siqueira@purpan.fr

The adoption of environmental practices is an important issue for livestock production. This study explores the main drivers of the adoption of nine environmental practices in the case of French dairy farms. First, we tested the role of internal farm factors related to the characteristics of the farmer, farm's structure, and governance. Second, we tested the role of external factors related with commercial and regulatory followed by spatial features. We used data of 47211 dairy farms from the 2010 French Agricultural Census to study the correlation between internal and external factors and each one of the nine environmental practices. The results show that among governance and managerial characteristics, attitudes towards uncertainties (insurance and succession) play a more important role than individual characteristics of the farmer (e.g., age, gender, or training). The results also suggest that farm size has a negative effect on the adoption of permanent grassland, leguminous for forage, no irriga-

Yulixaxis Ramayo Caldas

Yulixaxis Ramayo Caldas completed his PhD at the Universitat Autònoma de Barcelona (Spain) in July 2013. Afterward he was a post-doctoral research at INRA (France), and he was recruited in 2014 as Junior research scientific at INRA. Currently, he is working at IRTA's Animal breeding & genetics program (Barcelona, Spain) under Marie Skłodowska-Curie grant (P-Sphere) agreement funded by the European Union H2020 Research and Innovation programme. His research interests are related to applied statistical and computational tools to understand the genetic basis of complex traits through the use of both high throughput sequencing technologies and the implementation of holistic approaches combining multiple sources of

information. He is also interested in contributing to the knowledge in the area of metagenomics applied to animal production.



tion, crop rotation and no fertilisers and no pesticides practices. However, farm size has a positive effect on the adoption of no-till, manure treatment and agroecological structures as hedges, lines of trees, woods, and fallow lands. In terms of external factors, the statistical analysis highlights the strong correlation of positioning on alternative markets, short circuits, organic products, or quality markets on the adoption of these practices. As the literature commonly suggests, we show that environmental regulations also drive the adoption of farming environmental practices. The results also show the central role of the spatial environment of the farm and, more specifically, the environmental behaviour of neighbouring farms as a major driver of farm adoption behaviour. Finally, policies to promote locally farmer's experience exchange and to supporting diversification, high quality products and short circuits can further the adoption environmental practices on dairy farms.

Tiago Teixeira da Silva Siqueira

Tiago Teixeira da Silva Siqueira is an Assistant Professor in Agricultural Economics at INP Toulouse – Ecole d'Ingénieurs de PURPAN, France. Since 2016, he is also the coordinator of the International MSc European Animal Management and Sustainability. He is agronomist and has a PhD in Economics obtained at University of Toulouse. He is also a member of the research unit "Agroecologies, innovations and ruralities" at INRA (UMR 1248 AGIR). In the past 7 years, he has been evolving in projects to study the sustainability of livestock farming systems around the world. He is also interested on the organizational factors related to the adoption of sustainable agricultural practices. He uses interdisciplinary approaches (Animal sciences, Environmental sciences/Ecology and Economics/Management) to study this problematic.



Dairy farm of AgroParisTech, Grignon, France
Credit: Spedona, CC BY-SA 3.0

Table 1: The main drivers of environmental practices adoption for French dairy farms

Explanatory Variables		Practices									
		Permanent grassland	Leguminous fodder	Non-synthetic fertilizers	Chemical crop protection	Agroecological structures	Treatment of manure	Conservation tillage No-till/	Lack of Irrigation	Crop rotation	
FACTEURS INTERNES Characteristics of the farmer	Education (diploma)	-0.032*** -0.00049***	0.0096 -0.0016*	-0.00084 0.00078***	-0.0035* 0.000035	0.066*** 0.0055***	0.058*** 0.0020***	0.14*** 0.0017***	-0.033 -0.0017	0.0076 -0.00031	
	Age	0.016***	0.0016	0.013***	0.019***	-0.069***	-0.072***	-0.062***	0.14***	-0.033*	
	Male	0.016***	0.018	-0.0015	0.00085	0.0054	-0.021	-0.069***	0.099***	-0.055***	
	Known Successor	-0.017***	-0.17***	-0.044***	-0.014***	0.15***	0.072***	-0.13***	-0.018	-0.11***	
	Agricultural insurance										
Farm Governance	Legal Status:										
	Individual Property	Ref	Ref	Ref	Ref	Ref	Ref	Ref	Ref	Ref	
	Partnership farms	-0.032***	0.18***	0.038***	0.019***	0.0093	0.11***	0.15***	-0.40***	0.015	
	Others	-0.054***	0.079***	0.0070**	-0.014***	0.081***	0.068***	0.14***	-0.20***	0.031*	
	Owined land	-0.044***	-0.092***	0.0082*	0.014***	0.46***	0.031	-0.0100	0.055	-0.035	
Farm structure	Family work	-0.0026	-0.074**	-0.024***	-0.0031	-0.064**	-0.15***	-0.10***	0.16***	0.076**	
	Diversified										
	No	Ref	Ref	Ref	Ref	Ref	Ref	Ref	Ref	Ref	
	Yes (without dairy)	0.0037	0.091***	-0.0078	-0.016***	0.056**	0.066***	0.037	-0.0039	-0.058**	
	Yes (dairy processing)	0.013*	0.25***	0.043***	0.023***	-0.21***	-0.13***	0.24***	0.13	0.17***	
EXTERNAL FACTORS	Size/Turnover	-0.061***	-0.16***	-0.12***	-0.13***	0.17***	0.14***	0.098***	-0.19***	-0.13***	
	ICTs - specialized accounting software	-0.014***	0.080***	0.0040	-0.0067***	-0.060***	0.041***	0.12***	-0.22***	0.068***	
	ICTs - specialized technical software	-0.0095***	0.053***	-0.0076***	-0.016***	0.039***	0.027**	0.097***	-0.023	0.021	
Commercial and Regulatory environments	Organic:										
	No	Ref	Ref	Ref	Ref	Ref	Ref	Ref	Ref	Ref	
	Desired	-0.00028	0.16***	0.12***	0.074***	0.11***	0.13***	0.16***	-0.14***	0.051	
	Yes/under conversion	-0.018***	0.30***	0.56***	0.30***	0.0087	0.43***	0.043	-0.0064	0.82***	
	Quality label:										
	No	Ref	Ref	Ref	Ref	Ref	Ref	Ref	Ref	Ref	
	Yes (except dairy products)	0.0089**	-0.053*	-0.015***	0.0011	-0.020	0.11***	0.018	0.032	-0.0018	
	Yes (dairy products)	-0.036***	0.11***	-0.0055**	0.0041**	0.14***	0.085***	0.19***	0.063***	0.052***	
	Commercialization on short market chains:										
	No	Ref	Ref	Ref	Ref	Ref	Ref	Ref	Ref	Ref	
	Yes (except dairy products)	0.0070	0.058*	0.013*	0.020**	0.052**	0.11***	-0.029	-0.42***	-0.036	
	Yes (dairy products)	0.0052	0.041	0.052***	-0.00032	-0.041	0.19***	-0.038	-0.17***	-0.054	
	Paid for environmental services	0.087***	0.098***	0.11***	0.097***	-0.065***	0.058***	0.025	0.11***	-0.0076	
	Spatial environment	Agglomeration rate of dairy farms	-0.0057***	-0.16***	-0.012***	0.042***	-0.12***	0.098***	-0.037***	0.49***	0.10***
		Score of the neighbourhood practices	0.92***	1.95***	0.22***	0.26***	-0.46***	0.95***	0.85***	2.17***	0.74***
Geographical area:											
Plain		Ref	Ref	Ref	Ref	Ref	Ref	Ref	Ref	Ref	
Disadvantaged		0.023***	0.18***	0.038***	0.061***	0.029	-0.050***	0.068***	-0.61***	0.052**	
N	Piedmont	-0.0057	-0.28***	0.035***	0.12***	0.22***	0.24***	-0.23***	-0.95***	-0.27***	
	Mountain	-0.026***	-0.053*	0.037***	0.14***	0.26***	0.20***	0.027	-1.04***	-0.075***	
	High Mountain	-0.017	1.04***	0.32***	0.18***	-0.87***	-0.057	0.70***	-2.34***	0.47***	
		47211	47211	47211	47211	47211	47211	47211	47211	47211	
		7983.8	7983.8	7983.8	7983.8	7983.8	7983.8	7983.8	7983.8	7983.8	
chi2											
r2_p											

Source: 2010 French Agricultural Census

p-values: * p < 0.10, ** p < 0.05, *** p < 0.01



Rapeseed flowers
Credit: Gilles Tran

Feed-a-Gene communications presented in other EAAP sessions, DPP and EPC

The following pages include communications submitted by Feed-a-Gene researchers to the 69th EAAP meeting (outside the joint Feed-a-Gene/SAPHIR session), to the 14th Symposium on Digestive Physiology of Pigs, and to the 15th European Poultry Conference.

69th EAAP, 27-31 August 2018, Dubrovnik, Croatia



The main theme of the 69th Annual meeting of the EAAP is 'Conventional and traditional livestock production systems – new challenges' including topics such as sustainability, animal welfare, agro-ecology, and product quality. The programme contains various disciplines and latest findings regarding farm animals, such as genetics, nutrition, management, health, welfare and physiology for cattle, sheep, goats, pigs, horses, poultry, and fur animals.

14th International Symposium, Digestive Physiology of Pigs, 21-24 August 2018, Brisbane, Australia



The scientific program of the DPP is centered around the digestive system, focusing on specific aspects such as the emerging areas of the Microbiota and the nutrient chemosensory mechanisms in the pig gastrointestinal tract. DPP targets the latest advances in the field of digestive physiology, which will illustrate the future research trends.

15th European Poultry Conference, 17-21 September 2018, Dubrovnik, Croatia



The programme of the European Poultry conference will be focused on the main issues currently related to poultry research and production in order to add to and improve knowledge in a world where information and innovations are spread rapidly.

WP1 Alternative feed ingredients and real-time characterisation

The influence of faeces drying method on nutrient digestibility of growing pigs

EAAP 2018

A.D.B. Melo^{1,2}, B. Villca¹, E. Esteve-García¹, R. Lizardo¹

¹ IRTA, Centre Mas de Bover, Crta Reus-El Morell Km. 3.8, E-43120 Constantí, Spain,
² PUCPR, Prado Velho, Curitiba-PR, Brazil

Contact: rosil.lizardo@irta.cat

Elimination of moisture from faeces samples is crucial to preserve them before laboratory analyses, and it might affect estimation of nutrient digestibility. Freeze-drying is the standard method but is more expensive and time-consuming when compared with oven-drying methods. The aim of this study is

to evaluate the influence of drying methods on nutrient digestibility in growing pigs. One hundred forty-four growing pigs were housed by two in 72 pens, and *ad libitum* fed for 6 weeks. Titanium dioxide (0.5%) was included into diets as a tracer. Faeces samples were collected during the 5th week of experiment and aliquoted to oven-dry at 60°C for 72h or freeze-dry (condensation at -60°C, freezing at -35°C, lyophilisation at 25°C) for 72h. Samples were analyzed for dry matter (DM), gross energy (GE), crude protein (CP), ether extract (EE), crude fibre (CF), ash, organic matter (OM), N-free extracts (NFE) and titanium dioxide contents. Calculations were performed and data analyzed using the GLM procedure of SAS. In general, oven-dry method showed a lower coefficient of variation, which could explain slightly higher significant DM (83.2 vs. 84.2 %), GE (83.8 vs. 85.3%), CP (82.79 vs. 80.24%), EE (81.09 vs. 80.04%), CF (40.34 vs. 32.44%), ash (46.30 vs. 44.15%) and OM (85.5 vs. 86.4%) digestibility than freeze-drying. According to these results, it can be concluded that the oven-dry method (60°C, 72h) can replace freeze-drying to determine major nutrient digestibility for growing pigs.

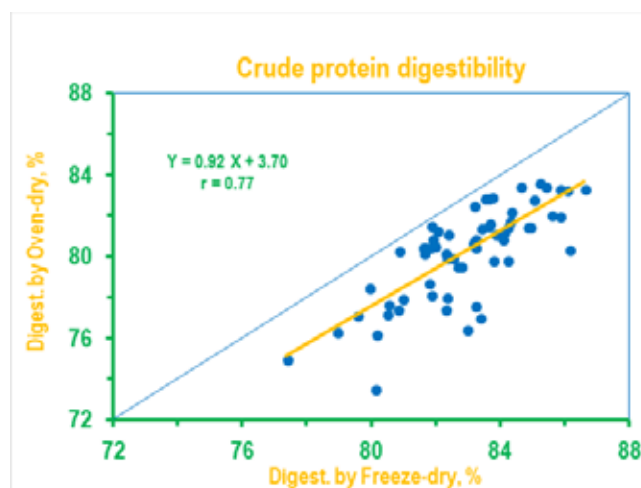


Figure 1. Effect of faeces drying method (freeze-drying or oven-drying) on crude protein digestibility in growing pigs

Rapeseed meal and enzyme supplementation on growth performance and nutrient digestibility in pigs

EAAP 2018

A.D.B. Melo^{1,2}, B. Villca¹, E. Esteve-García¹, R. Lizardo¹

¹ IRTA, Centre Mas de Bover, Crta Reus-El Morell Km. 3.8, E-43120 Constantí, Spain,
² PUCPR, Prado Velho, Curitiba-PR, Brazil

Contact: rosil.lizardo@irta.cat

The EU animal production relies on protein imports to satisfy the demand of the animal feed industry. However, these imports are subject of increasing concerns and the use of alternative EU protein sources is recommended. Rapeseed meal (RSM), a by-product of oil industry, contains large amounts of protein but also contains antinutritional factors (ANF) such as glucosinolates or a high

fiber content that limit its use. Processing of RSM to eliminate ANF might increase its protein content resulting more attractive for animal feeding. The aim of this study is to evaluate the influence of a high-protein RSM in combination with enzyme supplementation of diets for growing pigs. A 2x3 factorial arrangement of diets containing conventional (35% CP) or high-protein (40% CP) RSM in combination with supplementation of protease or NSPase and protease enzymes was used. One hundred forty-four pigs were allocated into 12 blocks of body weight and sex, and housed by 2 in 72 pens. The trial lasted 6 weeks and faeces samples were collected during the 5th week and oven-dried for 72h at 60°C before lab analysis. Productive performance and major nutrient digestibility parameters were used as response criteria. Data were analyzed using the GLM procedure of SAS. Body weight gain was not affected by the dietary treatments (NS). However, feed conversion ratio was improved (P<0.01) on

Table 1. Influence of processed rapeseed meal (RSM) and enzyme (ENZ) supplementation on growth performance, feed efficacy and nutrient digestibility of growing pigs fed RSM based diets.

Rapeseed meal	RSM-	RSM+	RSM-	RSM+	RSM-	RSM+	P values			
Enzymes	No	No	Prt	Prt	+NSPase	+NSPase	RSM	Enz	RSM*Enz	RSD
Bodyweight, kg	64.905	65.570	66.192	65.975	66.083	65.871	0.93	0.67	0.88	3.537
Weight gain, g/d	754.9	758.6	776.6	782.5	769.9	765.8	0.92	0.60	0.97	78.11
Feed intake, kg/d	1.642ab	1.596ab	1.663a	1.598ab	1.665a	1.565b	0.01	0.89	0.71	0.116
Feed conversion ratio	2.182a	2.112ab	2.150a	2.050b	2.165a	2.047b	0.01	0.36	0.79	0.124
Total tract digestibility										
Energy,%	84.8	85.5	85.8	84.7	85.4	85.1	0.57	0.94	0.08	1.30
Protein,%	82.1	82.6	83.8	81.7	83.0	82.7	0.25	0.75	0.12	2.11
Fat,%	78.7b	82.4a	81.0ab	81.0ab	80.9ab	81.2ab	0.02	0.84	0.03	2.39
Phosphorus,%	40.0c	49.3a	43.8b	46.3ab	43.0bc	46.5ab	0.001	0.91	0.02	4.23
NSPs,%	65.6	65.6	64.9	63.5	64.9	63.6	0.29	0.62	0.53	3.86

RSM- / RSM+ : conventional or technologically improved rapeseed meal to have a higher crude protein content; Prt, NSPase: exogenous protease or carbohydrase enzymes (ENZ) included into feeds; a,b,c : Means within the same row with different letterscript are different at P<0.05 .

pigs fed the high-protein RSM diets due to a reduction of feed intake ($P < 0.01$). On the contrary, enzymes inclusion into diets did not affect productive performances ($P > 0.05$). Digestibility of dry matter, nitrogen or energy were not affected by the diet. Only fat

digestibility was improved ($P < 0.01$) due to high-protein RSM utilization. In conclusion, high-protein RSM improves feed efficiency of growing pigs and can positively contribute to reduce EU protein imports for animal feeding.

Diego Melo

Diego Melo is a PhD student in Animal science at Pontifical Catholic University of Paraná (PUC-PR), Brazil. During his veterinary medicine degree at State University of Santa Cruz, Brazil, and Purdue University/USDA, USA, he developed studies to evaluate the effect of several feed additives in gut health of poultry and pigs. He obtained a Master in animal science at PUC-PR, focused on the use of feed additives to promote gut health in piglets. During the last year, he has been involved in the tasks 1.4 and 1.5 of the WP1 of the Feed-a-Gene project, carried out at IRTA, Spain; evaluating the use of technologically improved rapeseed meal for growing pigs. These investigations will be part of his PhD thesis.



Rosil Lizardo

Rosil Lizardo is a senior researcher on Swine Nutrition and Production at IRTA (Spain). He is graduated in Animal science from University of Évora (Portugal), with an MSc on Animal Production from CIHEAM-IAMZ (Zaragoza, Spain). He conducted his PhD exploring the adaptation of the digestive tract of the weaned piglet to feed substrates at INRA (St Gilles, France) where he also carried out a post-doc on pig growth modeling. His areas of interest have been focused on the development of liquid feeding of pigs, the interaction between nutrition and meat quality and the evaluation of feed additives (enzymes, probiotics, herbal extracts, acidifiers, clays, etc.) to improve swine productivity. Since 2015, he has been involved in characterization of alternative feed ingredients work package of the Feed-a-Gene project and his objective is to evaluate the technologically processed EU-grown rapeseed meals in combination with exogenous enzymes in diets for growing pigs.



Effect of novel soya bean meal processing technologies on broiler performance and digestibility

European Poultry Conference 2018

P. Sakkas¹, E. Royer⁴, S. Smith¹, P. Carré², A. Quinsac³, I. Oikeh¹, I. Kyriazakis¹

¹ Agriculture, School of Natural and Environmental Sciences, Newcastle University, Newcastle upon Tyne, United Kingdom, ² Olead, Pessac, France, ³ Terres Inovia, Pessac, France, ⁴ IFIP Institut du porc, Toulouse, France

Contact: panagiotis.sakkas@newcastle.ac.uk

Locally produced, expeller soybean meal (SBM) may be an important constituent of European broiler diets in the future. In the present trial 4 SBMs were produced from European grown soybeans, using different processing methods; this is the first time that the combination of these methods has been applied. Broiler starter (d0-14) and grower (d15-28) diets were offered to 288 Ross 308 male in a 2x2 design: 2 processing methods ((Extrusion-pressing (E) vs. Flaking-pressing-cooking (F)) x 2 hulling

methods ((de-hulling (D) vs. no dehulling (ND))). Variables measured consisted of ADG, ADFI, FCR, apparent ileal DM and CP digestibility, jejunal histomorphometry at d14 and d28 and ileal digesta viscosity at d28 of age. In addition, carcass and carcass part yield, organ weight, and empty gastrointestinal tract (GIT) weight and length per small intestinal segment were assessed at d28. Processing method did not affect any of the variables tested. On the other hand, hull presence increased ($P < 0.05$) ADFI over the starter period, but not over the grower period. In addition, hulled presence increased proventriculus, gizzard and jejunum weight, and reduced carcass yield at d28 of age, likely due to the higher fibre content. Method of processing and hulling significantly interacted ($P < 0.05$) for ADFI and ADG at the end of the starter period, being highest for the E/ND treatment, but overall broiler performance was similar between dietary treatments. Similarly, small intestinal architecture and DM and CP digestibility were not affected by dietary treatments at either d14 or d28 post hatch. Although there was some variation in soybean protein solubility and trypsin inhibitors amongst SBM products these factors did not appear to affect any of the measured variables. In conclusion, both treatments of locally produced SBM resulted in products which equally promoted

Table 1. Effect of soybean meal treatments, produced through the combination of different processing and hulling methods, on performance variables of broilers over the starter (d1-14) and grower periods (d15-28).

		BW		ADFI		ADG		FCR			
Days of age		0	1-14	15-28	1-28	1-14	15-28	1-28	1-14	15-28	1-28
Extrusion	De-hulled	37.2	36.7 ^a	110.3	73.5	27.5 ^a	65.5	46.5	1.33	1.65	1.58
	hulled	37.0	38.9 ^b	111.4	75.1	29.1 ^b	66.9	48.0	1.33	1.61	1.57
Flaking	De-hulled	37.0	37.6 ^{ab}	112.2	74.9	28.8 ^{ab}	67.2	48.0	1.30	1.64	1.56
	hulled	36.3	37.7 ^{ab}	114.1	75.9	27.6 ^a	68.9	48.2	1.37	1.62	1.57
SEM		0.45	0.48	1.39	0.76	0.43	1.09	0.59	0.019	0.025	0.025
Source		Probabilities									
Method		0.341	0.705	0.116	0.184	0.832	0.114	0.157	0.783	0.965	0.804
Process		0.298	0.032	0.295	0.104	0.660	0.186	0.164	0.094	0.279	0.975
Method*Process		0.571	0.043	0.758	0.698	0.004	0.913	0.293	0.090	0.709	0.513

broiler performance over the grower and the overall growing period. Although there were some differences in KOH solubility and TIU levels, these were poor predictors of DM and ileal CP digestibility. Hulled products resulted in similar performance, which could be ascribed to their effect on proximal GIT development. This nonetheless was achieved at an additional cost; slightly higher proportions of the hulled products were used to achieve similar CP content. Ultimately, the treatment with the least cost to produce should be employed in small scale production units, with other things being equal.

Panagiotis Sakkas

Panagiotis Sakkas is research associate at the School of Natural and Environmental sciences of Newcastle University. He obtained his PhD (2012) at the University of Edinburgh where he investigated host nutrition-parasite interactions in monogastric and ruminant hosts. Since obtaining his PhD he has worked as a research associate for Wageningen University (2012-2014) and for Newcastle University (2014-), with his research expanding on various nutritional research themes in monogastric animals with an emphasis on the interaction between nutrition and production diseases. Since 2015 he has been working on WP1. His objectives are to investigate the impact of novel processing methods of European soya for use in broiler diets (task 1.4) and the use of novel enzymes for the improvement of the nutritional value of feed ingredients.



WP2 New animal traits for innovative feeding and breeding strategies

Genome-wide association study of post-weaning growth in rabbits

EAAP 2018

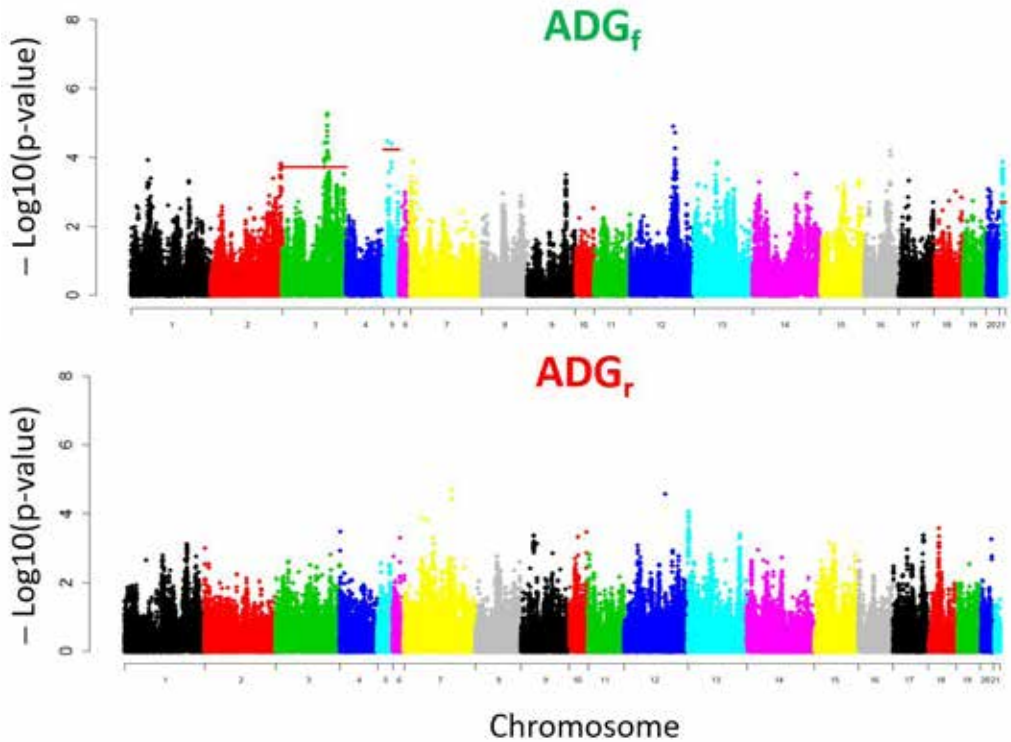
M. Ballester, M. Velasco, M. Piles, O. Rafel, O. González, J.P. Sánchez

Animal Breeding and Genetics Program, IRTA, Torre Marimon, Caldes de Montbui, 08140, Spain

Contact: maria.ballester@irta.cat

The aim of this work was to identify chromosomal regions and candidate genes associated with post-weaning growth in rabbits using a genome-wide association study. A total of 436 weaned rabbits from the Caldes line were distributed in two feeding regimes, 230 were fed *ad libitum* and 206 were restricted to 75% of *ad libitum* intake. Animal weight was recorded from 28 d to 56 d of age. Genotyping was performed using the Axiom rabbit array (Affymetrix) and after standard quality control a subset of 114604 annotated SNPs were retained for subsequent analysis. The maximum likelihood approach implemented in Qxpack 5.0 was used to test one snp at a time, separately for each trait; ADG on restricted (ADGr) or full feeding (ADGf). The model accounted for additive (polygenic) genetic effect, litter and cage effects, as well as the systematic effect of batch (5 levels). The R package q-value was used to adjust raw p-values to a False Discovery Rate of 0.05. While no significant as-

Figure 1. Plot of GWAS for ADG on restricted (ADGr) and full feeding (ADGf). The X-axis represents chromosome positions in Mb relative to OryCun2.0 assembly of the rabbit genome and the Y-axis shows the $-\log_{10}(\text{p-value})$. Horizontal lines mark the chromosome-wide significance level (FDR-based q-value ≤ 0.05).



Maria Ballester

Dr. Maria Ballester has a BSc in veterinary medicine from the Autonomous University of Barcelona (UAB). In 2005 she received the PhD degree in Animal Production from the UAB. She continued her scientific career as a post-doctoral researcher at INRA (France) and in the CRESA and CRAG



centres in Catalonia (Spain). On September 2015, she joined the IRTA's Animal breeding & genetics program with a Ramon and Cajal contract. She has a broad experience in animal genetics, functional genomics and bioinformatics applied to identify, characterize and functionally validate genetic variants affecting important economical traits in livestock species. Since 2017, she has been involved in the Feed-a-Gene project (WP5) with the objective to study the genetic determinism of feed efficiency traits. The identified genetic markers may be used to increase the accuracy of genomic predictions and long-term response to genomic selection.

sociations were found at whole-genome level for any trait; a total of 55 significant trait-associated SNPs (TAS) distributed in *Oryctolagus cuniculus* Chromosomes (OCC) 3, 5 and 21 were declared to be associated with ADGf at chromosome-wise level. No associations were evidenced for ADGr at this level. In order to identify positional candidate genes related to ADGf, four genomic QTL intervals (OCC3:101-114 Mb, OCC5:8-10 Mb, OCC5:18-20 Mb and OCC21:6-9 Mb) were annotated using Bio-mart. Out of the 55 TAS, 27 (49%) were mapped

in protein-coding genes. Remarkably, several genes related to growth such as *ATXN2*, *ACAD10*, *TRAFD1*, *PTPN11*, *NDUFAF6* and *FTO* were mapped in these QTL regions. Polymorphism in the rabbit *FTO* gene has previously been reported to be associated with growth and meat quality traits. Further analysis will be performed to determine the role of these candidate genes for rabbit growth.

Table 1. Description of the four chromosomal regions associated with ADG under *ad libitum* feeding

Chr	Mb	N sig. SNPs	Strongest SNPs effect (g/d)	MAF	Candidate Genes
3	101-114	27	-6.6	0.23	<i>NDUFAF6</i>
5	8-10	1	-3.6	0.11	<i>FTO</i>
5	18-20	2	-5.6	0.29	--
21	6-9	25	-3.5	0.06	<i>ATXN2, ACAD10, TRAFD1, PTPN11</i>

Operational measures of efficiency: make them measureable on large scale

EAAP 2018

H. Gilbert¹, E.F. Knol²

¹ INRA, UMR GenPhySE, 31320 Castanet Tolosan, France, ² Topigs Norsvin Research Center, bv, Schoenaker 6, 6641 BEUNINGEN GLD, the Netherlands

Contact: helene.gilbert@inra.fr

Finisher pigs tend to be 3-way crossbreds kept in pens of 8-15 in Europe and 20-30 in the Americas, with many exceptions. In theory it is possible to feed finisher pigs individually, but costs and management requi-

rements of automatic feeding systems, and availability of easy to handle decision making software limit their use on commercial farms. Management unit is, therefore, the pen, even though there is still a lot of variation among individual animals (among others, mendelian sampling). In addition, there is phenotypic variation, since piglets differ in birth weight (which is a maternal trait), in colostrum intake and in establishment of gut microbiome coming from their (foster) dam, and later depend on their pen mates influence (activity, hierarchy) and farm ambient conditions. Measuring feed efficiency, and predicting it to feed animals according to requirements given a certain environmental condition, thus remains a challenge, but yet animal sorting options are being put into practice to optimize feeding on a pen level.

Alternatives to individual electronic feeder measurements are also tested to produce individual measurements, including on-farm identification of drivers of the biological basis of feed efficiency (genomic and bio-markers) and measurements of components of feed efficiency (body composition, activity, gut microbiome composition). Feed efficiency is (still) mainly energy efficiency, and it has been the main driver of selection until now. However, energy requirements are now most often properly covered, protein efficiency is coming up and other efficiencies (vitamins, minerals) are being explored and might become of interest. In addition, by feeding animals high quality easy to digest feed, feed efficiency is essentially metabolic efficiency, but the increasing diversity of feed resources, including industry byproducts with higher dietary fiber contents, questions the opportunity to now focus on the genetic variability of digestive efficiency.

Effects of birth weight on nitrogen digestion and utilization in grower pigs

Digestive Physiology of Pigs 2018

A.J.M. Jansman, C.M.C. van der Peet-Schwering

Wageningen Livestock Research, P.O. Box 338, 6708 WD Wageningen, The Netherlands

Contact: alfons.jansman@wur.nl

A low foetal growth and birth weight leads to a lower number of muscle fibres formed prenatally and a lower body protein content in low birth weight (LBW) piglets. Therefore, LBW piglets may show a lower performance and nutrient efficiency later in life. The aim of the present study was to evaluate the effect of BW on N-digestion and N-utilization in growing pigs. Two groups of 20 piglets with a low (LBW, 1.11 kg) and high birth weight (HBW, 1.79 kg), balanced for litter were selected and subjected to N-balance measurement using quantitative urine and faeces collection over 5 d periods.

Hélène Gilbert

Hélène Gilbert is a Senior Scientist at INRA, France, working in quantitative genetics applied to livestock species. She obtained a PhD in Animal Genetics at INA P-G (now AgroParisTech), France, in 2003. In the past 15 years, she has been working on feed efficiency in numerous species, with a specific focus on pigs and the impact of selection for feed efficiency measured as residual feed intake on production and reproduction traits, animal physiology and responses to diverse challenges. Since 2015, she has been involved in the Feed-a-Gene project as the WP leader of WP5 "Use of traits in animal selection". Her objectives are 1. to quantify the effect of selection for feed efficiency in pigs on the HPA axis activity and on the gut microbiota, and 2. to evaluate the use of new measurements, of new genetic models and of genomic data for selection for feed efficiency without impairing the animals' robustness.



Pigs were fed a protein sufficient (NCP; CP 15.5%; 100%) or a protein restricted (RCP; CP 11.8%, 70% of sufficient) diet in a change-over design starting at 14 weeks of age. Diets were fed at 2.8xM over two meals per day. LBW and HBW pigs weighed 44 and 55 and 54 and 65 kg, respectively, at the start of the sequential balance periods. Faecal digestibility of DM, N and energy were not affected by BW, while faecal N digestibility was higher for the NCP compared to the RCP diet (91.4 vs. 88.8%, $P < 0.001$). N-retention was 27.7 and 19.0 g/d for the LBW pigs on the NCP and RCP diets, respectively, and 32.0 and 21.8 g/d for the HBW pigs ($P < 0.001$). Both N-efficiency (N-retention/N-intake; 0.629 vs 0.635, respectively) and marginal N-efficiency (0.68 and 0.69, respectively) did not differ between LBW and HBW pigs. IGF-1 (210 vs 265 $\mu\text{g/l}$) and insulin (11.0 vs 17.1 uU/ml) concentrations in plasma were lower in LBW compared to HBW pigs ($P < 0.05$). Birth weight is a determinant for BW gain and N-retention later in life, however, N-efficiency at later age is not affected by birth weight. This study is part of the Feed-a-Gene Project, funded from the European Union's H2020 Program under grant agreement no 633531.

Alfons Jansman

Alfons Jansman is Senior Scientist at Wageningen Livestock Research in Wageningen, The Netherlands. After graduating from Wageningen University in 1987, he obtained his PhD at the same university in 1993 with a thesis entitled "Tannins in feedstuffs for simple-stomached animals". Since 2003, he has been working for Wageningen Livestock Research as Senior Scientist in animal nutrition. His main areas of expertise are nutritional evaluation of feed ingredients, digestive physiology in pigs, requirements and metabolism of amino acids, and nutrition and health in pigs and poultry. He is leader of WP2 in Feed-a-Gene focusing at "New traits and technologies for measuring and improving digestive efficiency and gut health in pigs, poultry and rabbits". His personal objective is to contribute to finding new traits related to N-efficiency in pigs.



Plasma metabolites related to nitrogen efficiency in low and high birthweight pigs

Digestive Physiology of Pigs 2018

**L.M.G. Verschuren^{1,2}, A.J.M. Jansman²,
M.P.L. Calus², R. Bergsma¹, M.S.
Hedemann³**

1 *Topigs Norsvin Research Center B.V., Beuningen, 6640 AA, The Netherlands*, 2 *Wageningen UR, Livestock Research, Wageningen, 6700 AH, The Netherlands*, 3 *Aarhus University, department of Animal Health, Tjele, 8830, Denmark*

Contact:

lisanne.verschuren@topignorsvin.com

Birthweight of piglets has a major effect on average daily gain later in life, and therefore possibly influences nitrogen efficiency of pigs. Concentrations of particular plasma metabolites might be markers for nitrogen efficiency. The present study investigated differences in nitrogen metabolism between low and high birthweight pigs at grower-finisher age (between 98-126 days of age) using untargeted metabolomics. Plasma samples were collected of 40 grower-finisher pigs (three-way crossbreeds, low or high birthweight) at onset of the experiment (D0), and after the first (D17) and second (D28) experimental period. In a change-over design, pigs were either fed a protein adequate (100%) or a protein restricted (70%) diet. Plasma metabolites were characterized by untargeted liquid chromatography-mass spectrometry, and results were subjected to a discriminant approach combined with principal component analysis to discriminate pigs based on birthweight, diet fed, and diet fed within birthweight groups. Low vs. high birthweight pigs could be distinguished based

on a limited number of metabolites. Pigs fed a protein adequate or restricted diet also had very distinct metabolite profiles. However, different metabolites were important for distinguishing the effect of diet in the low compared to the high birthweight piglets. Further identification of the metabolites linked several metabolites to possible differences in nitrogen metabolism between pigs with diffe-

Lisanne Verschuren

Lisanne Verschuren is a junior researcher in pig genetics and nutrition at Topigs Norsvin Research Center B.V., The Netherlands. She has a Master in Animal Science obtained at Wageningen University in 2016 and started as external PhD candidate at Wageningen University & Research Animal Breeding and Genomics in the same year. In the past two years, she has been working on microbiota, metabolites and digestion in relation to feed efficiency in pigs. Since 2015, she has been involved in the Feed-a-Gene project and her objective is to investigate the underlying components of feed efficiency and their potential to develop more effective measures for genetic selection in pigs to improve pen performance on farm level.



rent birthweight. In conclusion, our results show a clear effect of birthweight and dietary protein restriction on plasma metabolites, the effect of dietary protein restriction being birthweight dependent. This study is part of the Feed-a-Gene Project, funded from the European Union's H2020 Programme under grant agreement no 633531.

WP4 Management systems for precision feeding to increase resilience to fluctuating environments and improve feed efficiency

Precision feeding of lactating sows: development of a decision support tool to handle variability

R. Gauthier^{1,2}, F. Guay³, L. Brossard¹, C. Largouët⁴, J.Y. Dourmad¹

1 PEGASE, INRA Agrocampus Ouest, 35590 Saint-Gilles, France, 2 Groupe ESA, 49007 Angers, France, 3 Université Laval, G1V0A6 Québec, Canada, 4 IRISA, Agrocampus Ouest, 35000 Rennes

Contact: raphael.gauthier@inra.fr

Nutritional requirements of lactating sows mainly depend on milk yield and greatly vary across individuals (Figure 1). Moreover, because the same diet is generally fed to all sows, and feed intake is low and highly variable, nutrient supplies are often insufficient to meet the requirements, especially those of primiparous sows. Conversely, sows

with high appetite may be fed nutrient in excess. Acquiring data on sows and their environment at high-throughput allows the development of new precision feeding systems with the perspective of improving technical performance and reducing feeding cost and environmental impact. The objective of this study was thus to design a decision support tool that could be incorporated in automated feeding equipment. The decision support tool was developed on the basis of InraPorc® model. The optimal supply for a given sow is determined each day according to a factorial approach considering all the information available on the sow (i.e. parity, litter size, milk production, body condition...) or predicted from real-time data (i.e. expected feed intake (EFI)).

Raphaël Gauthier

Raphaël Gauthier is a PhD student in both animal nutrition at INRA PEGASE and data science at INRIA LACODAM, France. He has a Master in Animal Science obtained at Ecole Supérieure d'Agricultures of Angers in 2017. Since March 2017, he has been involved in WP4 of the Feed-a-Gene project and he works on the development of new feeding systems with real-time data management. He is interested in pig production, new technologies and big data, in order to both improve the efficiency and the sustainability of swine breeding systems.



The approach was tested using data from 817 lactations. Precision feeding (PF_{EFI}) with the mixing of two diets with different nutritional values was then simulated in comparison with conventional feeding (CF) with a single diet. In sows fed in excess, PF_{EFI} reduced average digestible lysine excess from 10.9 g.d⁻¹ to 3.3 g.d⁻¹, whereas in deficient sows the deficiency was reduced from - 5.7 g.d⁻¹ to - 2.7 g.d⁻¹ (Table 1). Overall, PF_{EFI} reduced average lysine intake by 8.0 %. At the same time, with PF_{EFI} lysine requirement was met for a higher proportion of sows, especially in younger sows, and a lower proportion of sows, espe-

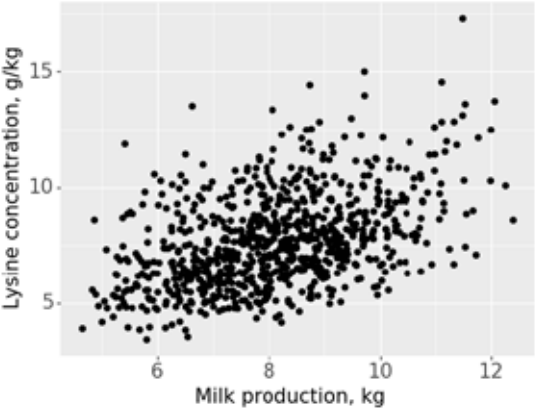
cially older sows, received excessive supplies. PF_{EFI} also reduced average phosphorus intake while limiting the occurrence of excess and deficiency. This study confirms the potential of precision feeding in order to better achieve nutritional requirements of lactating sows and reduce their nutrient intake and excretion. This work was supported by the French National Research Agency under the Investments for the Future Program, referred as ANR-16-CONV-0004. This project has received funding from the European Union's Horizon 2020 research and innovation program, grant agreement No 633531.

Table 1. Comparisons between conventional feeding (CF) and Precision Feeding with predicted feed intake (PF_{EFI}).

	CF	PF_{EFI}		PF_{EFI}
	Mean		p.value	Rate of change
Feed intake, kg.d⁻¹	5.84	5.85	ns	
Average intake				
Digestible Lysine, g.kg ⁻¹	8.50 ^c	7.82 ^a	***	-8.0%
Digestible Phosphorus, g.kg ⁻¹	3.20 ^c	2.94 ^a	***	-8.0%
Average balances				
Sows with negative balances				
Lysine, g.d ⁻¹	-5.66 ^c	-2.73 ^b	***	-52%
Phosphorus, g.d ⁻¹	-2.37 ^b	-1.15 ^a	***	-52%
Sows with positive balances				
Lysine, g.d ⁻¹	10.89 ^b	3.29 ^a	***	-70%
Phosphorus, g.d ⁻¹	3.91 ^b	1.26 ^a	***	-68%

Note: *** p.value < 2.2e⁻¹⁶

Figure 1. Simulation of the optimal lysine concentration per sow, on average across lactating period



Precision feeding with a decision support tool dealing with daily and individual pigs' body weight

EAAP 2018

N. Quiniou¹, M. Marcon¹, L. Brossard²

1 IFIP, BP 35, 35650 Le Rheu, France, 2 PE-GASE, INRA, Agrocampus-Ouest, 35042 Rennes, France

Contact: nathalie.quiniou@ifip.asso.fr

Nutritionists, feed companies and equipment manufacturers look for solutions that help farmers to improve sustainability of pig production. Based on experimental results obtained *in silico* or *in vivo*, a better adequacy between amino acid supplies and requirements increases feed efficiency and farmer's income and reduces the environmental impact of growing pigs, highlighting the interest for precision feeding. Data are collected to characterize daily animal traits (e.g., body weight, BW) and their variation from one day to another (e.g., growth rate, ΔBW). They are used to determine the requirement for maintenance and growth on the next day, respectively. Therefore, adequacy between requirements and supplies depends on these predicted BW and ΔBW . The double exponential smoothing (Holt-Winters) method with a smoothing parameter $\alpha = 0.6$ ($HW_{0.6}$), presents a low sensitivity to the number of latest values used to forecast BW. It seems to allow for a secured prediction of BW soon after the beginning of the growing phase (at least after 4 days). A group of pigs was used in restricted feeding conditions to compare results obtained either with a 2-phase feeding strategy, considered as the control treatment, or a precision feeding

strategy based on BW forecasting with the $HW_{0.6}$ method. Pigs allocated to both treatments were group-housed in the same pen, equipped with the decision support system built in the Feed-a-Gene project to manage the data, to determine in real-time the corresponding nutritional requirements, and to adapt the feed characteristics provided to

Nathalie Quiniou

Nathalie Quiniou is a research engineer in pig and sow nutrition at IFIP (France). She graduated in animal science at Agrocampus Ouest in Rennes (master's degree in 1992, PhD in 1995) and Rennes 1 University (HDR). Her PhD at INRA focused on growth modelling and effects of energy allowance on growing pigs. Since 2006, she has been involved in modelling of nutrient requirements in pigs at the population scale and she co-directed with Ludovic Brossard (INRA) a PhD student, whose results are integrated in the InraPorc® software. Between 2013 and 2017, Nathalie directed a project funded by the French environment and energy management agency (ADEME) toward precision feeding of restrictively fed pigs. Since 2015, she has been involved in the Feed-a-Gene project, especially into the design of the procedure used to adapt the quality and quantity of feed provided daily and individually to group-housed pigs, and the validation of precision feeding prototypes.



each pig through the blend of two diets (9.75 MJ net energy/kg, 0.5 or 1.0 g of digestible lysine per MJ). Available results from 24 pigs per treatment indicate that overall average growth performance were not influenced by the feeding strategy ($P > 0.58$ for both average daily gain and feed conversion ratio) but digestible lysine intake was reduced by 6%

(1774 vs. 1879 g, $P < 0.01$) and N output by 7% ($P < 0.01$) with precision feeding. Results will be completed by a second group using the same treatments. This study is part of the Feed-a-Gene project and received funding from the European Union's H2020 program under grant agreement no. 633531.

Figure 1. Comparison of the average measured body weight to the average predicted value with the Holt-Winter method (37 pigs from the MP group)

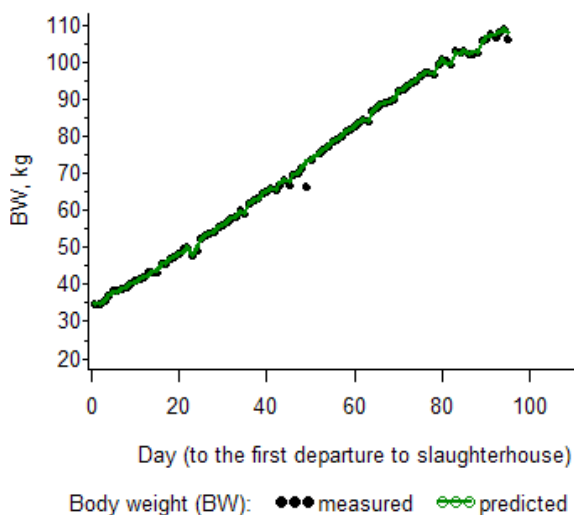
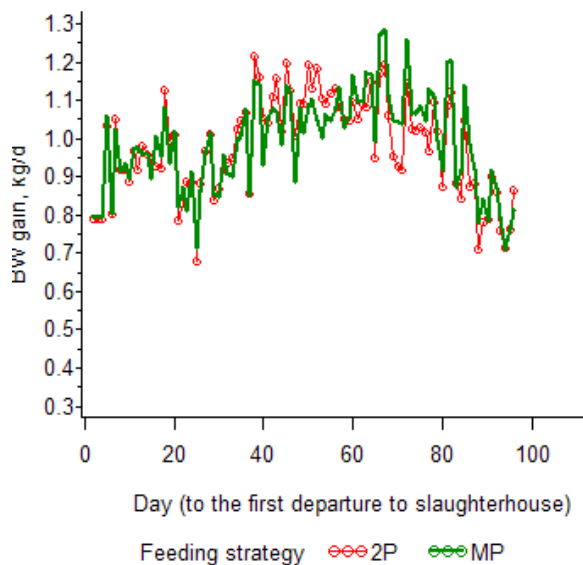


Figure 2. Comparison of the predicted daily BW gain for pigs fed according to the 2-phase (BP) or multiphase (MP) feeding strategy (24 pigs/group) (from day 70 to 84, the procedure was not secured enough to achieve the calculation in case of lacking data)



WP5 Use of traits in animal selection (Genetic parameter estimations, genetic model developments & evaluation of breeding schemes)

Genetic bases of individual performance variation in pigs

EAAP 2018

L. Bodin¹, N. Formoso-Raferty², H. Gilbert¹

1 INRA GenPhySE, 31326 Castanet-Tolosan, France, 2 Dept. of Animal Production, Universidad Complutense de Madrid, Madrid, Spain

Contact: loys.bodin@inra.fr

Part of the variability of performances in animal production is due to the genetic variation in the level of a trait between animals; that is the keystone of all genetic improvement programs and has to be maintained to guarantee the long-term sustainability of the selection progress. Another part of the performance variability comes from the individual variation of responses to various environmental conditions, called environmental sensitivity, which can have a highly negative impact on the final profitability of the production. Joint estimations of breeding values (EBV) and genetic parameters of the individual environmental sensitivity of a trait can be obtained along with those of the level of the trait. Moreover, use of these two kinds of EBV in genetic programs partly depends on

their correlations as well as their genetic relationships with other traits. In pigs, homogeneity of litter size is desired and in many cases its mean level should not decrease. Similar relationships between objectives exist for the birth weight components (mean and variability); homogeneity is desired to ensure good perinatal viability and subsequent growth, but the mean birth weight should also not decrease. The genetic parameters and relationships between components (mean and variability) of birth weight and litter size in pigs will be presented along with similar parameters estimated in a mice experiment. Furthermore, similar estimations were obtained for production traits, such as residual feed intake and growth, which will be discussed in the perspective of producing more efficient and robust animals.

Loys Bodin

Loys Bodin is a senior scientist at INRA who has been working for a long time on the improvement of sheep litter size and on the discovery of major genes for ovulation rate. The progresses which were obtained on litter size led to address the reduction of performance variability around an optimum value. He put effort on genetic modelling of environmental variability (i.e. canalisation) and participated in pioneering articles on this subject. He has been also the source of the selection experiment on BW variability undertaken on rabbit in France.



Figure 1. Residual feed intake (RFI) and average daily gain (ADG) in pig: genetic values for the variability/generation/line

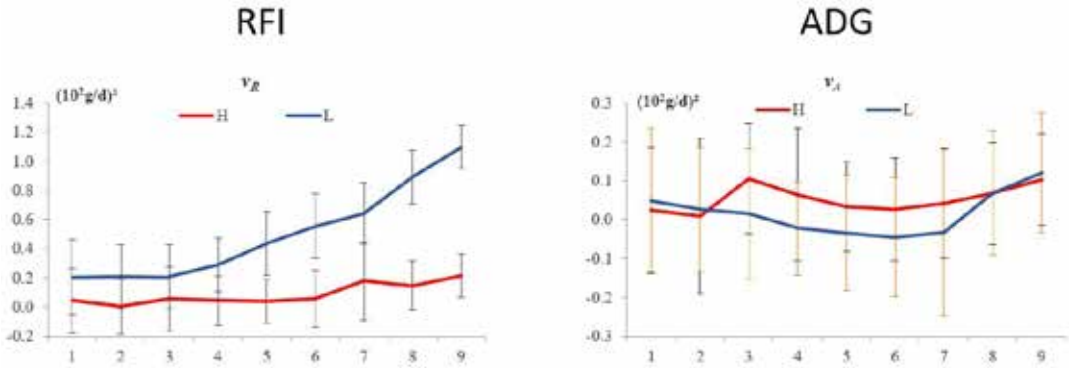


Figure 2. Litter size (LS) and birth weight (BW): genetic parameters for the mean and the variability of litter size and birth weight in pig

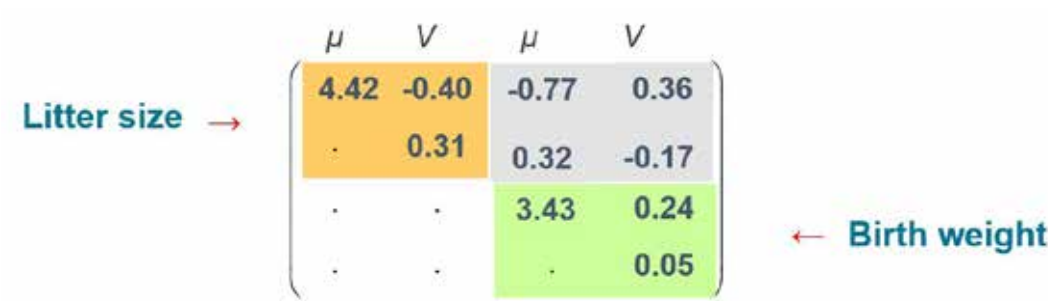
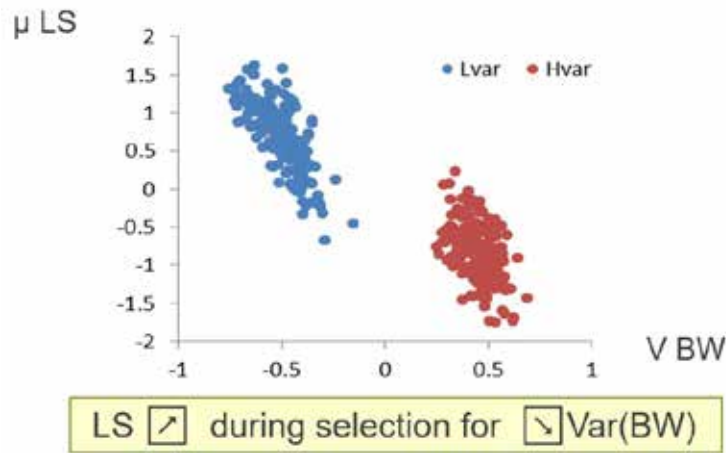


Figure 3. Plot of genetic values: mean of litter size - variability of birth weight in mice



Structured antedependence model for longitudinal analysis of social effects on ADG in rabbits

EAAP 2018

I. David¹, J.P. Sánchez², M. Piles²

1 *GenPhySE, Université de Toulouse, INRA, ENVT, 31326 Castanet Tolosan, France,*
2 *IRTA, Torre Marimon s/n, 08140 Caldes de Montbui, Barcelona, Spain*

Contact: ingrid.david@inra.fr

Even if there are evidences that the intensity of social interactions between partners vary with time, very few genetic studies have investigated how social genetic effects (SGEs) vary over time. To overcome this issue, the objectives of the present study were to analyze longitudinal records of average daily gain (ADG) in rabbits and to evaluate, by simulation, the response to selection for such longitudinal trait. Five weekly ADG records from 3,096 rabbits under feed restriction after weaning and raised in pen of 8 were used

for the analysis. A linear animal mixed model including SGEs with week specific random effects that follow structured antedependence (SAD) functions was fitted to the data using ASReml and the Fortran program that we have developed (freely available on Zenodo). The social heritability (Table 1) was higher in week 1 (0.44) than in weeks 2 to 5 (ranging from 0.16 to 0.23). The genetic variance-covariance matrix is presented in Figure 1. The correlation between the SGEs of different weeks was moderate to high for weeks 2 to 5 (0.62 to 0.91) and weaker between the first week and the other weeks (0.33 to 0.47). The direct-social genetic correlations were negative at any time. Based on the same data design, the same variance components but considering 3 different sets of direct-social genetic antagonism (strong, moderate, weak), we simulated 7 generations of selection using a SAD model including SGEs or not to estimate breeding values. Results obtained showed that the increase in ADG with selection decreased with the direct-social genetic antagonism and was improved (~by 30%) when SGEs were taken into account (Figure 2). In conclusion, results confirmed that SGEs vary over time and do not correspond to

Ingrid David

Ingrid David is a Senior Scientist at INRA, France, working in quantitative genetics applied to livestock species. She is a veterinarian; she holds an MSc in epidemiology and an MSc in biostatistics.

She received her PhD in animal breeding and genetics in 2008. Her research focuses on the development of models to study the mechanisms underlying interaction between individuals on the expression of a phenotype, genotype by environment interactions and interactions between genes in the broad sense. Since 2015, she has been involved in the Feed-a-Gene project and her objectives is to propose models accounting for indirect effects and genotypes x environment interactions, together with multiple repeated longitudinal data, for the estimation of variance components of traits of interest.



the same trait after mixing than later in life, probably as a consequence of social hierarchy establishment observed at that time.

Accounting for SGEs in the selection criterion maximizes the genetic progress.

Table 1. Heritability estimates for average daily gain across weeks

Week	Direct heritability	Social heritability	Total heritability
1	0.17 (0.03)	0.44 (0.13)	0.19 (0.10)
2	0.24 (0.03)	0.23 (0.07)	0.09 (0.06)
3	0.22 (0.02)	0.18 (0.06)	0.05 (0.04)
4	0.15 (0.02)	0.16 (0.06)	0.06 (0.04)
5	0.08 (0.02)	0.18 (0.11)	0.12 (0.10)

Figure 1. Estimates of genetic variances for each week (on the diagonal, s.e. in brackets) and of correlations between weeks and between direct and social genetic effects (below the diagonal).

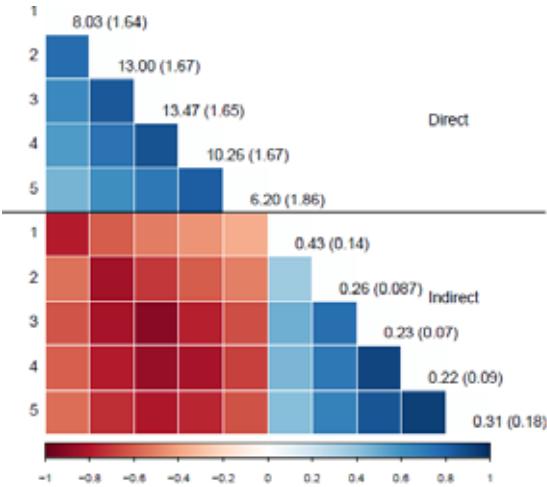
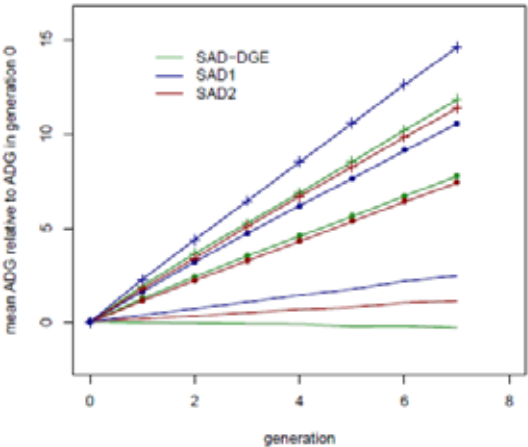


Figure 2. Changes in the mean ADG across generations for each selection strategy

SAD-DGE- selection criterion: sum of the weekly direct EBV obtained with a SAD model without SGE; SAD1- selection criterion: sum of the weekly TEBV obtained with a SAD model with SGE; SAD2- selection criterion: TEBV of the first week obtained with a SAD model with SGE. Straight line, line with ● and line with + represent strong, moderate and weak simulated genetic antagonism between direct and social effects, respectively.



Effect of gut microbiota on production traits, interaction with genetics

EAAP 2018

H. Gilbert¹, S. Lagarrigue², L.M.G. Verschuren³, O. Zemb¹, M. Velasco⁴, J.L. Gourdine⁵, R. Bergsma³, D. Renaudeau², J.P. Sanchez⁴, H. Garreau¹

1 *GenPhySE, INRA, 31320, Castanet Tolosan, France*, 2 *PEGASE, INRA, Agrocampus-Ouest, 35042, Rennes, France*, 3 *Topigs Norsvin Research Center B.V., Schoenaker 6, 6641 Beuningen, The Netherlands*, 4 *Institute for Food and Agriculture Research and Technology (IRTA), Torre Marimon, 08140, Spain*, 5 *URZ, INRA, 97170 Petit-Bourg, France*

Contact: helene.gilbert@inra.fr
or herve.garreau@inra.fr

Gut microbiota is a key contributor to feed use in monogastric species, in particular via the digestion dietary fibres. Molecular techniques are now available to run large studies and decipher the potential of gut microbiota to improve livestock. Studies on human and mice are more advanced: different factors have been demonstrated to influence the gut microbiota composition and functions, including maternal transmission, environment (diet composition and quantity, humidity and heat), age and physiological status. Studies also evaluated if the host controls its gut microbiota. In pigs, chicken and rabbits, microbiota differences between animals of extreme phenotypes within populations, and between lines divergently selected for specific traits, are reported. Other studies reported that some microbiota abundancies are heritable. Linear mixed models have been used to evaluate its contribution to trait variability, or microbiability, with different

data (full vs. 16S sequencing of gut or faecal contents) and different variance matrices. They showed significant contribution to production traits, reaching more than 30%. However, confounding effects exist, such as the maternal inheritance of the microbiota and the genetic determinism by the host: many studies show reduction of the genetic additive variance, in addition to reduction of the residual variance with microbiability. Specific datasets, testing a given genetic in different environments or using cross-fostering, are used to better understand the relative contribution of each effect (host genetics and microbiota) to the trait variance, and propose solutions to livestock. This work is part of the European Union's H2020 Feed-a-Gene Project (grant 633531).



Credit: Cobb

Feed-a-Gene



Contact information

Project coordinator

Jaap van Milgen

INRA, Domaine de la Prise F-35590 Saint-Gilles, FRANCE

Phone: +33 (0) 2 23 48 56 44

Email: jaap.vanmilgen@inra.fr

Project manager

Vincent Troillard

INRA Transfert, 3 rue de Pondichéry F-75015 Paris, FRANCE

Phone: +33 (0) 1 76 21 61 97

Email: vincent.troillard@inra.fr

Communication and dissemination

Gilles Tran

Association française de zootechnie, 16 rue Claude Bernard
F-75231 Paris Cedex 05, FRANCE

Phone: +33 (0) 1 44 08 18 08

Email: gilles.tran@zootechnie.fr



The Feed-a-Gene Project has received funding from the *European Union's Horizon 2020 research and innovation programme* under grant agreement No 633531

Conception and design

Association française de zootechnie, July 2018

Cover

Gilles Tran / AFZ

Printed by Grafeez
11 Rue de l'Épée de Bois
F-75005 Paris