Feed-a-Gene

Book of abstracts

Communications and posters

- 68th EAAP Annual meeting, Feed-a-Gene session, 30 August 2017, Tallinn, Estonia
- 8th EC-PLF European Conference on Precision Livestock Farming, 12-14 September 2017, Nantes, France

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

Photo credit: Cobb

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)
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- IFIP institut du porc
- ITAVI
- Terres Inovia
- Association française de zootechnie (AFZ)
- INRA Transfert (IT)

Abstracts published at the 68th EAAP meeting and at the 8th EC-PLF

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Feed-a-Gene

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

Feed-a-Gene is composed of 6 research & innovation work packages (WP), one dissemination WP and one management WP.

WP1 Alternative feed ingredients and real-time characterisation

WP2 New animal traits for innovative feeding and breeding strategies

WP3 Modelling biological functions with emphasis on feed use mechanisms

WP4 Management systems for precision feeding

WP5 Use of traits in animal selection

WP6 Sustainability assessment

WP7 Dissemination, training and technology transfer

WP8 Project management

The Feed-a-Gene project 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 started on March 2015 for a 5-year period and has been 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 the innovative technologies developed by the project 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

For more information, register at the stakeholder platform:
www.feed-a-gene.eu

Jaap van Milgen

Project coordinator

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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.

WP1 Alternative feed ingredients and real-time characterisation

WP1 leader: Knud Erik Bach Knudsen, Aarhus University
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Partners: AU, WUR, UNEW, IRTA, KU, CAU, Hamlet Protein, Bühler, DuPont, IFIP, Terres Inovia

Objectives

WP1 aims to develop novel high-quality European based feed protein ingredients and develop methodologies for characterisation of chemical and nutritional properties of feed in real-time. The WP will focus on:

- alternative European feed resources and improving the potential of EU protein feeds
- the exploration of novel feed processing and enzyme technologies to improve the nutritional value of feeds
- the development of new methodologies for the real-time characterisation of chemical composition and nutritional value of feeds

The novel feed ingredients, enzyme technologies, and feed characterisation methodologies will be used for the development of novel feed efficiency traits (WP2), as inputs for modelling digestion (WP3), and the development of precision feeding systems (WP4).

Approach

This WP integrates state-of-the-art knowledge from other on-going research programmes for the development of its different tasks. We will investigate the potential of alternative European feedstuffs to increase their production in quantity and quality in Europe. The focus will be on protein as a response to the increased need, thereby helping Europe to reduce its dependency on imported protein sources. We will also identify and qualify the impact of feed technologies such as heat treatment and enzyme technologies to improve the nutritive values of feedstuffs. An additional approach is the development of new analytical technologies that can be used to predict the chemical composition and nutritional value of feedstuffs in real-time. This WP has strong links with the activities in WP2, WP3, WP4, WP6 and WP7.

Tasks

Task 1.1 Production of novel feed protein from rapeseed and European grown soybeans

Task 1.2 Production of novel feed protein from green biomass

Task 1.3 Novel feed-processing technology to upgrade alternative feed ingredients

Task 1.4 Nutritional evaluation of novel feed ingredients

Task 1.5 Improvements in nutritive value by use of novel enzymes

Task 1.6 New methodologies for characterisation of nutrient composition and value

Photo credit: Aarhus University

Knud Erik Bach Knudsen

Professor Knud Erik Bach Knudsen works in the Department of Animal Science at Aarhus University. His main focus for the last 25 years has been on carbohydrates and bioactive phytochemicals. The emphasis has been on: 1) Development and implementation of analytical methods for the determination of carbohydrates in foods, feeds and digesta materials; 2) Studies on nutritional and physiological properties of carbohydrates emphasizing the importance of degradation, absorption and influence on the gut microflora; 3) Studies on the role of carbohydrates in the prevention of digestive disturbances and establishment of parasites in pigs; 4) Studies on the nutritional and health effects of carbohydrates and phytochemicals in monogastric species including human subjects. His most recent works have been in the interface to human nutrition emphasizing the use of animal models for understanding the mode of actions of carbohydrates and phytochemicals. He is actively involved in the establishment of a LC-MS/MS based metabonomic platform at the department and is currently the principal supervisor of several PhD projects.

Nutritional evaluation of dehulling and thermal treatments for production of expeller soybean meal

Oral communication, EAAP 2017

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The objective of this study was to determine the influence of different processes on the nutritional quality of expeller soybean meal (SBM). Extrusion or cooking processes in combination with dehulling and pressing were used to produce 4 partly defatted SBM with low residual trypsin inhibitor (TI) activity. European soybeans were ground using a roller mill, then dehulled or not with a cleaner separator. The 2 products were either extruded using single-screw extrusion at 140°C at around 100 kg/h (EP), or cooked at 150°C during 60 minutes (FCP) after flaking. All beans were then pressed to extract the oil. Extrusion allowed a higher oil extraction than cooking (residual oil: 4.9 vs. 8.6 g/100 g DM in whole EP and FCP meals, and 5.2 vs. 6.4 g/100 g DM in dehulled EP and FCP meals, respectively). The dehulling step resulted in an increase of almost 3 g/100 g protein (58.8 and 58.4 g/100 g for dehulled EP and FCP meals, respectively, and 56.0 and 55.8 g/100 g for whole EP and FCP meals, respectively, on a fat free DM basis). The KOH protein solubility was increased by dehulling for EP (70 vs. 76%) and FCP processes (82 vs. 89%, for whole and dehulled meals, respectively). The TI values were 2.6, 3.5, 3.6, and 7.6 TIU/mg for whole and dehulled EP and FCP meals, respectively. The lower dryer outlet temperature measured for the dehulled beans compared to whole beans (90 vs. 97°C) may explain the lower TI inactivation for the dehulled FCP meal. The amino acid and reactive lysine content and the *in vitro* rate of degradation based on hydrolysis of protein bonds (pH-stat) are determined and related to the chemical composition to evaluate the nutritional value of the meals. All 4 processes may produce good quality SBM with 46-52 g/100 g crude protein, 4-8 g/100 g residual oil, and a TI content below 8 TIU/mg. Extruded-expelled SBM produced in medium-sized crushing plants from local and GMO-free crops have a nutritional and economic potential in Europe.

Photo credit: Gilles Tran / AFZ

Eric Royer

Eric Royer is an engineer and senior scientist in pig nutrition at IFIP institut du porc, France, since 1997. He has an MSc in agriculture obtained at INP Toulouse (EI Purpan) and an MBA obtained at University of Toulouse. He has worked in extension and research in various topics (nutritional value of feedstuffs, effects of feed processing, liquid feeding, on-farm mixing...). His research in recent years was mainly focused on digestive health and feed and food safety. Since 2015, he has been involved in the alternative feed ingredients and real-time characterisation work package of the Feed-a-Gene project, and leads the production of novel feed protein from European-grown rapeseeds and soybeans.

WP2 New animal traits for innovative feeding and breeding strategies

WP2 leader: Alfons Jansman,
Wageningen University
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Partners: WUR, INRA, UNEW, UdL, IRTA, AU, CAU, Cobb, Claitec, IFIP, Topigs

Objectives

WP2 aims to explore and identify new animal traits directly or indirectly related to individual variation in the animal's response to feed and overall feed efficiency under different environmental conditions. The WP will focus on:

- between-animal variation in voluntary feed intake and feed intake behaviour and its consequences on feed efficiency
- nutrient digestibility with emphasis on the intermediary role of symbiotic intestinal microbiota
- nutrient metabolism as affected by nutrient and ingredient supply, feeding strategy, environmental conditions and genotypic differences within and between populations of animals
- the value of behavioural traits (i.e., physical activity, group behaviour and feeding behaviour patterns) on feed efficiency

The new and refined traits will be used for modelling the response of animals to the nutrient supply and environmental conditions (WP3), for further developing the concept of precision feeding (WP4) and for the development of future breeding strategies (WP5) with increasing emphasis on breeding feed-efficient production animals in a variety of production and feeding practices.

Approach

WP2 will use and refine existing data and samples available by the partners from national research programmes for the identification of new traits and integrative responses. In addition, animal trials will be performed focussing on the response of individual animals in terms of feed intake and behaviour, body weight gain, nutrient digestibility and gut health. We will explore the role of intestinal microbiota, and assess variation in nutrient metabolism as affected by nutrient and ingredient supply, feeding strategy, environmental conditions and genotypic differences within and between populations of animals. Specific attention will be given to metabolomics as a tool to identify new traits. New and state-of-the-art techniques will be used for the phenotypic description of the animal responses and for genotyping individual animals among and within animal lines. The identification of new traits will take place by measuring phenotypes in a variety of (defined) animal populations, including selected breeds and lines and defined phenotypes and genotypes, some of which will be subject to different dietary treatments and feeding strategies. WP2 has strong links with WP1, WP3, WP4 and WP5 in terms of delivery and receipt of data, samples and provision of new animal traits for use in optimised precision feeding and breeding strategies.

Tasks

Task 2.1 Individual feed intake and feeding behaviour in broilers and rabbits - New phenotypes to improve feed efficiency

Task 2.2 New traits and technologies for measuring and improving digestive efficiency and gut health in pigs, poultry and rabbits

Task 2.3 Nutrient metabolism related traits to improve feed efficiency

Task 2.4 Behaviour and welfare related traits influencing feed efficiency

Task 2.5 Metabolomics to identify new traits for improvement of feed efficiency

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.

Relationship between intestinal and blood metabolome and fecal digestive efficiency in chicken

Oral communication, EAAP 2017

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Digestive efficiency (DE) is an essential component of feed efficiency, especially in the context of increasing variety of feedstuffs with variable quality used in poultry diets. However, measuring fecal DE during balance trials is time-consuming and constraining as birds are placed in individual cages. Moreover, all the mechanisms controlling DE are still not known. The aim of our study was thus to identify biomarkers of DE using intestinal and blood metabolomics.

Our study used 60 chickens of an advanced intercross line (8th generation) between two broiler lines divergently selected for their fecal DE, based on metabolisable energy corrected to zero nitrogen retention (AMEn). At 3 weeks, fecal AMEn and coefficients of digestive use of lipids, nitrogen and starch were measured during a balance trial, ileal and caecal contents were sampled and blood collected. Metabolome was determined by proton high resolution NMR. Correlation models (canonical partial least squares) were fitted to assess the links between efficiency and metabolites of the 3 compartments.

Metabolites differences between animals with high or low levels of DE were mainly involved in amino-acids metabolism (lysine, isoleucine, methionine) and energetic metabolism (glutamate, glucose) in the 3 compartments. High positive correlations were especially found between glucose in caecal content and AMEn and coefficient of DE of nitrogen (Figure 1), which is consistent with the large divergence found in the divergent lines on these criteria. This result suggests an effect of microbial fermentation on DE.

These metabolic profiles give us information on mechanisms implied in feed digestion in chickens. Further analyses will estimate if blood metabolome could be used as an indirect criterion of selection of feed and DE. This study has been supported by the EU H2020 Feed-a-Gene project and by the INRA programme GISA-GALMIDE.

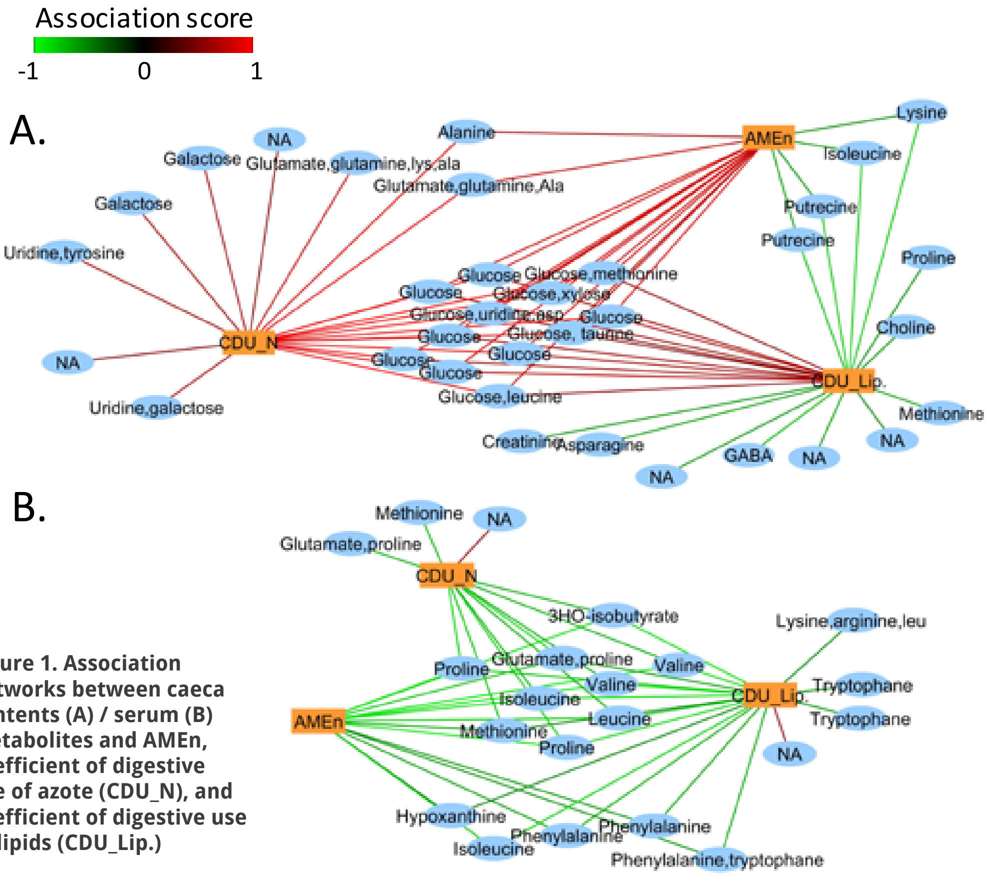

Figure 1. Association networks between caeca contents (A) / serum (B) metabolites and AMEn, coefficient of digestive use of azote (CDU_N), and coefficient of digestive use of lipids (CDU_Lip.)

Stéphane Beauclercq

Stéphane Beauclercq is a post-doctoral fellow in metabolomics at INRA Val de Loire, France. He has a PhD in Life Sciences obtained at the University of Tours (France) in 2017. During his PhD, he worked on chicken meat quality through high-throughput analysis such as metabolomics and transcriptomics. Since March 2017, he has been involved in the Feed-a-Gene project and his objective is to identify metabolic biomarkers of feed and digestive efficiency in chicken that may be further used in marker-assisted genetic selection.

Cross links between feed efficiency parameters and gut microbiota in pigs. Effect of productive type and diet protein levels

Poster, EAAP 2017

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The effects of two dietary CP concentrations (Normal or Low) and two productive types (castrated Duroc (C-Du) or entire Pietrain (E-Pi)) on productivity (ADFI, ADG and FCR), digestibility of nutrients and GHG emissions were assessed in a 98 d, three-phase feeding program. Thirty-two castrated male Duroc and 32 entire male Pietrain piglets were used. At the last day of each feeding phase and after 12 hours of fasting period, animals were submitted to rectal spot feces and blood sampling. Feed and feces samples at each phase were analyzed for their DM, CP, NDF contents. Genomic DNA was extracted from stool samples with a Qiagen stool mini kit, and the libraries were prepared using V3-V4 amplicons from the 16s rRNA gene. Sequencing was performed with Illumina Miseq, generating 902131 paired-end reads. Sequence data was analyzed following the UPARSE protocol. OTUs were classified taxonomically using RDPII database and Multivariate analysis was conducted using package “vegan” from R. Biodiversity indexes (Shannon Wiener, Simpson and Richness) and Spearman correlations between biodiversity and performance traits were also calculated.

Firmicutes was the most abundant phyla in both productive types (72.4±6.13 % in C-Du; 73.5±4.81 % in E-Pi), followed by *Bacteroides* and *Proteobacteria*. Among the main phyla, differences were observed between productive types in the relative titers of phyla *Bacteroidetes* (C-Du>E-Pi, $P<0.05$), *Proteobacteria* (E-Pi>C-Du, $P<0.01$), and *Actinobacteria* (C-Du>E-Pi, $P<0.1$). The effect of CP supply on phyla distribution was negligible. Thirteen genera presented changes in their relative abundance between productive types and six among diets. Richness index of diversity showed significant differences between genotypes and diets, being Normal CP diets more diverse than Low CP ones, and E-Pi more diverse than C-Du ($P<0.05$ in both cases). Microbial community structure showed to be highly affected by productive types ($P<0.001$), and productive types X diet interaction ($P=0.01$). Canonical Correspondence Analysis (CCA) indicated that CP and Starch digestibility, as well as Ammonia and CO_2 levels were related with microbial community structure ($P<0.014$, see Figure 1). Diversity correlated with ADG in C-Du and nutrients digestibility in E-Pi.

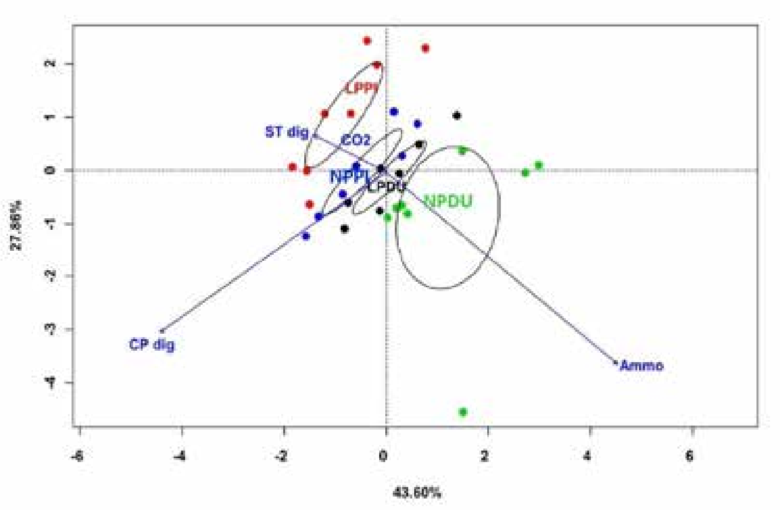

Figure 1. CCA illustrating the relationship between the structure of the bacterial community with performance traits. Arrows show the direction of the gradient and their length is proportional to the correlation. Confidence interval (95%) is indicated for each interaction between productive type (Duroc (DU) or Pietrain (PI)) and diet (Normal CP (NP) or low CP (LP)).

CP dig: apparent digestibility of CP; ST dig: apparent digestibility of Starch; Ammo: Ammonia emissions; CO_2: CO_2 emissions.

Gabriel de la Fuente

Gabriel de la Fuente Oliver has been working since 2015 as a Lecturer at Lleida University (Spain). He has a DVM (2003) and a PhD in Animal Nutrition (2010) from the University of Zaragoza. He then developed his scientific career in Aberystwyth University (UK), where he studied the microbial community structure in the gut, and identified significant shifts in stability due to drastic changes in the diet or to inclusion of additives or probiotics. Since his return to Spain, he has been involved in the Feed-a-Gene project looking for metabolic and digestive traits to predict feed efficiency in pigs, as well as their links with the intestinal microbiota. By understanding the relationships that occur between the gut microbiota and the diet, it becomes possible to induce changes that can yield products that are more efficient (increasing the utilisation of the feeding and reducing the waste products) and more environment-friendly (reducing the impact of greenhouse gases (GHG)).

Molecular indicators of feed efficiency as proposed by a meta-analysis of transcriptomics data

Oral communication, EAAP 2017

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Improving feed efficiency is an important challenge for pig production. This study aimed at proposing molecular traits able to predict feed conversion ratio (FCR) in growing pigs. A total of 71 pigs from two divergent lines selected for residual feed intake (RFI) and fed under different conditions (*ad libitum* or restricted) and different diets (low fat high starch or high fat high fiber) were considered, so that a broad range of FCR data was obtained (Figure 1). Transcriptomics data from the loin muscle and blood were obtained using porcine microarrays. The dataset (22,288 molecular probes per tissue and pig) was split into 70% for machine learning methods and 30% for cross-validation. Random forests were used to propose a reasonable set of 359 genes identified as very important predictors (VIP) of FCR. The FCR was well predicted (RMSE = 0.16; R^2 = 0.63) by a model combining the expression levels of 50 genes in muscle (out of the 359 VIP). These genes were involved in various biological pathways, including the response to insulin, homeostatic processes, signal transduction, regulation of cell proliferation, apoptosis, protein metabolism, and inflammatory responses (Table 1). About 82% of the muscle VIP were also expressed in the blood. The FCR was also predicted correctly (RMSE = 0.21; R^2 = 0.52) by using the same model of genes expressed in blood. Technical validation is in progress to evaluate the predictive potential of the model when expression levels of these genes are measured by

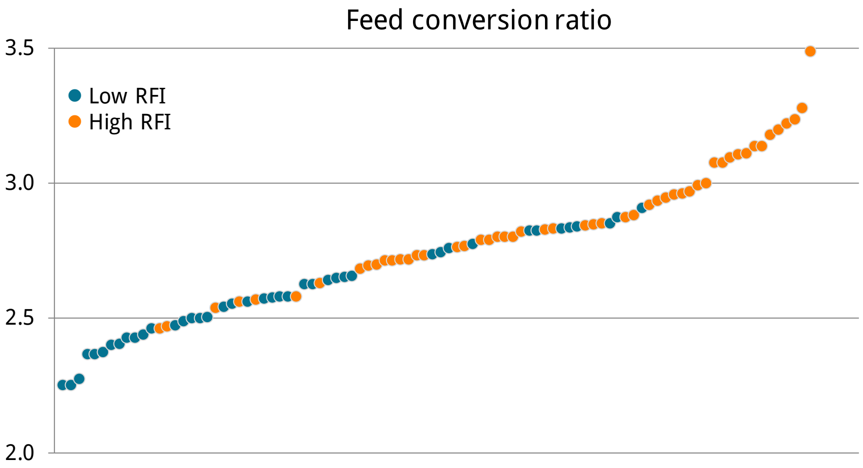

Figure 1. Distribution of feed conversion ratio among experimental pigs.

target methodology (qPCR) in blood of the same pigs. Further tests will be performed on blood samples taken at earlier growth stages to obtain early predictors and by using different pig populations to obtain generic predictors. In conclusion, identifying molecular traits related to feed efficiency could be helpful to identify important genomic regions and new biomarkers for genetic selection.

Table 1. Main biological processes shared by the most important muscle gene predictors of feed conversion ratio in pigs[1]

Biological pathway	Number of genes
For the 359 very important predictors (VIP)	
Regulation of apoptosis	30
Regulation of metabolic process	27
Response to organic substance (incl. response to insulin)	23
Homeostatic process	23
Cell adhesion	22
Cell cycle process	17
Cell response to stress	12
Regulation of cell cycle	12
Muscle organ development	13
Protein metabolic process	8
Regulation of DNA binding	8
For the first top 50 VIP	
Signal transduction	8
Regulation of cell proliferation	7
Regulation of apoptosis	5
Homeostatic process	5
Cell adhesion	4
Response to hormone stimulus (incl. response to insulin)	3
Inflammatory response	3
Protein metabolic process	3

[1] A same gene can be involved in different processes

Florence Gondret

Florence Gondret is a Senior Scientist working on the biology of pig lean and adipose tissues at INRA (UMR Pegase, Saint-Gilles, France). She has a PhD in animal sciences obtained at AgroParis-Tech (Paris) in 1997. She was awarded by the Physiology Commission at EAAP in 2001. In the past 5 years, she has been working on the biological basis of feed efficiency in growing pigs, with a specific interest in determining how different metabolic routes for nutrient use, energy production and energy dissipation in fat and lean tissues could be related to energy (in)efficiency. Since 2015, she has been involved in the Feed-a-Gene project and her objectives are to find omics predictors of feed efficiency using different datasets. This may add candidate genes for the studied trait to help in the design of next selection programmes and suggest early predictors to rank animals for feed efficiency.

Influence of productive type and dietary CP levels on the metabolomic pattern, gas emissions and feed efficiency in swine

Poster, EAAP 2017

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The effects of two dietary CP concentrations (Normal or Low) and two productive types (castrated Duroc or entire Pietrain) on productivity (ADFI, ADG and FCR), digestibility of nutrients and GHG emissions were assessed in a 98 d, three-phase feeding program. Thirty-two castrated male Duroc and 32 entire male Pietrain piglets were used. Digestibility trial was conducted using chromic oxide as an external marker. At the last day of each feeding phase animals were submitted to rectal spot feces and blood sampling. The indoors environmental and outdoors fresh air samples were sampled using syringes which were immediately analyzed for concentration of CO_2, N_2O, NH_3 and CH_4. Feed and feces samples at each experimental phase were analyzed for their DM, CP, NDF contents following the procedures of AOAC. Non targeted chromatographic analyses of both polar and global extracts from plasma at 18 weeks of age were performed with a Hypersil GOLD C18 selectivity LC column (6 µm particle size; 2.1×100 mm; Thermo Fisher). Metabolites were eluted using a gradient of formic acid and analyzed by using an Orbitrap Fusion mass spectrometer (ThermoFisher, San Jose, CA). Data were acquired for 22 min in positive and negative modes; the full mass scan range was m/z 65-1500 with a resolution of 240,000 and a maximum injection time of 1 ms.

No differences were observed in the overall ADFI, but C-Pietrain presented a higher ADG ($P=0.01$). DM Digestibility was higher in Low CP diets ($P<0.001$), and CP digestibility increased in E-Pietrain types ($P=0.01$). Both types showed differences in the metabolic pattern in global extracts (PERMANOVA, $p<0.024$ in negative mode), although that effect was not considered significant in the polar extracts, suggesting that the non-polar fraction of metabolites could be responsible of the metabolomic differences among productive types. Diet also influenced global metabolomics pattern ($p<0.015$ in negative mode), but no effect was observed in the interaction diet X productive types (Figure 1). Further work identifying key metabolites related with specific metabolomics patterns will help to deepen the understanding of the link between metabolism and productive types.

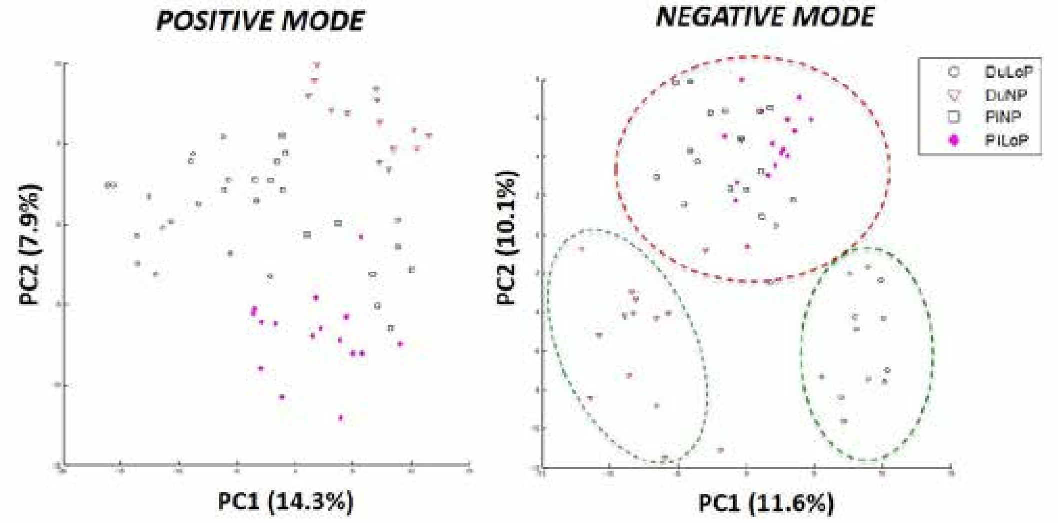

Figure 1. Principal Component Analysis (PCA) representing the metabolomic profile of animals under the study (N=61) in both negative and positive modes, from LC-MS data. Different symbols mean the interaction between productive type (Duroc (Du) or Pietrain (Pi)) and diet (Normal CP (NP) or Low CP (LoP)).

Ahmad Reza Seradj

Ahmad Reza Seradj received his PhD from University of Lleida (UdL) in 2015 and since then he has been engaged in research activities as a post-doctorate fellow working in Agrotecnio Research Center and UdL in Spain. During the past 5 years he has been working in various investigation projects focused on ruminants (using secondary plant metabolites to ameliorate ruminal fermentation and suppress methane emission; the effect of fat encapsulation of urea on ruminal microbial synthesis, efficiency and digestibility of rations) as well as monogastrics (study of the effect of nutrition and manure management on emissions of gases (NH_3, CH_4 and N_2O) in growing pigs), analyzing those merits which are related to the utilisation of nutrients and feed efficiency of the pigs. Since 2016, he has been involved in the Feed-a-Gene project aiming to determine fractional protein synthesis rate in two races of pigs (Duroc vs. Pietrain) receiving normal and low levels of crude protein.

Effect of feeding regime and presence of antibiotics in diet on rabbit's microbial gut composition

Oral communication, EAAP 2017

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Simultaneous *Bacteria* and *Archaea* detection by 16S rDNA-based MiSeq sequencing was performed to assess rabbit gut microbiota composition subjected to different factors: feeding regime (*ad libitum* (aL) vs. restricted (R)), presence/absence of antibiotics in the diet, and the global environmental conditions defined by the farm. Caecum samples from 66-days-old rabbits (236 fed aL and 215 fed under R) were collected from two different farms (375 farm A and 94 farm B). 24 samples from farm B came from animals fed with the same standard feed but without antibiotics. Average daily gain (ADG) was individually recorded and its association with microbiome composition was studied. Globally, a total of 4,613 OTUs without singletons were clustered from 15,296,317 filtered contigs with a QIIME pipeline. Taxonomic assignment, based on Greengenes database gg_13_5_otus, revealed that intestinal microbiota was dominated by *Firmicutes* (79.2%), *Tenericutes* (6.6%) and *Bacteroidetes* (5.4%) phyla; *Archaea* domain was present at low percentage (1.5‰) (Figure 1). PCoA based on weighted Unifrac distance matrix showed that farm exerted a more relevant effect than feeding regime or the presence/absence of antibiotics (Figure 2). Nevertheless, 3 OTUs belonging to *Clostridiales* order (*Firmicutes*) and *Methanobacteriaceae* family (*Euryarchaeo-*

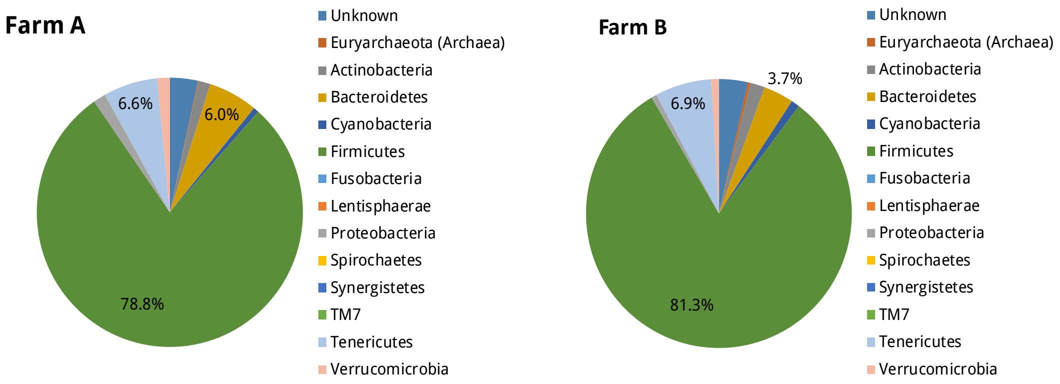

Figure 1. Microbial composition, at phylum level, by farms A and B

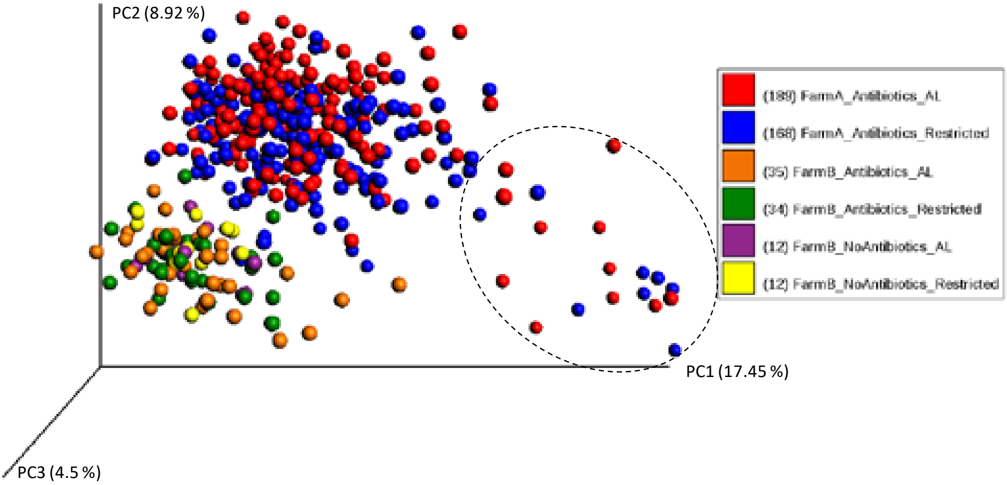

Figure 2. PCoA representing 451 caecum samples assigning different colors to the levels of the combination between farms, presence of antibiotics in diet and feeding regime. Grouped samples belong to animals with low microbial richness.

María Velasco

María Velasco is a PhD student in Animal Production at Autonomous University of Barcelona (Spain) who is currently working in her doctoral thesis “Characterization of caecal microbiota of meat rabbits. Genetic relationships between microbiota and feed efficiency” at the Genetics and Animal Breeding department of Institute for Food and Agriculture Research and Technology (IRTA) in Spain. She has a degree in Genetics (Autonomous University of Barcelona) and an MSc diploma in Animal Breeding and Reproduction Biotechnology obtained with *Maxima cum laude* mention at Polytechnic University of Valencia and Autonomous University of Barcelona in 2016. Since 2015, she has been involved in the Feed-a-Gene project and her objectives are to characterize phenotypically and genetically the caecal microbiota of two groups of meat rabbits fed with different feeding regimes (*ad libitum* vs. restricted), to quantify the effect of the feeding regime and the presence of antibiotics in the diet on the host’s microbiota, to study the genetic determinism of the rabbit on its caecal microbiota and to study the relationship between microbiota and productive traits.

ta) were overrepresented in samples from animals fed aL relative to those under R. Moreover, 57 OTUs were differentially represented in animals receiving diet with or without antibiotics. On the other hand, significant associations with ADG were found for 45 OTUs. This was negative for 13 families and 5 phyla, and positive for 3 families and 2 phyla. OTU richness was positively associated with ADG (Figure 3). Our results point to the fact that bacterial taxa abundance might explain an important percentage of ADG variability since the content in half of the detected phyla is associated to ADG.

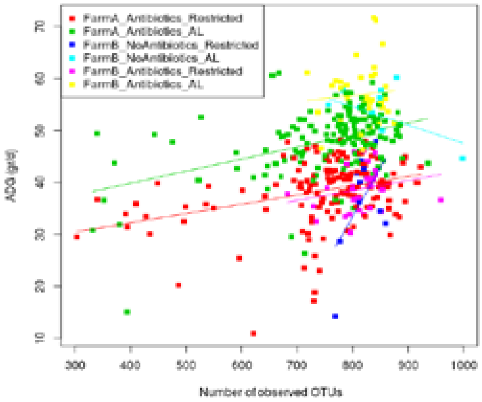

Figure 3. Association between average daily gain (ADG) and the number of observed OTUs at 10,000 reads

Fecal microbial composition associated with variation in feed efficiency in pigs depends on diet and sex

Oral communication, EAAP 2017

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Feed efficiency (FE) is an important trait in the pig industry, as feed costs are responsible for the major part of production costs. Availability in the market and cost of feed ingredients dictate changes in feed composition. As a result, fibre level and composition can vary between pig diets. Microbiota in the gastrointestinal tract play an important role in fibre digestion, because they produce enzymes that break down fibre structures and deliver volatile fatty acids to the pig. These volatile fatty acids can be used as metabolic energy source. As such, microbial fermentation could influence FE in pigs. The aim of this study was to investigate the association between FE and faecal microbiome in commercial grower-finisher pigs. Three-way crossbred grower-finisher pigs (154) were either fed a diet based on corn/soybean meal (CS) or a diet based on wheat/barley (WB). Faecal samples were collected on the day before slaughter (mean bodyweight 122 kg) and sequenced for the V3V4 16S ribosomal DNA regions. Sequences were clustered according to operational taxonomic units (OTU) for each individual, forming a table of OTU abundancy. A partial least square regression was applied to the dataset, together with a discriminant analysis using principal components of FE extreme groups (10 high and 10 low FE animals for each diet x sex-combination). Pigs on different diets and males vs. females had a very distinct microbiome, needing only two OTUs for diet (P=0.018) and 18 OTUs for sex (P=0.002) to separate the groups. Faecal microbiome was not related to FE groups fed the CS diet, but there were sex specific OTUs related to FE in the male and female pigs in the groups fed the WB diet. In conclusion, our results show a diet and sex dependent relationship between the faecal microbial composition and FE in grower-finisher pigs at slaughter weight.


Photo credit: Topigs Norsvin

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 this past year, she has been working on microbiota 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.

WP3 Modelling biological functions with emphasis on feed use mechanisms

WP3 leader: Veronika Halas,
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Partners: KU, INRA, UNEW, IRTA,
Cobb, AFZ

Objectives

The aim is to develop models and a tool for predicting and assessing feed and nutrient utilisation in pigs and poultry of different genotypes maintained under different environments, including access to different feeds. Emphasis will be given to the interactions between genotype and nutrition at digestive, metabolic and output levels, including nutrient excretion. The framework will be used as the basis to develop a Decision Support System (DSS). The specific objectives are:

- develop a simulation model to predict digestive utilisation of feed and nutrients in pigs and poultry
- develop a simulation model to predict the metabolic utilisation and partitioning of nutrients
- develop models to account for (environmental) disturbances and robustness in pig and poultry systems
- include variation in the different components of the system (i.e., environment, feed composition and animal genotype) to account for their effect and for variation in the response among individual animals
- deliver a Decision Support System integrating the concepts and models described above

Approach

In the proposed models, a dynamic and mechanistic deterministic approach will be used. The core of the digestive and metabolic models is the same for pigs and poultry and the differences are attributed to species specific model parameters and, if required, additional model equations (e.g. predicting feather growth). This approach enables a generic representation of digestion and metabolism in different monogastric species. It focuses on biological commonalities among monogastric animals, while allowing the representation of aspects that are species or production specific. Apart from quantitative aspects of feed efficiency and nutrient transformation, qualitative aspects of meat production will also be addressed. An innovation in the developed models is that they can cope with disturbances of environmental factors and the response of the animal to these disturbances, and predict the variation in the responses among individual animals within a herd or a flock.

Results

The core of the digestive model has been developed, and it is being quantified for chickens and pigs for standard diets with literature database. The metabolic model predicting nutrient partitioning, particularly energy and amino acid utilisation in pigs has been extended with a Ca and P metabolism module. The pig model has been adapted for broiler chickens, and the preliminary tests show reasonable fit of simulated to measured data. A perturbation has usually prompt impact on feed intake, therefore the intake curve of individual animals is suitable to detect environmental disturbance. A module is being developed to detect the perturbation and resistance and resilience of the animals. A method has been provided to determine the ideal trajectory of cumulative feed intake. In stochastic model development a phenotypical landscape work has been done using the Bayesian statistical approach. A model for estimating difficult-to-measure individual-specific traits, such as dynamic body composition (protein, lipid) and maintenance heat, without using data on any of these traits was developed.

Implication

The aim of the working package is to develop biological models of livestock functioning to better understand and predict nutrient and energy utilisation of animals along their productive trajectory, and, based on these, develop Decision Support Systems (DSS). The projected models are available to predict digestible nutrient content of feeds as well as the animal (pig and poultry) performance upon different feeding and environmental conditions and cope with the representation of individual variance and herd/flock response to different scenarios.

The DSS will be available for users to run the models with various input data and thus test different concepts. The innovation in WP3 is the ability of the animal model to represent the effect of certain stress situations or unknown incidence on the animal response. The environmental perturbation on the animal response is modelled as a spring-damper system describing the phe-

Veronika Halas

Veronika Halas is an associate professor in Department of Animal Nutrition at Kaposvár University, Hungary. She has a PhD degree in animal sciences obtained at Wageningen University in 2004. In the past 15 years, she has been working on modelling and experimenting nutrient partitioning in pigs, and involved in digestibility studies in pigs and poultry. Since 2015, she has been involved in the Feed-a-Gene project as a leader of the modelling work package.

nomenon as a composition of a resistance period followed by a resilience period in the presence of an external force. The WP also deals with stochasticity by predicting the individual variance of the animals as a trait of the population, herd or flock upon different scenarios. This approach is rarely represented in today's models. Bayesian statistics are applied to account for correlation among model parameters and for the variability (stochasticity) in parameters among individuals. Bayesian methods are used also to predict future performance by sampling from the estimated posterior distribution of parameters and simulating the model. This store of information can be applied directly to the management of commercial units to support nutritional or technological decisions as well as breeders to improve their genetic selection.

Tasks

Task 3.1 Digestive utilisation of feed and nutrients

Task 3.2 Metabolic utilisation of feed and nutrients

Task 3.3 Accounting for environmental variability, system disturbance and robustness

Task 3.4 Accounting for variation among individuals (stochasticity) in nutrient digestion and metabolism processes

Task 3.5 Delivery of a Decision Support Tool

Preliminary model to predict P-requirement of growing pigs

Oral communication, EAAP 2017

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Phosphorus is an essential nutrient and, as phosphate, is involved in most of the metabolic activities of the body as well as in bone formation. There is evidence that long term P deficiency reduces the growth rate of animals. However, oversupply results in high rate of excretion that is critical from environmental point of view. Modelling P metabolism allows to improve our understanding on the main factors affecting the P requirement. The aim of the work was to develop a mathematical model predicting the dynamics of P partitioning and retention in growing and fattening pigs over time. The model is a comprehensive description of the underlying mechanisms of digestible P and Ca utilisation. Input parameters are related to the diet and include dry matter, the Ca and P content of the feed, as well as Ca and P digestibilities, and to the animal such as daily feed intake, protein and fat deposition rate. The model presents the distribution of true digestible P and Ca within the body. Absorbed P and Ca are used for maintenance purposes, soft tissues (muscle and backfat), and bone tissue development. Surplus P and Ca is excreted via urine. Retention of P in the body

is the sum of P retention in soft tissues and skeleton. It is presumed that soft tissues have a priority in utilizing the absorbed P. Thus, an insufficient P supply results in a reduction in or even negative bone ash retention to ensure P for the development of soft tissues. However, there is a limit for rate of demineralization and, under the threshold level, the absorbed P has priority to be retained in bone over soft tissues. The bone formation depends on P bioavailability and Ca supply, and limited by potential bone P retention. The model is able to predict P-retention, urinary P excretion and digestible P requirement of swine at different body weights and with a different body composition. The results show that the P requirement depends on growth rate and particularly on protein deposition of the pigs.

Model testing confirms that P deficient diet (2 g/kg P) reduces the simulated live weight due to the reduced protein deposition (Figure 1). However, it also confirms that slightly lower P content feed compared to a feed containing sufficient P does not compromise the growth rate and the protein and fat deposition, even if the P-retention is lower. The model behaviour has been checked by sensitivity analyses; particularly the predicted apparent digestible P requirement is tested in response to protein and lipid deposition rate (PD and LD) as well as Ca to protein ratio (Ca/prot). The default values of PD, LD and Ca/prot are changed by ±20 and ±40% at 30, 60 and 100 kg BW. The results show that the model is highly sensitive to changes in daily protein deposition and to Ca/protein ratio in the body, and 40% change in PD and Ca/protein ratio resulted in 44% and 24% changes in P requirement. However, changes in LD do not make significant changes in P requirement. The relative changes in digestible P requirement in response to changes in the checked sensitivity parameters are identical in each BW.

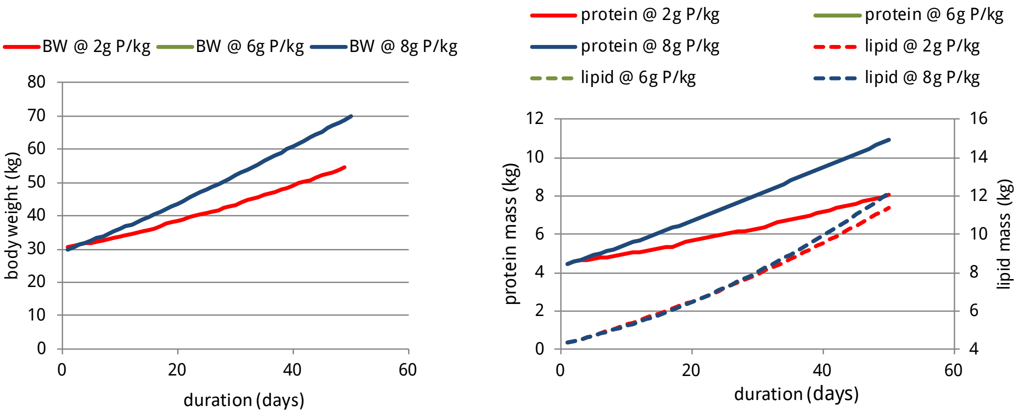

Figure 1. Simulated body weight and protein and fat mass in pigs fed diets with different P content

Table 1. Result of the sensitivity analyses: predicted apparent P requirement as a function of changes in protein and fat deposition rate, and Ca to protein ratio in the body

		Change in default value				
BW		60%	80%	100%	120%	140%
30 kg	PD (default 101 g/kg)	2.27	3.14	4.00	4.87	5.75
	LD (default 89 g/kg)	3.99	3.99	4.00	4.01	4.01
	Ca/protein ratio (default 0.05)	3.04	3.52	4.00	4.48	4.97
60 kg	PD (default 142 g/kg)	3.18	4.44	5.67	6.92	8.17
	LD (default 204 g/kg)	5.65	5.66	5.67	5.69	5.71
	Ca/protein ratio (default 0.05)	4.29	5.00	5.67	6.35	7.03
100 kg	PD (default 125 g/kg)	2.77	3.84	4.92	6.01	7.11
	LD (default 301 g/kg)	4.86	4.89	4.92	4.95	4.97
	Ca/protein ratio (default 0.05)	3.72	4.32	4.92	5.51	6.11

Re-parametrization of a swine model to predict growth performance of broilers

Oral communication, EAAP 2017

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The aim of the study was to investigate whether a pig growth model is suitable to be modified and adapted for broilers. As monogastric animals, pigs and poultry share many similarities in their digestion and metabolism. The common basis and the generic approach are feasible, considering that many structures (body protein and lipid stores) and the nutrient flows of the underlying metabolic pathways are similar among species. For that purpose, the InraPorc model was used as a basis to predict growth performance and body composition at slaughter in broilers. Firstly, the backbone of InraPorc was translated to Excel and examined whether the equations were suitable for growing birds by evaluating the parameters and model behavior. After determining of differences the model was modified for predicting growth in broilers in relation to the nutrient supply. The model core is very generic in terms of representing the most important nutrient flows and the transformation from absorbed nutrients to protein and fat accretion during growth. The idea of nutrient utilisation is mainly based on concepts used in net energy and ideal protein systems. The model is driven by feed intake (FI), the partitioning of energy between protein and lipid deposition, and availability of dietary protein and amino acids. Parameters of the Gompertz function were adjusted using li-

terature data to express maximum feather-free body protein deposition. A separate Gompertz equation was used to estimate feather growth and protein content of feather was assumed to be a nonlinear function of age. The amino acid loss with feathers was considered as a part of the maintenance requirement and the sum of fasting heat production (460 kJ/(kg BW)$^{0.70}$/day) and energy for activity (33% of FHP) was used as the net energy requirement for maintenance. FI for broilers was expressed on a net energy basis and estimated by a Gamma-function (which expresses the feed intake as multiples of maintenance), as in InraPorc. Parameters of the Gamma function were adjusted to experimental data from different broiler studies. For model calibration growth data of Cobb broilers were used. Five data series were assigned to test the model. The Gamma function was fitted to observed feed intake at different time points. The aim of the model evaluation was to examine if Gamma function estimates the FI, and the model response for different feed intake patterns. For that reason the model was run with precisely estimated feed intake of each pen. The nutrient content of the feed was assumed to be identical with Cobb recommendations. All other input parameters were the same for each pen (precocity: 0,045; mean PD = 14 g/d; initial BW = 45 g; nutrient content of the feed). Simulated BW as a response to different feed intake patterns was an output of the model and values for 7, 14, 21, 28, 33 and 39 day of age were compared to observed data. The mean square prediction error (MSPE) was calculated according to Bibby J & Toutenburg H (1977) to evaluate the predictive potential of the model:

$$\text{MSPE} = \Sigma\,(O_i - P_i)^2 / n$$

where O_i and P_i are observed and predicted values; i = 1, ..., n, and n is the number of experimental observations. The root MSPE is a measure in the same units as the output and is expressed as a percentage of the observed mean. The MPSE can be decomposed into three fractions. MSPE = B + R + E, where B – error attributed to overall bias; R – deviation of regression slope from one; E – disturbance proportion. The results show that the Gamma function can be used to estimate precisely the feed intake pattern of broilers during growth (Fig. 1). In conclusion, a modified pig model appears to be suitable to predict the response of broilers to different feed intakes (Fig. 2, Table 1).

Galyna Dukhta

Galyna Dukhta is a PhD student at Department of Animal Nutrition at Kaposvár University, Hungary. One of her MSc diploma is in Animal Nutrition and Feed Safety completed at Kaposvár University in 2013. Since March 2016 she has been involved in WP3 of the Feed-a-Gene project and she works on metabolic utilisation of feed and nutrients, and prediction model of poultry performance.

Table 1. Comparison of observed pen data of Cobb broilers with model simulations: mean square prediction error (MSPE) and decomposition of the MPSE

	Feed Intake (g/d)					Body Weight (kg)				
	Root MSPE	relMSPE %	B%	R%	E%	Root MSPE	relMSPE %	B%	R%	E%
1 pen	4.160	0.02	16.6	35.0	48.4	0.078	3.74	56.1	19.9	24.0
3 pen	6.071	0.04	17.6	34.1	48.2	0.063	3.12	56.9	38.8	4.2
6 pen	3.269	0.02	12.7	27.4	59.9	0.122	6.92	82.0	7.3	10.7
21 pen	4.286	0.02	15.0	34.0	50.9	0.141	5.87	56.6	41.6	1.9
98 pen	3.772	0.04	14.7	27.7	57.7	0.079	5.58	40.1	2.7	57.3

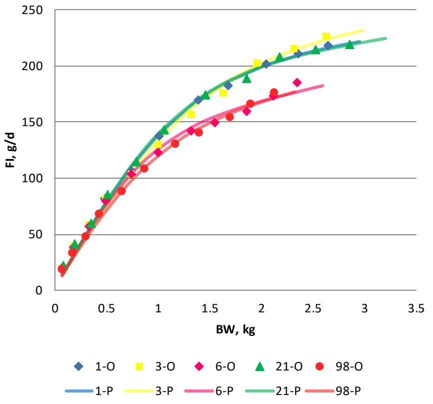

Figure 1. Observed feed intake (dots) and feed intake predicted with a Gamma-function of maintenance (line) based on body weight for five different datasets of Cobb broilers

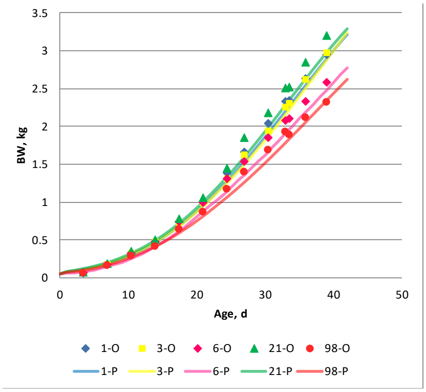

Figure 2. Observed BW (dots) and predicted BW (line) from five different datasets of Cobb broilers

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Modelling individual uncertainty and population variation in phenotypical traits of livestock

Oral communication, EAAP 2017

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Characterising between-animal variation and its population-level consequences is key to effective livestock management and selective breeding. The aim may be to predict trait development (e.g., performance) from early growth or to estimate unobserved traits (e.g., maximum growth or maturity parameters). A usual sequence of steps is: 1) To develop a mathematical model of chosen animal-level traits. 2) To estimate individual parameters across a sample of animals. 3) To estimate a population distribution of parameters. 4) To generate a population distribution of traits

by simulating the model across distribution 3. The challenge is in the parameter estimation given typical data limitations. We use a Bayesian inference methodology to estimate the population distribution of predicted traits. The approach i) accounts for individual-level uncertainty in parameters (2) due to their correlation and data limitations, e.g., short growth span or infrequent records, and ii) does not invoke distributional assumptions and estimation of variance-covariance parameters (3). We present results derived from individual data with usual limitations. We apply the approach to estimate individual-specific performance traits that are difficult to measure, such as dynamic body composition and maintenance heat (Figure 1), without requiring data on these traits. We show the within-breed inter-individual variability in protein and lipid growth parameters and in metabolic heat production (HP) and the predicted population distributions of body composition, and compare body composition and extent of its variation across monogastric species (pigs, chicken, rabbits). Literature body composition estimates usually condition on input of average HP data; by estimating composition and HP jointly, their individual-level correlation is included and no metabolic data is needed. For pigs, HP estimates distributed about 0.7 MJ/kg/d in line with literature, and body fat content variation was much larger than that of body protein. For broilers, HP estimates also agreed with literature and relative body fat content was lower than in pigs. We suggest this approach has general application in model parameterisation and prediction of trait development in populations using limited individual data.

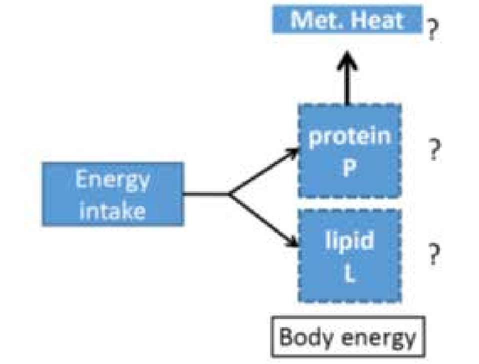

Figure 1. Schematic representation of the energy flow model. Question marks indicate the non-observed variables estimated through the model and statistical approach.

João Filipe

João Filipe, Newcastle University, UK, specialised in mathematical modelling and Bayesian statistics in systems biology and epidemiology, previously at the University of Cambridge and the London School of Hygiene and Tropical Medicine. He is involved in the Feed-a-Gene project since December 2015 developing modelling approaches for characterising phenotypical variability in monogastric animals.

Characterizing animal response to environmental challenges: new traits of more efficient animals

Oral communication, EAAP 2017

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Farm animals are constantly facing perturbations due to changing environmental and farm conditions. Characterization of the animal response when it is facing these perturbations that influence animal performance and health is of main concern to ensure sustainable livestock production. Indeed, a better understanding of the adaptation mechanisms used by the animal to cope with a single and multiple challenges (through resistance and resilience) is a prerequisite to propose adequate farm management strategies and for the development of precision livestock farming systems. Several experimental studies have been conducted to investigate the influence of the environment on animal performance. Mathematical models can be used to consider and to quantify the systemic aspects of the animal's response to a perturbation. Existing models of farm animal performance have accounted to a limited extent for environmental perturbations. With novel monitoring technologies, it is now possible to evaluate the impact of these perturbations on animal performance in real time and with a high frequency.

We propose a mechanistic model to describe the influence of a generic and perturbation of unknown origin on feed intake of growing pigs. The model is based on two sub-models: InraPorc, a model to describe growing pig performance in a standard environment, and the well-known spring-and-damper system used in physics to describe the behavior of a system in presence of external force. The InraPorc model was used to describe the phenotypic performance of the animal in the absence of acute perturbing factors. The spring-and-damper system included two parameters to characterize the adaptive response of animals when facing a perturbation. The main interest of this characterization is to define new standards to rank animals based on feed efficiency together with their adaptive capacity, and to find out potential correlation between these parameters. Future development of the model will adapt it to simulate successive perturbations of known or unknown origins. Moreover, based on these new parameters, the model can propose model-derived traits for genetic selection of more efficient and robust animals.

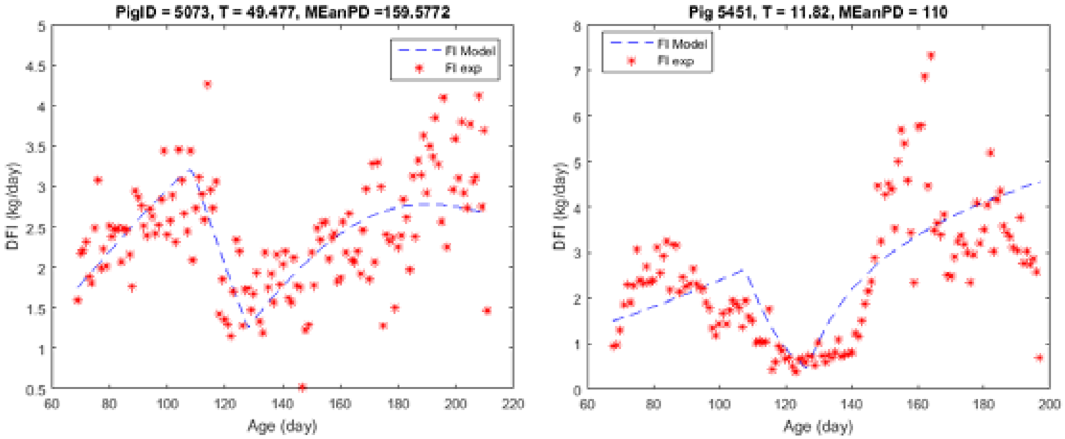
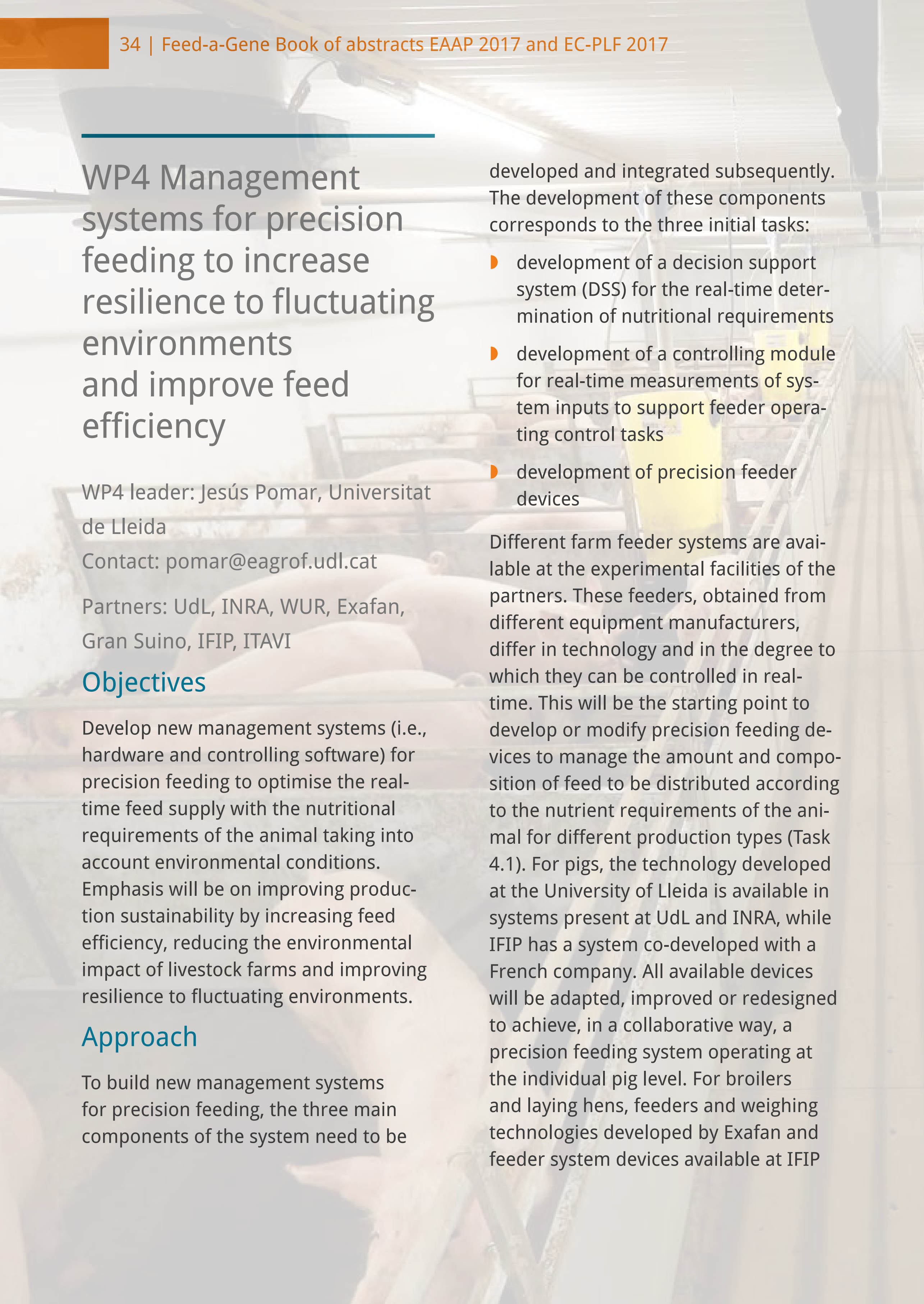


Figure 1. Characterization of the responses of two growing pigs faced with a given perturbation

The figure shows the responses of two growing pigs faced with a given perturbation. The animal of Figure b has a fast recovery after the perturbation compared to the animal of the Figure a. This recovery capacity is quantified by the parameter T of the model. The prediction of the model (blue dashed line) fits well the data of daily feed intake for two growing pigs (red asterisk).

Masoomeh Taghipoor

Masoomeh Taghipoor is a scientist in theoretical biology and mathematical modelling of complex systems in animal science at INRA, France. She has a PhD in Biomathematics obtained at Tours University in 2012. In the past 5 years, she has been working on the use of mathematical models for a better understanding of the animal adaptation faced with nutritional or environmental challenges at different scales. Since 2015, she has been involved in the Feed-a-Gene project and her objectives are a better characterization of animal response to a generic and unknown perturbation. The main interest of this characterization is to define new standards to rank animals based on feed efficiency together with their adaptive capacity.



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

WP4 leader: Jesús Pomar, Universitat de Lleida

Contact: pomar@eagrof.udl.cat

Partners: UdL, INRA, WUR, Exafan, Gran Suino, IFIP, ITAVI

Objectives

Develop new management systems (i.e., hardware and controlling software) for precision feeding to optimise the real-time feed supply with the nutritional requirements of the animal taking into account environmental conditions. Emphasis will be on improving production sustainability by increasing feed efficiency, reducing the environmental impact of livestock farms and improving resilience to fluctuating environments.

Approach

To build new management systems for precision feeding, the three main components of the system need to be developed and integrated subsequently. The development of these components corresponds to the three initial tasks:

- development of a decision support system (DSS) for the real-time determination of nutritional requirements
- development of a controlling module for real-time measurements of system inputs to support feeder operating control tasks
- development of precision feeder devices

Different farm feeder systems are available at the experimental facilities of the partners. These feeders, obtained from different equipment manufacturers, differ in technology and in the degree to which they can be controlled in real-time. This will be the starting point to develop or modify precision feeding devices to manage the amount and composition of feed to be distributed according to the nutrient requirements of the animal for different production types (Task 4.1). For pigs, the technology developed at the University of Lleida is available in systems present at UdL and INRA, while IFIP has a system co-developed with a French company. All available devices will be adapted, improved or redesigned to achieve, in a collaborative way, a precision feeding system operating at the individual pig level. For broilers and laying hens, feeders and weighing technologies developed by Exafan and feeder system devices available at IFIP and INRA will be adapted in a collaborative way to achieve precision feeding at the group level (Tasks 4.2 and 4.3).

The aim of Task 4.4 is to integrate the three components obtained in the previous tasks to build systems that enable accurate and automatic feeding according to the requirements of individual or groups of animals including a preliminary validation and refinement of prototypes. The last stage (Task 4.5) involves prototype demonstrations. Once prototypes pass validation in experimental conditions, they will be demonstrated at the farm level to illustrate their potential and, if needed, refine their characteristics under field conditions.

Tasks

Task 4.1 Development of decision support tools for the real-time determination of animal nutritional requirements (composition and amount) and improvement of performance

Task 4.2 Development of a controlling module (software and hardware) to support feeder control tasks and real-time measurements

Task 4.3 Development of precision feeder devices

Task 4.4 Build and validate precision feeding system prototypes

Task 4.5 Demonstration activities

Jesús Pomar

Jesús Pomar is professor at Universitat de Lleida, Spain. After graduating from the Universidad Politécnica de Madrid, he obtained his PhD at Universitat Politècnica de Catalunya in 1985. His R&D activities have focused on the development and application of ICT in the agricultural sector, initially in the development of information systems and intelligent decision-making support for the livestock sector (Sistema BDporc®, GTEP-X), resulting in the first «Electronic Pig management information systems». Since 2005, his work has focused on the advance of methods and technology for the development of smart farming livestock. As result an innovative robotised precision feeding system for pig production farms has been developed and patented. This robotised system uses an innovative distributed multi-agent architecture that supports intelligent and complex analysis functions. Lately, he has been involved in Feed-a-Gene as a leader of the development of new management systems for precision feeding group.

Development of a decision support system for precision feeding application in pigs and poultry

Oral communication, EAAP 2017

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Precision feeding is a promising way to improve feed efficiency and thus economic and environmental sustainability of livestock production. A decision support system (DSS) was built to determine in real-time the nutritional requirements of animals and feed characteristics (composition, amount). This tool will be associated with a controlling module to be part of an automatic feeding system and exchange data with different devices for an application of precision feeding in pig and poultry commercial farms (Figure 1). This DSS tool, dedicated to animals managed individually or in group, is designed with a modular structure for adaptation to different feeder devices, species and production stage (growing pigs, gestating and lactating sows, broilers, laying hens) (Figure 2). The modules are built to perform specialized tasks in a cooperative way. It includes a data management module with a proper characterization of data by meta-data definition for precision feeding. It ensures standard encoding to allow data interoperability from any platform. Other modules are dedicated to data checking and correction for database filling, prediction of most probable body weight (BW) gain and feed intake (*ad libitum* or restricted feeding) and calculation of nutritional requirements. The BW and feed intake prediction is based on dynamic data analyses. For that, specific methods have been studied and selected depending on the number of available data, their type (BW or feed intake) and recording frequency. The calculation of nutritional requirements is performed using nutritional models specific to a species or a production stage. These two last modules are currently designed for healthy animals and will be refined to extent prediction to a larger range of field situations (e.g. health problems, climatic conditions) with nutritional models in development/refinement in other workpackages of the project. The general specifications of this DSS and dynamic data analyses will be illustrated for growing pigs.

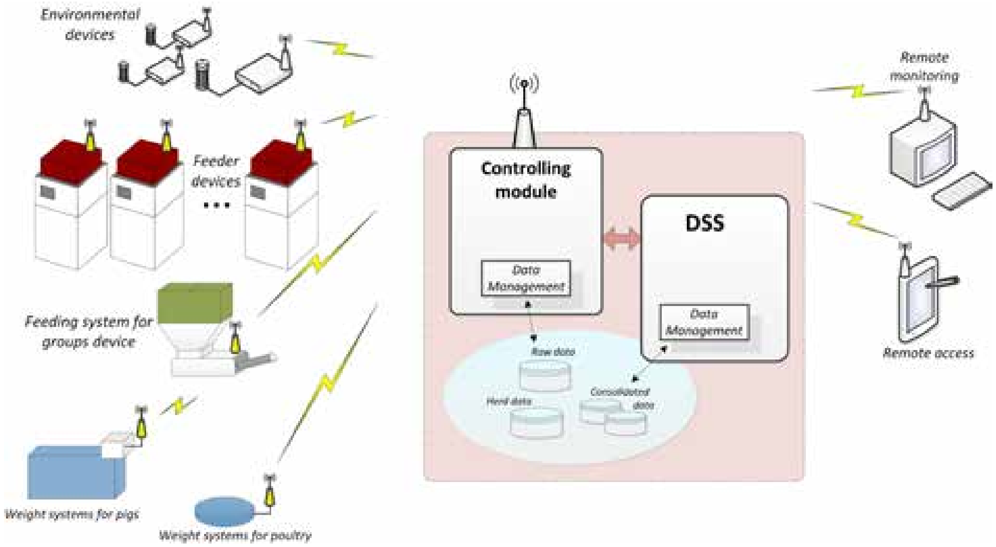

Figure 1. General structure of proposed precision feeding system (DSS: decision support system) for application of precision feeding in pig and poultry commercial farms

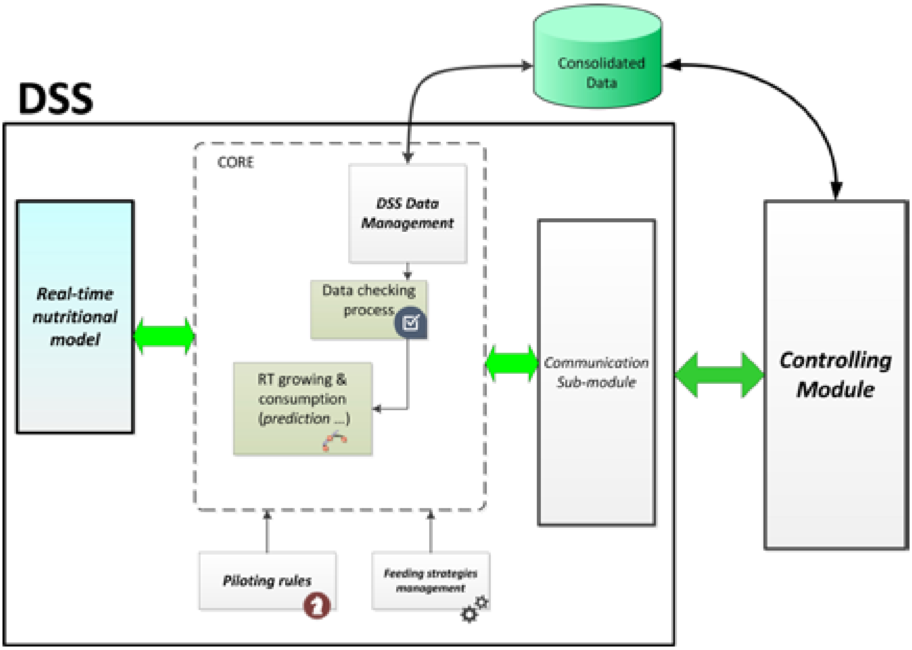

Figure 2. Modular structure of decision support system (DSS) developed in the Feed-a-Gene programme to determine in real-time the nutritional requirements of animals and feed characteristics (composition, amount) in precision feeding

Selection of methods to analyze body weight and feed intake data used as inputs for nutritional models and precision feeding in pigs

Oral communication, EC-PLF 2017

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The progress of technologies (sensors, automates) in precision livestock farming enables the development of innovative feeding techniques such as precision feeding of individual animals. In addition to the design of adapted feeders, precision feeding requires decision-support tools to manage data and apply nutritional models that calculate the optimal feed composition and allowance. These calculations require to forecast body weight (BW) and feed intake (FI) of individual pigs according to past performance. To select the most accurate forecasting method, three statistical methods were tested on a dataset of measurements of BW and FI for 117 pigs: the double exponential smoothing (DES) method, multivariate adaptive regression splines (MARS), and the k-nearest neighbours (kNN) method. The principles of these methods are described. The three methods were tested in relation to data sampling frequency (i.e., daily or weekly measurements) and data availability (number of historical data, i.e. latest previous data, to consider for calculation). The DES method was tested also by varying a parameter used to weigh differently past and recent observations. The capacity to forecast BW or FI was evaluated through the mean error of prediction. The kNN method appeared suitable if few historical data are available as it requires no more than 3 historical data. The MARS method was better than the DES method to forecast daily BW, especially using 13

Table 1. RMSEP (kg) of daily BW forecasting using the double exponential smoothing (α value ranging from 0.1 to 0.9) or MARS methods and 8, 13, or 20 historical data[1].

Nb. of data	Method									
	MARS	Double exponential smoothing (α value)								
		0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9
8	1.34^{a}	2.00^{b}	1.23^{c}	1.29^{ac}	1.21^{cd}	1.19^{cd}	1.22^{c}	1.27^{ac}	1.34^{a}	1.46^{e}
13	1.13^{a}	1.79^{b}	1.27^{c}	1.21^{cd}	1.18^{ad}	1.19^{ac}	1.22^{cd}	1.27^{c}	1.34^{c}	1.46^{e}
20	1.11^{a}	1.43^{b}	1.26^{c}	1.19^{cd}	1.18^{ad}	1.19^{cd}	1.22^{cd}	1.27^{ce}	1.34^{e}	1.46^{b}

1. Least-square means. The main effects of method, number of historical data and their interaction were significant at $P < 0.001$ (residual standard deviation of the model = 0.31 kg). Within a row, values followed by common letters are not significantly different for the method effect ($P < 0.05$).

or 20 historical data (Table 1). The DES method was better in forecasting the daily cumulated FI, with 8 to 20 historical data, the best forecasting being obtained by giving a higher weight to more recent data (weighing parameter α = 0.6 to 0.8; Table 2). The DES method also seemed more appropriate for weekly BW data, requiring only 3 historical data to make a forecasting, even if the mean error of prediction was higher than for daily data. These different methods can be used for performance forecasting in a decision-support tool for precision feeding.

Table 2. RMSEP (kg) of cumulated FI forecasting using the double exponential smoothing (α value ranging from 0.1 to 0.9) or MARS methods and 8, 13, or 20 historical data[1].

Nb. of data	Method									
	MARS	Double exponential smoothing (α value)								
		0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9
8	0.52^{a}	1.06^{b}	0.67^{c}	0.60^{d}	0.54^{ae}	0.50^{ae}	0.48^{a}	0.48^{a}	0.49^{a}	0.51^{a}
13	0.60^{a}	1.04^{b}	0.73^{c}	0.61^{a}	0.54^{d}	0.50^{de}	0.49^{e}	0.49^{e}	0.49^{e}	0.52^{de}
20	0.70^{a}	1.02^{b}	0.75^{c}	0.61^{e}	0.54^{f}	0.51^{fg}	0.49^{g}	0.49^{g}	0.50^{fg}	0.52^{fg}

1. Least-square means. The main effects of method, number of historical data and their interaction were significant at $P < 0.001$ (residual standard deviation of the model = 0.17 kg). Within a row, values followed by common letters are not significantly different for the method effect ($P < 0.05$).

Ludovic Brossard

Responsible of a research team working on pigs in livestock systems, Ludovic Brossard is research engineer in nutrition and growth modelling for pigs at INRA (UMR Pegase), France. He has a PhD in Biology and Agronomy obtained at ENSA Rennes in 2004. In the past 5 years, he has been working on heterogeneity among individuals to integrate it in growing pig nutritional models and study its implication in definition of feeding strategies considering animal performance, economic results and environmental impact. This includes the development of precision feeding concepts. Since 2015, he has been involved in the Feed-a-Gene project and his objectives are to contribute to refinement of nutritional models and to develop a decision support tool to real-time calculation of individual nutrient requirements for pigs, sows and poultry allowing improvement of performance while reducing feed costs and environmental impact. This tool will be included in automatic feeding devices allowing the application of precision feeding on farm.

Development of a decision support tool for precision feeding of pregnant sows

Oral communication, EAAP 2017

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Nutritional studies indicate that nutrient requirements for pregnancy largely differ among sows and according to the stage of pregnancy, whereas in practice the same diet is generally fed to all sows from a given herd. In this context, the availability of new technologies for high-throughput phenotyping of sows and their environment, and of innovative feeders that allow the distribution of different diets, offers opportunities for a renewed and practical implementation of prediction models of nutrient requirements, in the perspective of improving feed efficiency and reducing feeding costs and environmental impacts.

The objective of this study was thus to design a decision support system (DSS) that could be incorporated in automated feeding equipment as illustrated in Figure 1. 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: genotype, parity, expected prolificacy, gestation stage, body condition (i.e. weight and backfat thickness), activity and housing (i.e. type of floor and ambient temperature).

The approach was tested using data from 2500 pregnancies on 540 sows. Energy supply was calculated for each sow to achieve, at farrowing, a target body weight established based on parity, age at mating and backfat thickness (18 mm). Precision feeding (PF) with the mixing of two diets was then simulated in comparison with conventional (CF) feeding with a single diet. Compared to CF, PF reduced protein and amino acid intake, N excretion and feeding costs. At the same time, with PF, amino acid requirement was met for a higher proportion of sows, especially in younger sows, and a lower proportion of sows, especially older sows, received excessive supplies (Figure 2).

The results from this study indicate that, in the same way as in fattening pigs, precision feeding of gestating sows appears a win-win strategy which allows improving nutritional supplies of sows whilst reducing total protein and phosphorus supplies and consequently reducing their excretion. The effect on feeding cost was not yet evaluated but it may be expected that it is also reduced. The DSS developed in this study allows adapting the amount and composition of feed to each sow according to her body condition at mating and expected prolificacy, and to stage pregnancy. This DSS will also allow taking account of information collected by sensors during gestation, such as BW, backfat thickness or physical activity, on the environment, such as ambient temperature.

The data used for the simulations were issued from a project conducted within the AgriInnovation Program from Agriculture and Agri-food Canada.

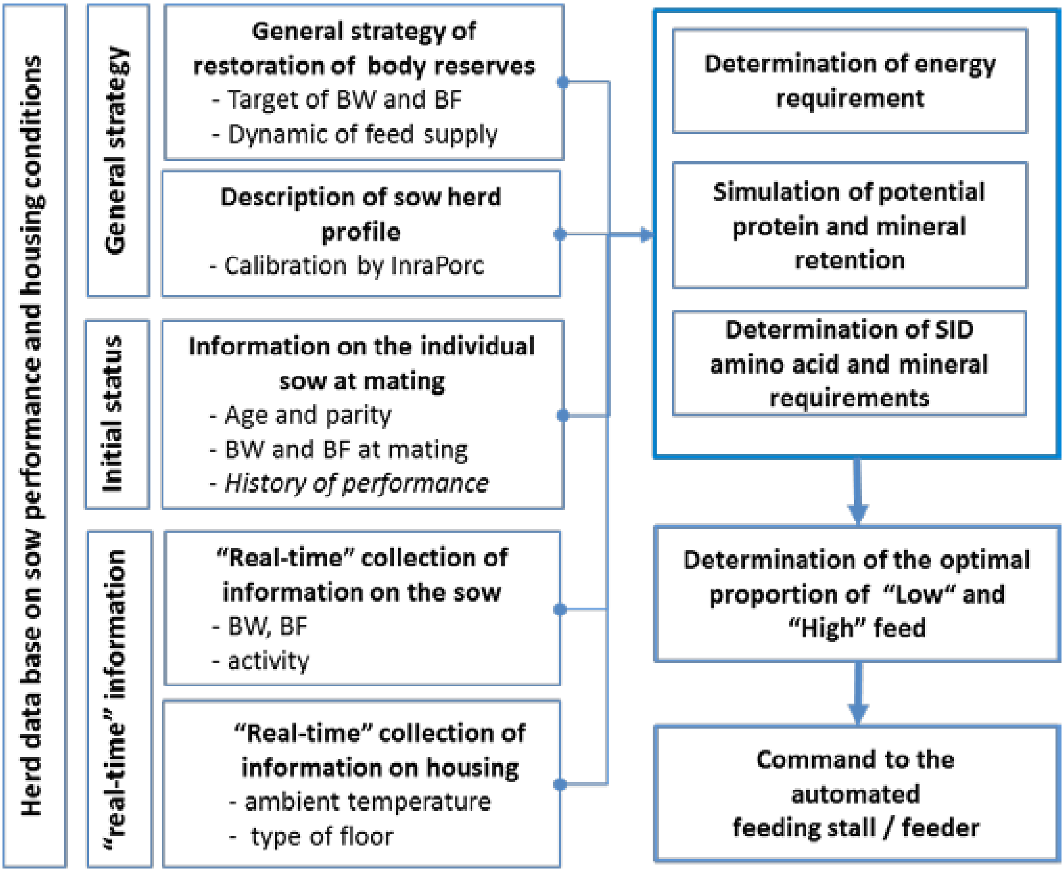

Figure 1. General description of the approach

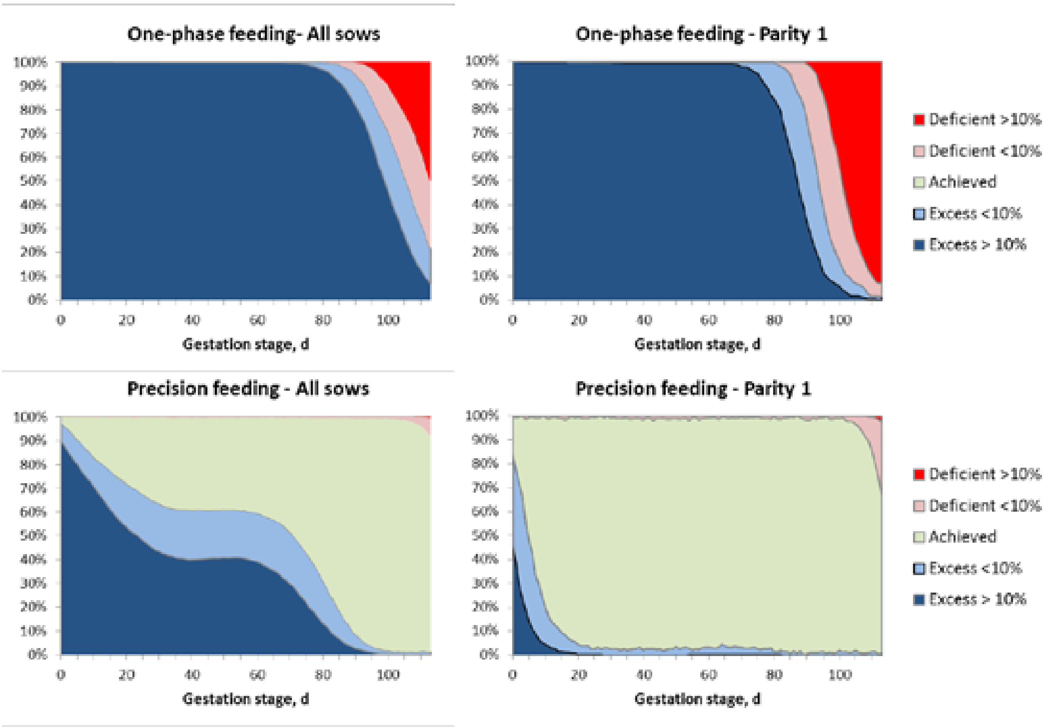

Figure 2. Effect of feeding strategy (one-phase vs. precision feeding) during gestation on the proportion of sows (left, among all sows and right, among parity-1 sows) that received deficient, adequate or in excess lysine supplies

Jean-Yves Dourmad

Jean-Yves Dourmad graduated in 1981 from INA P-G (now AgroParisTech), France, where he obtained his PhD on nutrition of the reproducing sow. He joined INRA in 1983 and contributed to a research program on energy and protein requirements of sows, and more recently, on the evaluation and reduction of the environmental impact of pig production systems. His research is based on both experimental and modeling approaches. He coordinated the development of the sow module of the InraPorc® model and software tool. He belongs to the «Pig farming system» research group of INRA UMR Pegase Unit (Rennes) and chairs the national transdisciplinary «Pig research committee» of INRA. In Feed-a-Gene he is involved in WP3 and WP4 on modelling and precision feeding of gestating and lactating sows.

Assessment of the dynamic growth of the fattening pigs from body weight measured daily and automatically to elaborate precision feeding strategies

Oral communication, EC-PLF 2017

Quiniou N.[1], **Brossard L.**[2], **Marcon M.**[1]

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Growing pigs are often fed below *ad libitum* to increase their feed efficiency and carcass leanness. When energy supply is under control, precision feeding is implemented through the amino acids (AA). As the AA requirement depends on the body weight (BW) for the maintenance part and on its daily variation (ΔBW) for the growth part, the adequacy between requirements and supplies on day D+1 depends on the adequacy of predicted BW_{D+1} and ΔBW_{D+1}. Data sets from four trials were used to forecast BW from time series analyses based either on multivariate adaptive regression splines (MARS) or double exponential smoothing (HWα) methods using the *k* latest data (8, 14 or 20). Pigs (n = 117) were group-housed and restrictively fed, and their BW was recorded daily and individually with an automatic scale (n = 11 736). With $HW_{0.6}$, the RMSEP of BW_{D+1} was the smallest one (1.21 kg) and not influenced by *k*. Linear regression on the *l* latest forecasted BW was used to assess ΔBW_{D+1}. At the beginning of the trial, ΔBW_{D+1} was more difficult to predict from BW forecasted with MARS than with $HW_{0.6}$. Descriptive statistics of individual variation of ΔBW_{D+1} based on

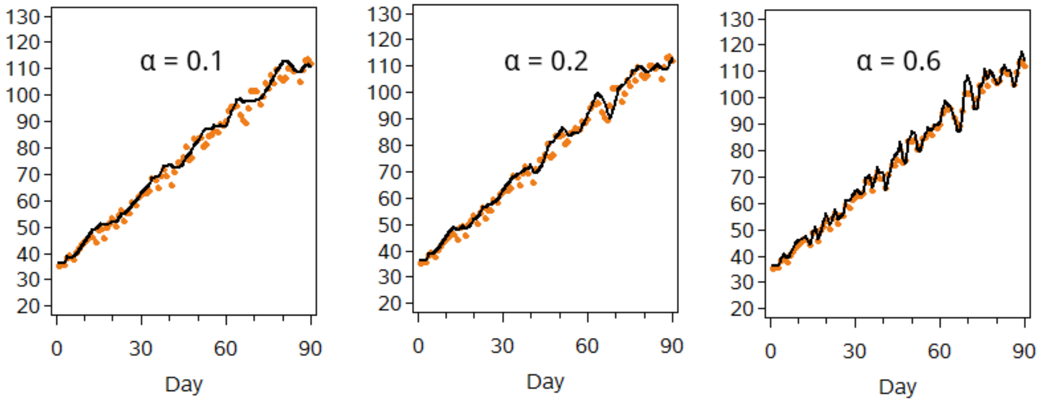

Figure 1. Example of comparison of measured (●) to forecasted (—) BW with the HW method implemented with 20 different historical values and three values for the smoothing parameter α (pig 310 in trial 1)

MARS and $HW_{0.6}$ were comparable with $k = l = 20$ only after removal of the first 19 days. Compared to other methods studied, the method $HW_{0.6}$ seems to be the best compromise to forecast BW_{D+1} and ΔBW_{D+1} of restrictively fed pigs.

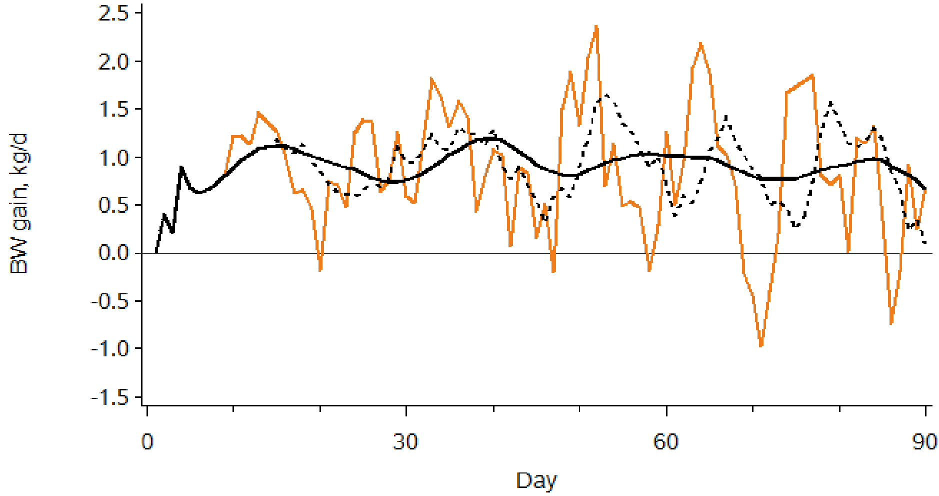

Figure 2. BW gain assessed from BW predicted with methods HW with α = 0.6 by linear regression with *k* = 20 and *l* = 8 (—), 14 (---) or 20 (—) (pig 310 in trial 1)

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 (task 4.1) and the validation of precision feeding prototypes (task 4.4).

Photo credit: Hamlet Protein

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

WP5 leader: Hélène Gilbert, INRA
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Partners: INRA, WUR, IRTA, Topigs, Cobb, INCO, IFIP

Objectives

The objective of WP5 is to explore new traits and models for estimating breeding values for feed efficiency, and to identify new strategies to use these in breeding programmes without impairing product quality, welfare and robustness considering the diversity of production environments and feed resources in the EU, and anticipating the effects of climate change on production systems. In this WP, we will:

- validate the potential of new on-farm measured heritable traits to predict breeding values for feed efficiency, robustness and welfare
- propose criteria and methodologies to quantify variability in gut microbiota as a heritable trait influencing feed efficiency, robustness and welfare
- produce new genetic models to better predict the individual variability of feed efficiency, robustness and welfare
- develop new selection strategies for feed efficiency to account for crossbred performance and genomic information, accounting for correlated impacts on the animals' sensitivity to environmental changes, product quality, environmental impact and welfare traits
- validate the importance and use of social effects and crossbred data for improving selection for feed efficiency

WP5 will benefit from new knowledge and data generated in the Feed-a-Gene project in terms of new feed resources for animals (WP1), new traits for innovative feeding and breeding (WP2) and model-derived traits of feed efficiency and robustness (WP3).

Approach

WP5 will revisit existing data and samples available from the partners, involving different breeding systems or climatic conditions. WP5 will carry out genetic analyses on trials designed to propose novel traits for feed efficiency (WP2). Specific trials will be run to generate new data, in particular including records on welfare, robustness and product quality associated to new feed resources (WP1), and for demonstration of selection strategies. Data will originate from purebred and crossbred pigs from conventional (Topigs, IFIP, and INRA) and alternative breeding systems (IRTA, INRA), from crossbred poultry from conventional populations (Cobb), and from experimental lines in pigs, poultry and rabbits (INRA and IRTA). Genetic parameters for new traits related to feed efficiency will be derived using conventional genetic approaches, and revisited models will be developed. New breeding strategies, including genomic information, crossbred data, and indirect indicators of feed efficiency will be explored to propose new selection indexes while accounting for the economic impact on welfare, robustness, and product quality. Results will be shared for the generation of new feeding strategies (WP4) and new models and tools of nutrient utilisation (WP3). The results will also be used for the sustainability assessment of new production systems (WP6).

Tasks

Task 5.1 Genetics of components of feed efficiency and robustness indicators

Task 5.2 Genetic relationships between the gut microbiota and feed efficiency

Task 5.3 Statistical-genetic modelling of feed efficiency and robustness features

Task 5.4 Selection strategies to account for crossbred and genomic data for a sustainable selection for feed efficiency

Task 5.5 Demonstration of the value of social interactions and crossbred information in selection to improve feed efficiency

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.

Responses of pigs divergently selected for cortisol response or feed efficiency to an ACTH challenge

Oral communication, EAAP 2017

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Selection for feed efficiency can impair the animal's ability to respond to stress. A key driver of this response is the hypothalamo-pituitary-adrenal (HPA) axis, which releases cortisol in response to stressors. Injection of a normalized dose of adrenocorticotropic hormone (ACTH) to stimulate cortisol release by the adrenal cortex is a standardized method to evaluate the activity of the HPA axis independently of the animal's perception of stress. It has been used to select during three generations a highCortisol line and a lowCortisol line, that had divergent cortisol levels 1 h after ACTH injection (H1, peak of the response). A trial was set up to compare the responses to ACTH of these two lines and those of two other lines divergently selected for residual feed intake (RFI, measure of net feed efficiency) during nine generations. At 6 weeks of age, 48 pigs per line were tested. Blood samples were collected before and 1 (H1) and 4 h after injection (H4) when cortisol is expected to return to basal level. In the Cortisol lines, plasma cortisol was twofold higher ($P<0.0001$) in the highCortisol pigs than in the lowCortisol pigs at the 3 times (Figure 1a). In both lines, cortisol was 2.3 to 2.6 fold higher at H1 compared to H0 (Figure 1b). The highRFI (less efficient) line had a similar response to the ACTH injection as the Cortisol lines (Figure 1b). The lowRFI line had higher cortisol levels at H0 ($P=0.08$) and H1 ($P=0.0002$) than the highRFI line. This difference was increased at H4 ($P<0.0001$), due to higher H4 than H0 cortisol levels in lowRFI pigs ($P<0.0001$) (Figure 1b). Blood counts, urea, glucose, IGF-I and free fatty acids (FFA) measurements were used to better understand the responses to ACTH, suggesting different underlying metabolisms. In contradiction with previous hypotheses, increased feed efficiency is not associated with a decreased HPA axis activity, but might be related to different dynamics of responses after stress.

Photo credit: INRA

Figure 1a

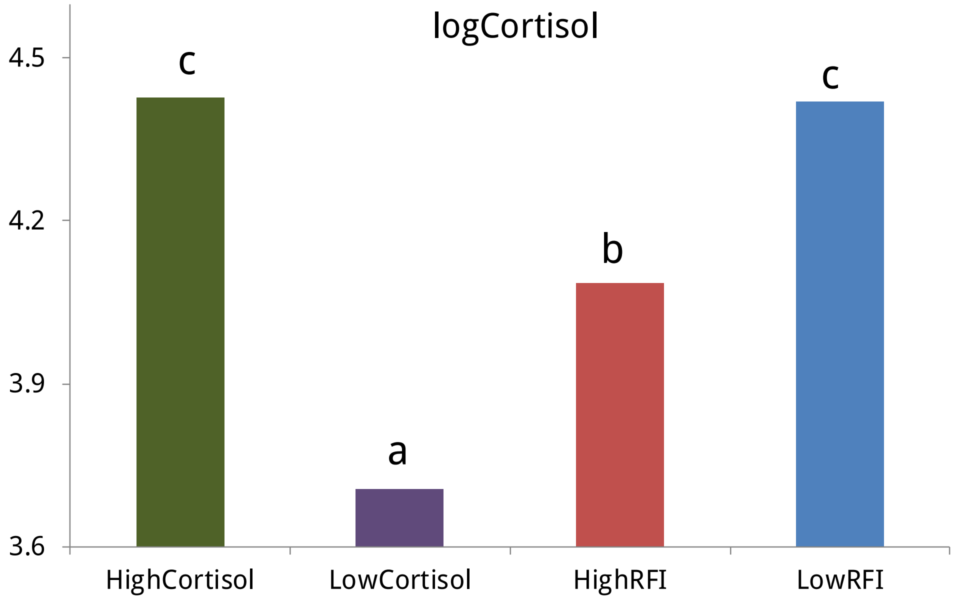

Figure 1b

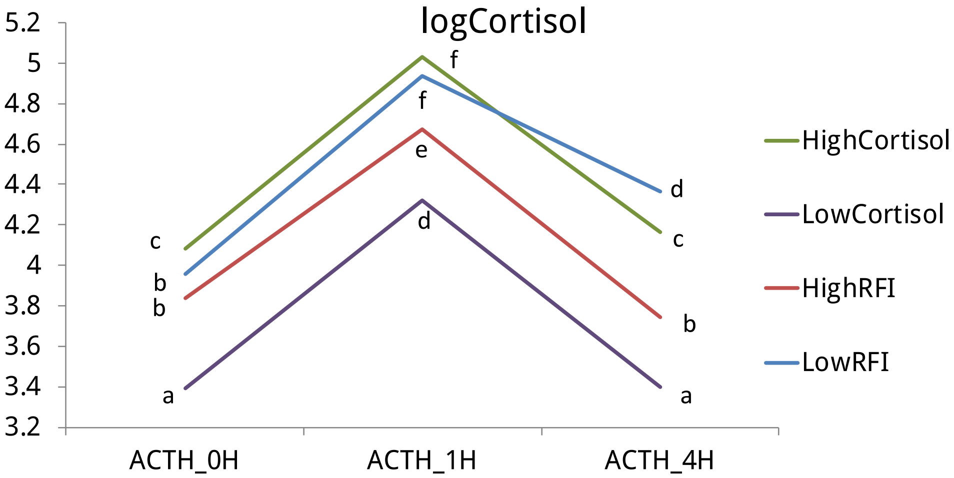

Figure 1. Least square means for line effect (a, P<0.0001) and the line x time interaction (b, P<0.0001) from a linear model including the fixed effects of batch (4 levels), herd of test (2 levels), sex (2 levels), line (4 levels), time (3 levels), and all relevant interactions, including line x time. Values with different letters differed at P<0.05.

A review of the purebred-crossbred correlation in pigs: theory, estimates, and reporting

Oral communication, EAAP 2017

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Pig and poultry production relies on crossbreeding of purebred populations to produce production animals. Thus, the breeding goal is to improve crossbred performance, while selection typically takes place within the purebred populations. The genetic correlation between purebred and crossbred performance (r_{pc}) is known to be lower than unity for many traits. A low value of r_{pc} indicates that use of crossbred performance in selection is required to achieve sizable genetic progress. We aimed to 1) review estimates of r_{pc} in pigs, 2) review the different components of r_{pc} and their contribution to it, 3) give guidelines for future studies estimating r_{pc}. In total, 195 r_{pc} estimates from 27 studies were used, published between 1964 and 2016. The r_{pc} estimates had an average value of 0.63, with 50% of the estimates between 0.43 and 0.88. Standard errors were on average 0.16, with 50% of the values between 0.07 and 0.2. Standard errors of r_{pc} reduced with increasing numbers of common sires between purebred and crossbred animals (Figure 1). For all different trait categories, e.g. growth, meat amount, meat quality, feed, and fertility, the average r_{pc} was below 0.8 (Figure 2). The r_{pc} has three components: 1) genotype by environment interaction between nucleus and commercial herds, 2) differences in genetic background of purebred and crossbred animals, and 3) differences in trait definition or measurement used in purebred and crossbred animals. Genotype by environment interaction appeared to have

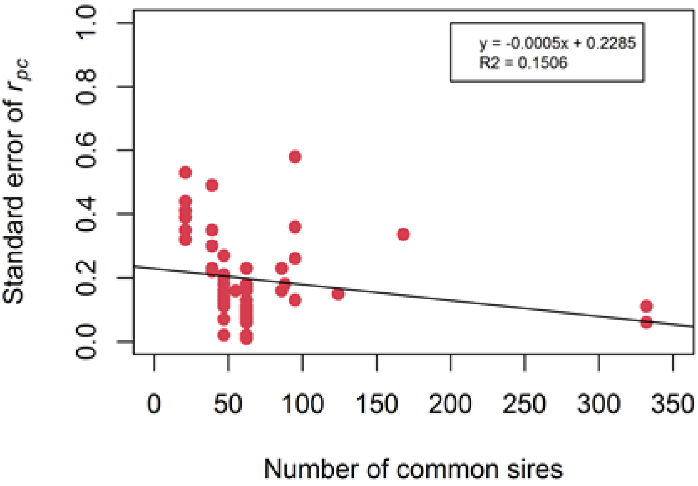

Figure 1. Number of common sires between purebred and crossbred animals versus the standard error of the r_{pc}

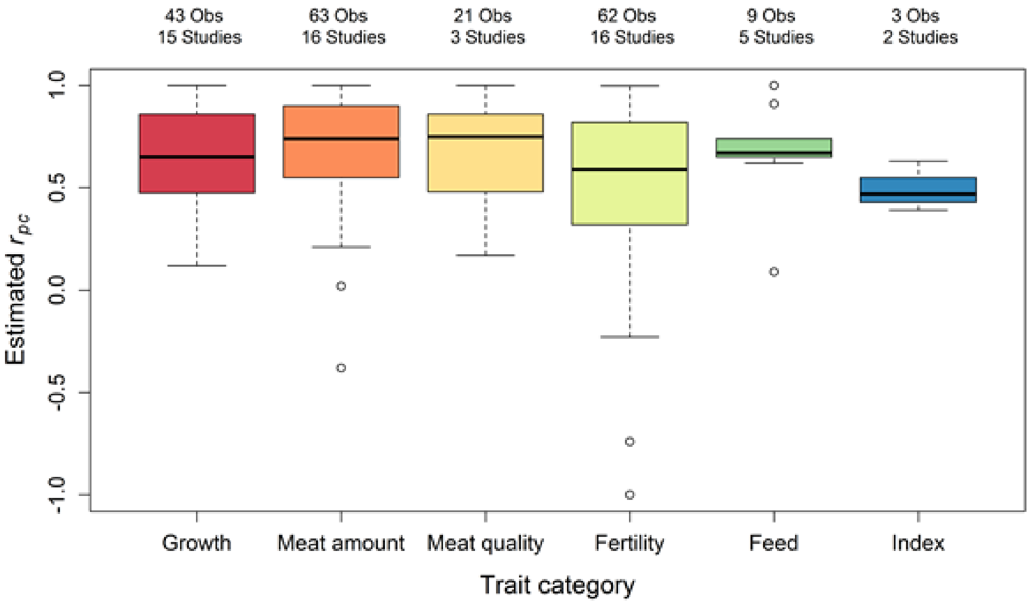

Figure 2. Estimated r_{pc} values for the six different trait categories

a smaller contribution to r_{pc} than differences in genetic background. Across traits and studies, the r_{pc} did not show a relation with the heritability of the trait. Future studies are advised to consider to keep both purebred and crossbred animals under nucleus and commercial conditions, report characteristics of the herd environments in detail, estimate separate r_{pc} for different pure lines, and genotype the animals under study.

Mario Calus

Mario Calus is a Senior researcher in Quantitative Genetics at Wageningen University & Research, The Netherlands. He has a PhD in Animal Breeding and Genetics obtained at Wageningen University in 2006. In the past 10 years, he has been working on the development of genomic prediction, both in terms of science and application. Since 2015, he has been involved in the Feed-a-Gene project and his objectives are to develop tools to enable and optimize genomic prediction for crossbred performance in livestock populations.

Genetic and maternal effects on growth and feed efficiency in rabbits

Oral communication, EAAP 2017

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The aim of this study was to evaluate the significance of neonatal environment (ultimately including the microbiota composition) on feed efficiency. For that purpose, rabbits of the G10 line, selected for 10 generations on residual feed intake (RFI), were fostered by does of a non-selected control line G0, and vice versa. In parallel, collaterals were adopted by mothers from their original line. Around 900 animals were produced in 3 successive batches and raised in individual or collective cages. Traits analyzed in this preliminary study were weights at weaning (32 days) and at the end of the test (63 days), average daily gain (ADG), feed intake between weaning and 63 days (FI), feed conversion ratio (FCR) and RFI. Line of the rabbit, type of housing and batch were significant effects for all traits. G10 does had a negative effect on FCR (+0.06, P = 0.04), irrespective of the line of young rabbits. G10 animals were lighter than G0 at 32 days (-83 g) and at 63 days (-161 g). They also had a lower ADG (-2.36 g/day), FCR (-0.36), RFI (-548 g/day) and a lower FI (-839 g), confirming a better feed efficiency.

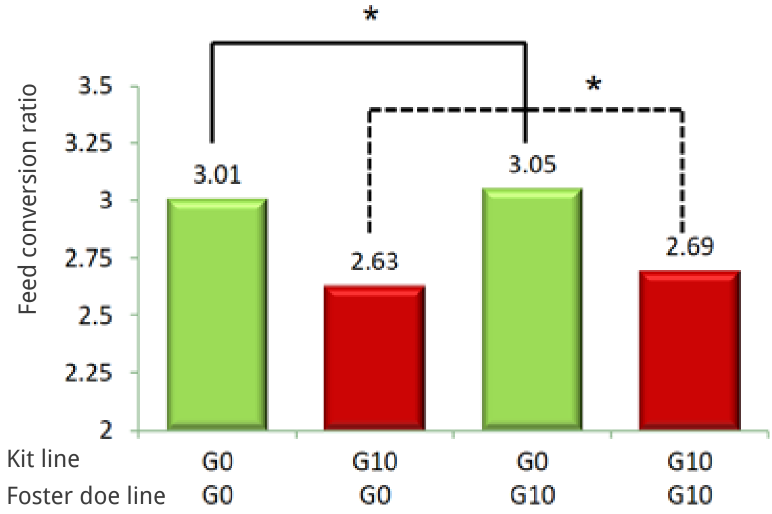

Figure 1. Kit line and foster doe line effects on feed conversion ratio. *: P < 0.05 ; ***: P < 0.001.

Table 1. Level of significance of fixed effects

		P	
Trait	Kit line	Foster doe line	Type of housing
Body weight at 32 days	***	ns	/
Body weight at 63 days	***	ns	***
Average Daily Gain	***	ns	***
Feed Conversion Ratio	***	*	***
Residual Feed Intake	***	ns	***
Feed Intake	***	ns	***

ns = non significant; *: P < 0.05; **: P < 0.01; ***: P < 0.001.

Table 2. Least square means for kit line and type of housing

	Kit line		Type of housing		
Trait	G0	G10	collective	digestibility	individual
BW32 (g)	916 ± 6	833 ± 6			
BW63 (g)	2,624 ± 13	2,463 ± 12	2,436 ± 14^{a}	2,596 ± 20^{b}	2,599 ± 11^{b}
ADG (g/day)	51.76 ± 0.28	49.40 ± 0.26	47.77 ± 0.32^{a}	52.08 ± 0.46^{b}	51.88 ± 0.25^{b}
FCR	3.02 ± 0.02	2.66 ± 0.02	3.14 ± 0.02^{a}	2.69 ± 0.03^{b}	2.69 ± 0.01^{b}
RFI (g)	298 ± 18	-250 ± 17	333 ± 20^{a}	-117 ± 29^{b}	-144 ± 16^{b}
FI (g)	5,127 ± 23	4,288 ± 21	4,850 ± 26	4,645 ± 38	4,628 ± 21

a, b means with different letters are significantly different (P < 0.05).

Hervé Garreau

Hervé Garreau is a research engineer in genetics at INRA, France. He has an engineer diploma in agronomy obtained at ENITA of Bordeaux in 1991. In the past 10 years, he has been working in feed efficiency, longevity and disease resistance in rabbit. Since 2015, he has been involved in the Feed-a-Gene project as leader of task 5.2 (“Genetic relationships between the gut microbiota and feed efficiency”) and his objectives are to examine the relative importance of the host and of the microbiota composition in the variability of feed efficiency to propose new traits for selection and new breeding strategies.

Genomics to estimate additive and dominance genetic variances in purebred and crossbred pig traits

Oral communication, EAAP 2017

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This study aims at assessing the contribution of the additive and dominance genomic variances to the phenotype expression of several purebred Piétrain and crossbred (Piétrain x Large White) pig performances. A total of 636 purebred and 720 crossbred male piglets were phenotyped for 22 traits that can be classified into growth rate and feed efficiency, carcass composition, meat quality, behavior, boar taint and puberty groups of traits. Additive and dominance variances estimated in univariate genotypic models including additive and dominance genotypic effects and a genomic inbreeding covariate allowed us to retrieve the additive and dominance SNP variances for purebred and crossbred performances. These estimated variances were used, together with the allelic frequencies of the parental populations, to obtain additive and dominance variances in terms of genetic breeding values and dominance deviations. Figure 1 shows the ratio of dominance deviation variance with respect to the total genetic variance for the 22 analyzed traits in both populations (percentage above the bars indicates the amount of variance due to dominance deviations with respect to the phenotypic variance). Estimates of additive genetic variances across traits were consistent with previous results without dominance indicating that additive and dominance genetic effects were non-confounded. Some traits showed relevant amount of dominance genetic variance in both populations (i.e. growth rate 8%, feed conversion ratio 9-12%, backfat thickness 14-12%, lean meat 10-8%, carcass lesions 9%, in purebreds and crossbreds, respectively) or increased amount in crossbreds (i.e. ham cut 8-13%, loin 7-16%, pH *semimembranosus* 13-18%, pH *longissimus dorsi* 9-14%, dressing yield 5-15%, androstenone 5-13% and estradiol 6-11%). There was not a clear common pattern of dominance expression within and between groups of analyzed traits. Results suggest that accounting for dominance in the models of these traits could lead to an increased GEBV accuracy and that using crossbred information can be beneficial to evaluate purebred candidates to selection for crossbred performance. Further research will compare additive and dominance marker effects between crossbred and purebred performances.

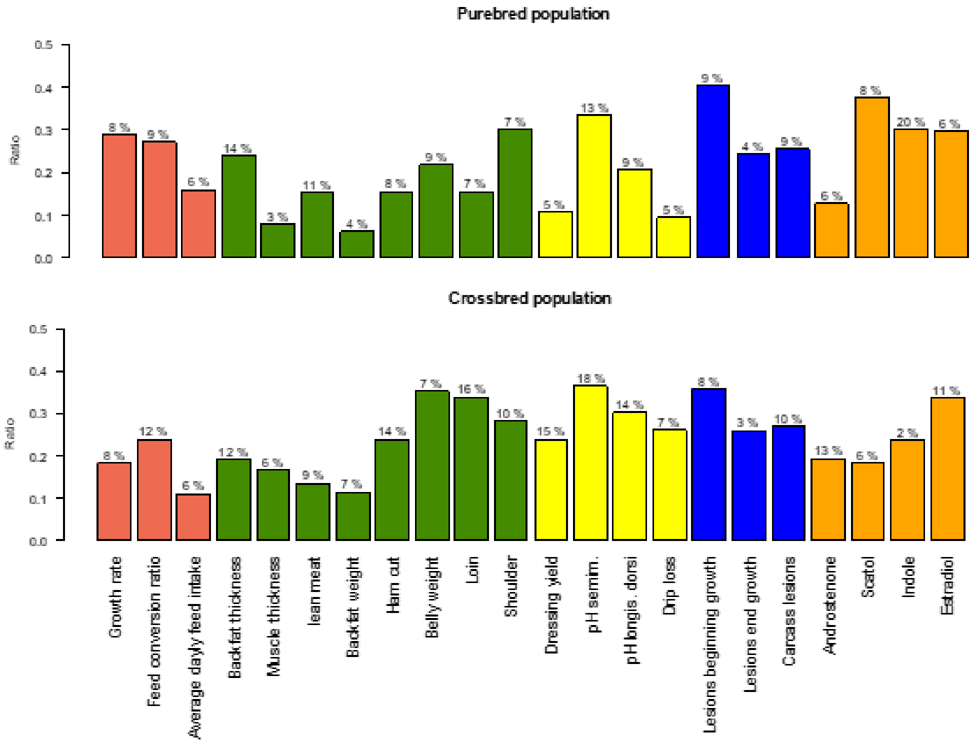

Figure 1. Ratio of dominance deviation variance with respect to the total genetic variance for the 22 analyzed traits in both populations. % above the bars indicate the amount variance due to dominance deviations with respect to the phenotypic variance.

Llibertat Tusell Palomero

Llibertat Tusell Palomero is a research scientist working on genomic selection in pigs with a special interest in selection of purebreds for improved crossbred performance at the GenPhySE department from INRA in Toulouse, France. She has a PhD in Animal Sciences performed at IRTA, Barcelona obtained at the Universitat Politècnica de València in 2017. In the past 7 years, she has been working in genome-enabled methods for predicting pig performance in purebred and in crossbred populations. Since 2015, she has been involved in the Feed-a-Gene project and her objectives are to develop model strategies to account for crossbred and genomic data for a sustainable selection for feed efficiency.

Feed restriction and growth of mice divergently selected for birth weight environmental variability

Poster, EAAP 2017

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Nowadays, the selection for feed efficiency is one of the main aims in animal breeding in order to decrease the production costs. On the other hand selection for less sensitivity with respect to environmental effects, as indicated by a low variation around the optimum trait value, may have benefits in the productivity and in the animal welfare. Therefore, the objective of this work was to analyze the influence of food restriction, understood as an environmental challenge, on weight at different ages in two lines divergently selected for birth weight variability in mice, low variability (LV) and high variability (HV) lines. A total of 40 females (four full-sib females from 10 random different litters from the 12, 13 and 14 generations of selection), were chosen within lines and fed either *ad libitum* or restricted from 21 to 70 days. Restriction consisted of feeding with 75%, 90% and 85% of *ad libitum* consumed in the respective three studied generations. Weekly weights from 21 to 77 days were analyzed (Figure 1). The model adjusted the diet (restricted or not), the line, the generation and the litter size, including also the interaction between the line, the generation and the diet. ASReml Release 4.1 program was used. Animals fed *ad libitum* of LV line had similar weights in all generations

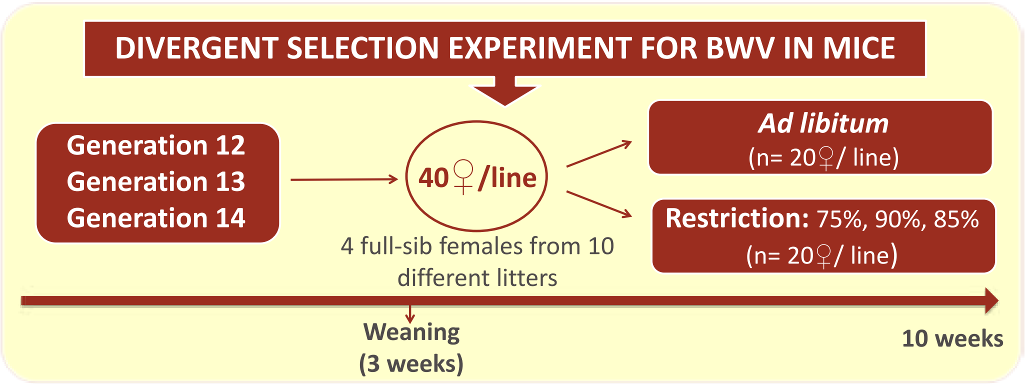

Figure 1. Divergent selection experiment for birth weight variability in mice

unlike those of HV line, which presented lower weights. The dietary restriction had a negative effect on the body weight of the animals but the interaction between line and diet was significantly different only after day 35, showing a differential response of the lines to the environmental challenge, animals from LV line were less sensitive to the feed restriction (Figure 2, Table 1).

Figure 2. Predictive values of weights at 49 days of life (W49) in each generation, diet and variability line

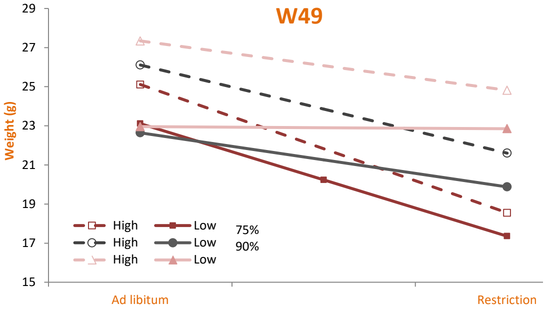

Table 1. Effect of feed restriction on mice weight at different ages

	W21	W28	W35	W42	W49	W56	W63	W70
Line	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.
Generation	n.s.	n.s.	***	***	***	***	***	***
Diet	--	***	***	***	***	***	***	***
Litter size	***	***	**	***	***	***	***	***
Line*generation	**	n.s.	n.s.	n.s.	**	n.s.	--	n.s.
Generation*diet	--	**	***	***	***	***	***	***
Line*diet	--	n.s.	***	***	***	**	***	**

W** (weight ** days); -- effect not taken into account; n.s. not significative; * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$

Nora Formoso-Rafferty

Nora Formoso-Rafferty is a scientist researcher working on animal genetics at the Department of Animal Production of the Universidad Complutense de Madrid. She has a diploma in Agronomy Engineering obtained at the Universidad Politécnica de Madrid in 2010. Recently, she obtained a PhD in Veterinary Science at the Universidad Complutense de Madrid. Since 2015, she has been involved in the Feed-a-Gene project and her research interests include animal genetics, reproduction, strategies to improve feed efficiency and animal welfare.

Using metafounders to model purebred relationships in genomic prediction for crossbreeding

Oral communication, EAAP 2017

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Selection for feed efficiency in purebred pig and poultry breeding animals should ideally account for the performance of crossbred animals. As part of the Horizon 2020 Feed-a-Gene project, methodologies to account for crossbred data are being developed and optimized using simulated data. The advantage of using crossbred data instead of purebred data in genomic evaluations for feed efficiency will be evaluated to propose new selection schemes for feed efficiency in monogastric animals. Simulations were set up using a three-way crossbred breeding program, with 10 generations of purebreds (PB), and 5 generations of two-way and three-way crossbred animals. The last generation of PB are validation animals. True breeding values are simulated for each line/cross (5 traits). Genetic correlations between all PB lines were randomly sampled in the range 0.2-0.8. Heritabilities were randomly sampled in the range of 0.2-0.4. Each PB generation consists of 2000 phenotyped individuals, and all genotyped animals were also phenotyped. Three scenarios will be tested with varying amounts of data available. In the first scenario 2000 phenotypes and no genotypes will be available, in the second 2000 phenotypes and 1000 genotypes, and in the third 2000 phenotypes and 2000 genotypes. The simulated genotypes follow the size and number of chromosomes of the pig genome (18 chromosomes). The number of SNP simulated is ~60k, with 4,500 QTL in total. Each simulation is replicated ten times. Breeding values of validation animals are predicted using pedigree-based BLUP, or single step GBLUP (SS-GBLUP) that either uses metafounders or not. Metafounders

Ilse van Grevenhof

Ilse van Grevenhof is a researcher in Quantitative Genetics at Wageningen University & Research, The Netherlands. She has a PhD in Animal Breeding and Genetics obtained at Wageningen University in 2011. In the past years, she has been working on complex (disease) traits. Since 2016, she has been involved in the Feed-a-Gene project and she is investigating methodologies to account for crossbred data using simulated data.

enable to estimate parental relationships between purebred lines using the genotype information of different lines in the G-matrix (usually no relationship is assumed between PB lines). Results will contain estimated variance components and accuracies of breeding values of purebred selection candidates for crossbred performance. We hypothesize that use of metafounders will lead to improved accuracies and more unbiased estimated variance components for SS-GBLUP.

Social genetic effects on productive and feeding behavior traits in growing Duroc pigs

Oral communication, EAAP 2017

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To explore the role of feeding behavior traits (FBt) and social genetic models for genetic evaluation of both FBt and performance traits (Pt), genetic parameters were estimated for daily gain (DG), daily feed consumption (DC), feed conversion ratio (FCR), backfat thickness (BF), feeding rate (FR), feeding frequency (FF), and occupation time (OT). Traits were recorded in 663 Duroc pigs. Two bivariate models were fitted: animal models (AM) and social interaction animal models (SAM). Estimations were done following Bayesian procedures. Heritability (h^2) estimates obtained with AM for all traits were medium-high (Table 1), due to additional heritable variation captured by social genetic effects (SGE). Higher estimates of the ratio of total genetic variance to phenotypic variance (T2) were obtained with SAM. Only OT direct genetic effects (DGE) seem to be positively correlated with DGE of DG, DC and BF (0.34(0.14), 0.61(0.18) and 0.38(0.09), respectively), when AM was used the respective genetic correlations were not different from zero. With AM, unfavorable genetic correlation between BF and DG (0.64(0.15)) were estimated (Table 2). With SAM either SGE or DGE correlations remained high and unfavorable, but the correlation between SGE of DG and DGE of BF was negative (-0.80(0.13)), being null that between SGE of BF and DGE of DG (Table 3). Large estimation errors of within-trait direct-social genetic correlations prevented to properly define their sign, but they seem to be of low magnitude. The role of FBt to improve Pt genetic evaluations is limited, except for OT. Consideration of SAM allows disentangling the social origin of certain unfavorable AM correlations. SAM could be used to explore indexes combining SGE and DGE of different traits to take advantage of favorable genetic correlations that might exist between them.

Figure 1. Schematic representation of the relationships between traits (1,2) and box mates (i,j) under Social Animal Model (SAM). Double rows represent genetic correlations.

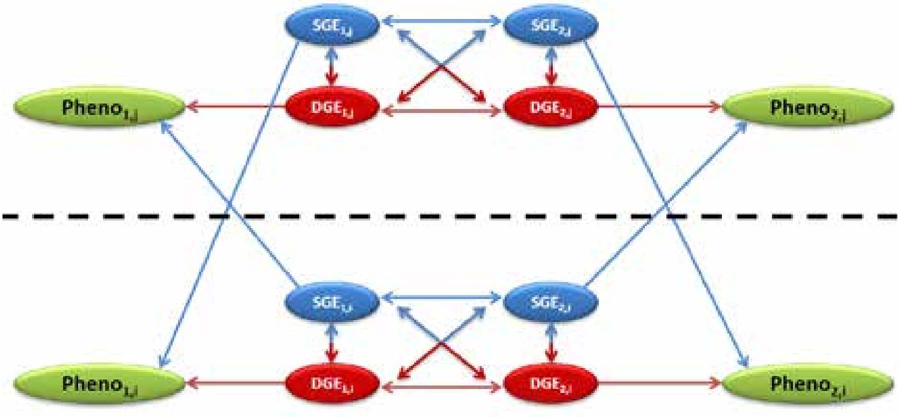


Table 1. Heritabilities for productive and feeding behavior traits

	AM	SAM		
Traits	h^2	T^2	Cor (DGE-SGE)	Dif. DIC
Average daily gain, ADG	0.46 (0.15)	0.52 (0.27)	-0.54 (0.41)	80.63
Average daily consumption, ADC	0.47 (0.12)	0.77 (0.42)	-0.19 (0.60)	49.81
Feed conversion ratio, FCR	0.25 (0.09)	1.12 (0.54)	0.37 (0.55)	13.21
Backfat thickness, BF	0.59 (0.12)	0.77 (0.33)	-0.13 (0.61)	55.05
Feeding rate, FR	0.43 (0.09)	0.69 (0.32)	-0.007 (0.64)	15.34
Occupation time, OT	0.39 (0.10)	0.27 (0.22)	-0.83 (0.25)*	44.35
Feeding frequency, FF	0.46 (0.10)	1.17 (0.62)	-0.03 (0.55)	46.29
Time between visits, FInt	0.41 (0.09)	0.40 (0.31)	-0.64 (0.34)*	41.14

DGE: direct genetic effect; SGE: social genetic effect; Cor (DGE-SGE): genetic correlation between DGE and SGE; DIC: deviance information criterion; *: probability of being greater than 0 >0.95 or <0.05.

Table 2. Genetic correlations between productive traits from animal model (AM) and between direct genetic effects (Above diagonal) and social genetic effects (Below diagonal) from social animal model (SAM)

	Animal Model			Animal Model with Social Effects			
	ADC	BF	FCR	ADG	ADC	BF	FCR
ADG	0.93 (0.05)*	0.64 (0.15)*	0.42 (0.42)		0.87 (0.05)*	0.55 (0.10)*	-0.17 (0.12)
ADC		0.87 (0.07)*	0.71 (0.25)*	0.83 (0.13)*		0.87 (0.05)*	0.43 (0.16)*
BF			0.86 (0.14)*	0.64 (0.24)*	0.75 (0.17)*		0.75 (0.09)*
FCR				0.51 (0.20)*	0.81 (0.27)*	0.63 (0.32)	

ADG: average daily gain; ADC: average daily consumption; FCR: feed conversion ratio; BF: backfat thickness; *: probability of being greater than 0 >0.95 or <0.05.

Table 3. Genetic correlations between direct genetic effects (rows) and social genetic effects (columns) for productive traits using SAM

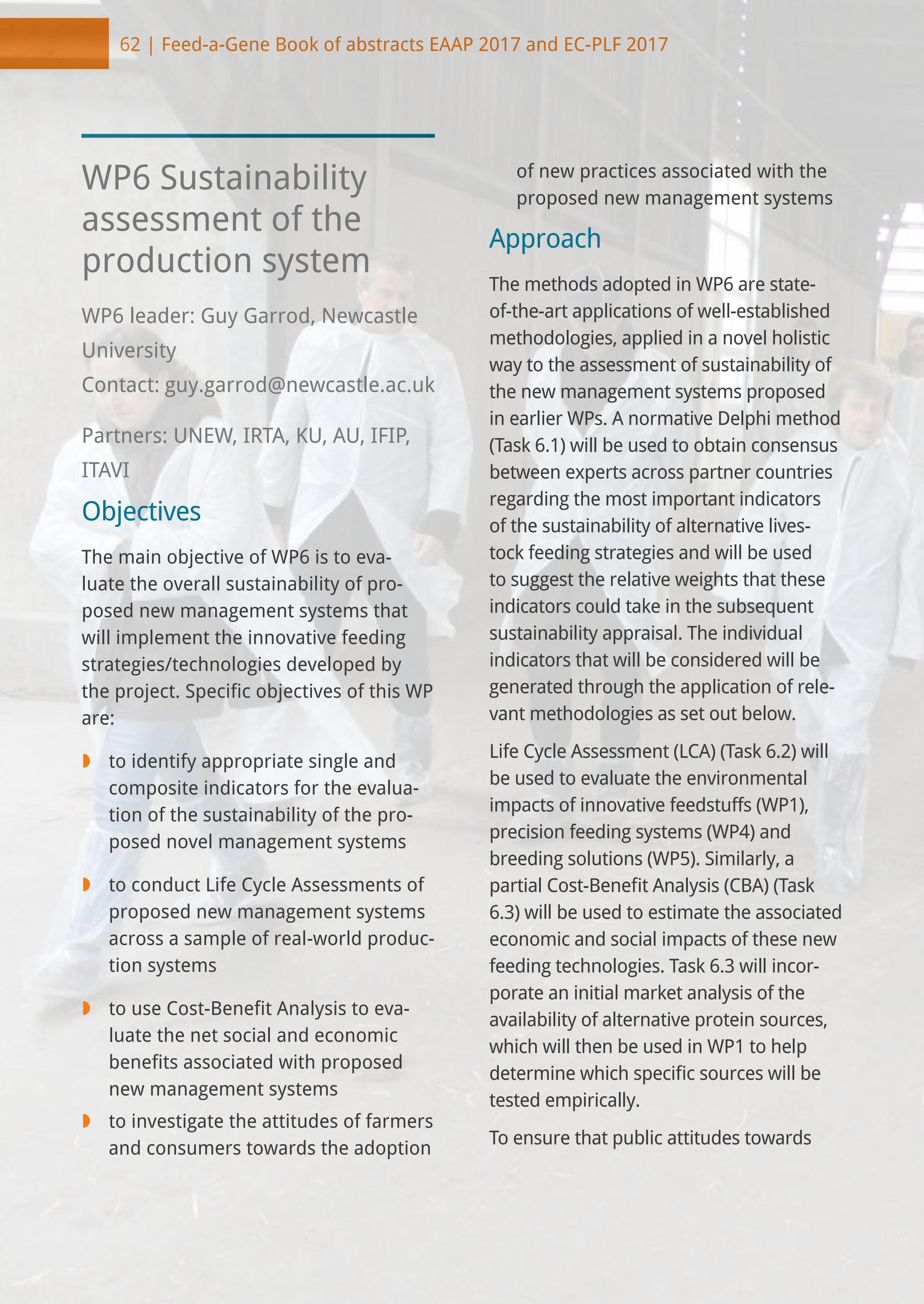
	DGE_ADG	DGE_ADC	DGE_BF	DGE_FCR
SGE_ADG		-0.13 (0.30)	-0.80 (0.13)*	0.84 (0.05)*
SGE_ADC	-0.41 (0.41)		-0.34 (0.25)	-0.23 (0.51)
SGE_BF	0.11 (0.47)	-0.54 (0.40)		-0.2 (0.25)
SGE_FCR	-0.43 (0.27)	-0.33 (0.32)	0.17 (0.37)	

DGE: direct genetic effect; SGE: social genetic effect; ADG: average daily gain; ADC: average daily consumption; FCR: feed conversion ratio; BF: backfat thickness; *: probability of being greater than 0 >0.95 or <0.05.

Credits: Nicolas Bertrand, INRA

William Herrera Cáceres

William Herrera Cáceres is a PhD student of Animal Production at Autonomous University of Barcelona. He is currently working on his doctoral thesis “Optimization of feed intake recording in genetic improvement programs for feed efficiency in swine” at IRTA. He holds a M.Sc. in Animal Breeding and Reproduction Biotechnology (Polytechnic University of Valencia, Spain, 2016). He has been working in animal breeding and feeding behaviour in swine during the last two years. Since 2015 he has been involved in the Feed-a-Gene project and his objectives are to explore direct and indirect selection mechanisms to propose strategies to improve feed efficiency in pigs, minimizing investments in devices to record individual consumption in animals raised in group.



WP6 Sustainability assessment of the production system

WP6 leader: Guy Garrod, Newcastle University
Contact: guy.garrod@newcastle.ac.uk

Partners: UNEW, IRTA, KU, AU, IFIP, ITAVI

Objectives

The main objective of WP6 is to evaluate the overall sustainability of proposed new management systems that will implement the innovative feeding strategies/technologies developed by the project. Specific objectives of this WP are:

- to identify appropriate single and composite indicators for the evaluation of the sustainability of the proposed novel management systems
- to conduct Life Cycle Assessments of proposed new management systems across a sample of real-world production systems
- to use Cost-Benefit Analysis to evaluate the net social and economic benefits associated with proposed new management systems
- to investigate the attitudes of farmers and consumers towards the adoption of new practices associated with the proposed new management systems

Approach

The methods adopted in WP6 are state-of-the-art applications of well-established methodologies, applied in a novel holistic way to the assessment of sustainability of the new management systems proposed in earlier WPs. A normative Delphi method (Task 6.1) will be used to obtain consensus between experts across partner countries regarding the most important indicators of the sustainability of alternative livestock feeding strategies and will be used to suggest the relative weights that these indicators could take in the subsequent sustainability appraisal. The individual indicators that will be considered will be generated through the application of relevant methodologies as set out below.

Life Cycle Assessment (LCA) (Task 6.2) will be used to evaluate the environmental impacts of innovative feedstuffs (WP1), precision feeding systems (WP4) and breeding solutions (WP5). Similarly, a partial Cost-Benefit Analysis (CBA) (Task 6.3) will be used to estimate the associated economic and social impacts of these new feeding technologies. Task 6.3 will incorporate an initial market analysis of the availability of alternative protein sources, which will then be used in WP1 to help determine which specific sources will be tested empirically.

To ensure that public attitudes towards

the positive and negative externalities of these approaches are properly considered, a choice experiment approach (Task 6.4) will be used to estimate consumer preferences for relevant management attributes. In addition, a qualitative analysis of farmers' attitudes (Task 6.4) will investigate any potential barriers to the uptake of new methods and technologies and will explore how these new approaches to animal nutrition and feeding can be made more acceptable.

In Task 6.5 a composite indicator of sustainability will be constructed using the individual indicators and weights suggested by analysis of the Delphi data in Task 6.1. This will be populated by data estimated in Tasks 6.2-6.4 relating to the environmental, economic, and social impacts of potential new management approaches. This composite indicator approach allows comparing a range of feeding and nutrition solutions in terms of their sustainability and relative economic, environmental and social performance. Sensitivity analysis will then be undertaken to investigate the robustness of the evaluations under changes in assumptions about the composition of the indicator.

Tasks

Task 6.1 Identification of sustainability indicators for proposed production systems

Task 6.2 Life Cycle Assessment of proposed management systems

Task 6.3 On-farm evaluation of proposed management systems

Task 6.4 Evaluation of consumer and farmer attitudes

Task 6.5 Sustainability appraisal

Guy Garrod

Guy Garrod is an environmental economist at School of Agriculture, Food and Rural Development of Newcastle University. His work focuses on valuing the environment in order to provide an effective rationale for not over-exploiting it, that is meaningful to practitioners in conservation, industry and policymakers. In framing problems for research, he includes the viewpoints of the people affected by them, using participatory modelling as a decision support tool for sustainable development. Since 2010 Guy Garrod has been Director of the Centre for Rural Economy (CRE), a Newcastle University research centre specialising in applied interdisciplinary social science, studying rural development and policy, food and society, and the wellbeing of rural communities.

Feed-a-Gene

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