FEED-A-GENE

Adapting feed, animals and feeding techniques for more efficient and sustainable monogastric livestock production systems

Deliverable D7.5

3rd annual newsletter and minutes of the two demonstration events and of the stakeholder meeting organised during the 3rd year of the project.

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Table of contents

1 Summary

This deliverable includes the 3rd Annual newsletter and the minutes of the two demonstration events and of the stakeholder meeting organised during the 3rd year of the project. The annual Feed-a-Gene newsletter aims at informing stakeholders and consortium partners about recent, on-going and planned events and activities, and about the progress made since the last meeting in April 2017. Progress reports were communicated by Work Package researchers during and after the second Feed-a-Gene annual meeting held in Newcastle in April 2018. The newsletter was disseminated by email to 370 stakeholders and is available as a PDF file on the website. The minutes of the events and meetings were recorded and edited by AFZ.

2 Newsletter

2.1 Introduction

The impact of the Feed-a-Gene project is heavily dependent on the ability of its partners to disseminate information to stakeholders during all the phases of the project. The dissemination plan includes the publication of 5 annual newsletters. The objective of this third newsletter is 1) to present recent, on-going and planned events activities related to Feed-a-Gene, 2) provide updates on the progress made in the project since the last annual meeting in April 2017, and 3) to make the project attractive to stakeholders, increase the target audience and maximise the impact of the project.

In addition to the "regular" newsletter that is published after each annual meeting and sent as a printable PDF, it was decided to publish shorter "intermediate" newsletters sent in email form only and containing links to recently published materials, such as videos and papers. Two intermediate newsletters have been sent: one in October 2017 and another one in January 2018.

2.2 Methodology

The newsletters were designed and edited by the AFZ team using texts and photographs created by AFZ and the consortium partners. Each Work Package leader contributed to the annual newsletter by writing a short progress report.

2.3 Results

2.3.1 Delivery format

The third Feed-a-Gene newsletter is provided in three formats.

- As a printable PDF brochure in A4 format. The document is 17-page long, in colour and it uses the visual identity guidelines defined in Deliverable 7.1.
- As an email sent to stakeholders and partners with links to individual articles.
- As a page on the Feed-a-Gene website that links to individual articles.

The PDF and the page are available at http://www.feed-a-gene.eu/newsletter/feed-a-gene-newsletter-3.

The PDF is presented in the following pages:

![Feed-a-Gene logo]

Newsletter #3

June 2018

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

Editorial

Dear readers,

We are proud to present the third newsletter of the Feed-a-Gene project funded through the Horizon 2020 programme of the European Commission. As our project is now two years from completion, it is entering a phase where it produces results on a regular basis, and this newsletter includes a large panel of the works presented during the 3rd annual meeting held on 24-26 April in Newcastle upon Tyne, United Kingdom.

Several demonstrations and workshops targeted at specific groups of stakeholders are being planned and will start in the second half of 2018. Two joint Feed-a-Gene/Saphir sessions are planned: the first one on 30 August at the EAAP meeting in Dubrovnik, Croatia, and the second one on 11 September at the SPACE agricultural show in Rennes, France. A stakeholder meeting dedicated to biological modelling will take place on 11 October in Budapest, Hungary.

We hope that this newsletter will give you a good idea of the progress made in the past three years.

Jaap van Milgen (INRA)
Feed-a-Gene project coordinator

The Feed-a-Gene Project has received funding from the European Union's H2020 Programme under grant agreement no 633531

Third Feed-a-Gene Annual meeting

Newcastle upon Tyne, UK

The University of Newcastle hosted the third annual meeting of the Feed-a-Gene programme. During this meeting, Feed-a-Gene partners presented the work done so far, shared their results and planned activities for the next year. All attendees appreciated the organization of the meeting by Prof. Ilias Kyriazakis and his team at University of Newcastle.

Feed-a-Gene project coordinator Jaap van Milgen and project manager Vincent Troillard would like to thank all the people at UNEW who made this meeting possible and enjoyable.

The third annual meeting of the Feed-a-Gene project took place on 24-26 April 2018 in Newcastle upon Tyne, United Kingdom. It was hosted by the Newcastle University, one of the project partners. The meeting was attended by 68 people.

A year of results

During the meeting, young researchers (PhD and post-doc) were put in the spotlight and presented 10 oral communications. Other researchers presented their results during a poster (14 posters) session. These presentations showed the progress done in all work packages since the last scientific event (EAAP meeting in Tallinn in August 2017) for which a book of abstracts had been published. It was stressed that results of dissemination and related communications had substantially increased since 76 documents have been submitted: peer-reviewed papers, communications, posters, book chapters, PhD dissertations and technical papers. 56 have already been published and among them 9 are peer-reviewed papers.

Prof. Ilias Kyriazakis presented PROHEALTH, a FP7 European animal health project funded to help combat production diseases of pigs and poultry. PROHEALTH aims to increase the understanding of animal pathologies linked to the intensification of production and it helps providing effective control strategies to reduce the impact on animal welfare, including health. The project is in its last year of implementation and many interesting results are already available (www.fp7-prohealth.eu).

Sharing data in the context of Open Science

Following the lectures held in the previous meetings about data management (*FAIR data management* by Richard Finkers/WUR in 2016; *Lightweight data management* by François Moreews/INRA in 2017), Feed-a-Gene coordinator Jaap van Milgen presented the results of a survey carried out this year among Feed-a-Gene researchers.

Out of 66 researchers who answered, 65% had made publications involving data, algorithm, software or prototypes, and 75% of those researchers were willing to make them available. The preferred mode of dissemination was a data repository (45%), followed by making the material available upon request (32%), and by providing the data as supplementary material (25%). No researcher was in favour of making the data available upon payment. The preferred type of repository was that of the researcher's organisation (43%). The preferred condition for making the material available in a public repository was that the authors be cited (42%).

From top to bottom, left to right:
- Meeting session at Newcastle University
- Ilias Kyriazakis (UNEW)
- Florence Gondret (INRA) during the poster session
- Jaap van Milgen (INRA) wearing his unique Feed-a-Gene tie
- Hélène Gilbert (INRA)
- Sandrine Espagnol (IFIP)
- At the Blackfriars restaurant in Newcastle: Candido Pomar (AAFC), Jaap van Milgen (INRA), Charlotte Gaillard (INRA), Ludovic Brossard (INRA), Joao Filipe (UNEW)

SAB recommendations: keep focusing on stakeholders expectations

The stakeholder advisory board (SAB) attended the 3rd annual meeting and reaffirmed its interest in the programme. Stakeholders highlighted the fact that the multi-actor, multi-approach used in Feed-a-Gene is a challenging experience but also a great opportunity for very positive outcomes such as the integration of breeding and feeding. While science and project management are well done and partners are fully involved in the project, care should be taken to fulfil stakeholders expectations, particularly those of farmers, industry and policy makers. Communication towards stakeholders should be in the form of practical abstracts, policy briefings, and press releases. For higher impact on these categories of stakeholders, Life Cycle Assessment results and answers provided in the consumers questionnaire should be highlighted in all communication materials.

SAB members: Erik Dam Jensen (FEFAC), Jan Venneman (Effab), Leo den Hartog (Trouw Nutrition)

Roadmap for demonstrations and workshops

Several demonstrations events and workshops are already planned.

August 2018	Joint stakeholder session Feed-a-Gene/SAPHIR, EAAP meeting, Dubrovnik, Croatia, 30 August
September 2018	Joint stakeholder workshop Feed-a-Gene/SAPHIR & demo of the precision feeding DSS (WP4), SPACE, Rennes, France, 11-14 September
	Feed-a-Gene conference, Feed Additives Global, Amsterdam, The Netherlands, 26-28 September
October 2018	Stakeholder meeting & hands-on demonstration of the biological modelling DSS (WP3), Budapest, Hungary, 11 October
November 2018	Joint Feed-a-Gene/SAPHIR event, EuroTier, Hanover, Germany, 13-16 November
Last quarter 2019	On-farm demos & workshops for the precision feeding DSS (WP4), Parma, Italy
Early 2020	Workshops on strategies for sustainable selection for feed efficiency (location to be defined)

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Stakeholder session
68th EAAP annual meeting, Tallinn, Estonia, 30 August 2017

A stakeholder session was organised during the EAAP meeting in Tallinn in August 2017. It was attended by about 120 people. The session included 16 oral presentations and 3 posters, a demonstration of the biological modelling DSS (WP3) by Masoomeh Taghipoor (INRA) and a discussion with the stakeholders.

Feed for thoughts from the session

If Warren Buffett wanted to invest in microbiota in order to influence animal performance in a positive way, should he put 10 million in feed company or 10 million in genetics or 50/50? Jaap van Milgen, INRA

Is the microbiome a result of an animal, its diet or environment, or does it have causal effect on animal? If it is causal, then the indicators of the microbiome are a good way to control the levers that are working. But, if it is just a consequence, why do we look at the microbiota at all? Jaap van Milgen, INRA

Experimental design is going to be very important to you. People are going to transplant microbiome from an animal to another which seems to be easy to do. If you can set up cross design don't worry. It seems that experimental designs are embryonic at the moment. Wait a couple of years for people to make mistakes that way and learn from that. We do not have enough data to figure out how to do it properly, we need more mistakes. Pieter Knap, Genus-PIC

The main part in these discussions is understanding what is going on and how to approach that. This may be experimental design, this may be increasing data sets, but the main thing about metabolomics is, yes, we can measure everything, but do we know what we are looking at? Lisanne Verschuren, Topigs Norsvin

Maybe we could have a look at human medicine where biomarkers were studied for diagnosis of different pathologies and, in fact, it has been successful only with very large sets of subjects to be analysed... We don't have to understand the mechanisms, we just have to find the biomarkers. We have to dissociate research of biomarkers and the understanding of the phenotypes. Florence Gondret, INRA

- Mario Calus (WUR)
- Galyna Dukhsa (KU)
- William Herrera (Univ. Barcelona)
- Stéphane Beauclercq (INRA)
- Masoomeh Taghipoor (INRA)

Progress reports for the Feed-a-Gene project

Alternative feed ingredients and real-time characterisation (WP1)

Production of novel feed protein from rapeseed and European-grown soybeans

- European-grown soybean meals (SBM) have been successfully processed by dehulling (or not), extrusion or flaking-cooking (FCP). They were analysed for chemical and antinutritional compounds and tested with piglets and broilers.
- The degree of hydrolysis was higher in the SBMs than in intact soybeans. The rate of hydrolysis was higher for the meal from extrusion processing. Dehulling lowered the fibre content and increased the maximum degree of hydrolysis in

meal from extrusion processing, but decreased the degree of hydrolysis in meal from flaking cooking. None of the processes caused lysine damage.

- In vitro laboratory tests were used to select proteases and NSPases for animal studies.
- A conventional European rapeseed meal (RSM) has been identified and upgraded at Hamlet Protein for studies with pigs.

Production of novel feed protein from green biomass

- 60% of the protein from green biomass extracted from grass and legumes was recovered in pulp and 40% in juice. Proteins in the juice were precipitated to produce a concentrate with 35-45% protein. There was no difference between acid and heat precipitation. Amino acid composition was similar to that of soybean. About 15% of the

protein of the plant remained in the residue.

- Two large-scale fractionation experiments in a pilot plant were performed in 2016 and 2017 and used for pig trials. Enzyme addition during protein extraction did not improve the protein yield but modified the carbohydrate fraction.

Novel feed-processing technology to upgrade alternative feed ingredients

- Large-scale RSM sifting and division into fine and coarse fractions have been carried out. The fine fraction had a higher protein content, while the amino acid composition did not vary between fractions.
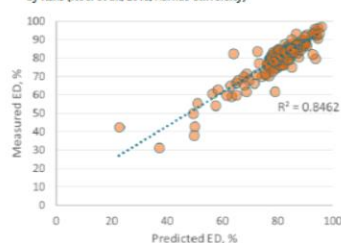- Samples of RSM from five different suppliers were divided in a lab-scale experiment into fine and coarse fractions. All fine fractions had lower crude fibre contents than the starting material.

Nutritional evaluation of novel feed ingredients

- The green protein concentrates were included at a level of 30% in experimental pig diets without negative impact on feed intake. There was no difference between the sources in standardized ileal digestible (SID) amino acid content, except for methionine and alanine. The SID of crude protein was 22-33%-units lower than that of SBM and SID of amino acids was on

average 15%-units lower (from -3 to 54).

- Pigs had significantly lower body weight and average daily gain, and higher feed conversion ratio when fed with the FCP dehulled SBM compared to control pigs. In line with performance data, amino acid digestibility was lower in the FCP dehulled SBM.
- In broilers, SBM processing did not affect any of the tested variables, and all 4 processes resulted in similar performance. Aside from increased carcass yield, hull removal did not confer a significant advantage, possibly due to the adaptive growth of the gizzard and proventriculus in the hulled treatments.

Improvements in nutritive value by use of novel enzymes

- Mechanical improvement of RSM increased its protein content, which improved feed efficiency due to a reduction of feed intake. No effect was observed on growth performance. No effect of enzyme

inclusion on dry matter, energy or nitrogen digestibility was detected.

New methodologies for characterisation of nutrient composition and value

- Predictive calibration models were obtained with NIR scans for 328 cereal samples. Models for chemical data (including amino acids) and biological data from pig trials have been evaluated. In general, NIR calibration models had good predictive ability and robustness, though they were not suitable to predict the mineral composition of cereals.
- The removal of anti-nutritional components from RSM and the isolation of a fine fraction both enhanced protein content, but did not substantially affect amino acid pattern. No substantial effects on lysine damage were observed, and lysine damage varied between 0 and 5% of total lysine.

Energy digestibility of cereal grains in pigs: measured vs predicted by NIRS (Noel et al., 2018, Aarhus University)

$R^2 = 0.8462$

Identification of feed efficiency traits related to individual diversity (WP2)

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

- The development of feeding stations to monitor feed intake and body weight of individual rabbits and broilers in group-housing systems was completed.
- Hardware and software were redesigned and modified to create devices, linked data collection software, and tools suitable to evaluate the effects of dietary and other interventions on individual feed intake in group-housed animals.

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

- New knowledge has been generated linking the composition of the intestinal and faecal microbiota to nutrient digestibility and systemic metabolic parameters in pigs, rabbits, and broilers.
- A new method using NIR technology to measure nutrient digestibility more easily in a large number of samples is being developed.

Nutrient metabolism related traits to improve feed efficiency

- Absolute N retention at later age is affected by birth weight of pigs. However, relative N efficiency is not affected by birth weight.

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▸ Analysis of the relationship between experimental treatments with metabolome profiles in blood is ongoing.
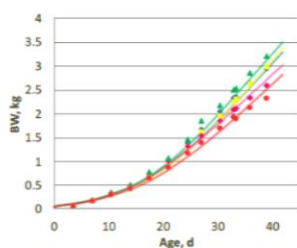
Behaviour and welfare related traits influencing feed efficiency

▸ A methodology capable of the automatic measurement of a variety of traits at a group level related to feed intake behaviour in pigs has been developed.

▸ A new method was developed to assess interactions between pigs, that uses electronic feed recording information for estimating the ranking of animals within a group as an indicator for behaviour in relation to feed efficiency.

Metabolomics to identify new traits for improvement of feed efficiency

▸ The blood metabolome of pigs and rabbits was shown to be affected by dietary treatment and genotype.

▸ In growing-finishing pigs, blood biomarkers measured at an early stage have been identified as indicators of feed efficiency.

Modelling feed use mechanisms and animal response to nutrient supply and environmental challenges (WP3)

Digestive utilisation of feed and nutrients

▸ A mechanistic-dynamic model of transit and digestion for pigs has been developed and improved. Its accuracy was confirmed by a comparison between observed and predicted digestibility values.

▸ This model was transposed to broilers. Inputs are the amount of nutrients ingested (proteins, free amino acids, lipids, starch, sugars, fibre, Ca, P). Equations represent the transit, hydrolysis, fermentation, and absorption of nutrients. Outputs are ileal and faecal nutrient digestibilities. Parameter quantification has been performed but the model needs to be validated.

Metabolic utilisation of feed and nutrients

▸ The initial version of the post-digestive pig model has been improved with a better amino acid and protein model, and by adding models predicting P utilization, P retention and feed intake.

▸ The pig model was transposed to broilers. The broiler model is able to simulate the partitioning of energy and protein and predict P retention and excretion.

▸ A module estimates the body fatty acid composition of pigs and lipid distribution in the different tissues.

Accounting for environmental variability, system disturbance and robustness

▸ Work has been done on the ability to detect perturbations automatically, using the deviation of cumulative feed intake from an ideal trajectory as a response criterion.

▸ In pigs, a mechanistic model was developed to describe the adaptative response to a generic perturbation.

▸ In broilers, Bayesian inference methods were used to estimate perturbations in the performance of birds undergoing intestinal parasitic infection. Results suggest evidence for compensatory growth.

Observed body weight (kg, dots) and predicted body weight (line) from five different datasets of Cobb broilers (Dukhta et al., 2018, Kaspovár University)

Accounting for variation among individuals in nutrient digestion and metabolism processes

▸ A Bayesian inference approach was used in pigs, broilers, and rabbits to obtain posterior distributions of parameters and traits reflecting within-individual variation and data uncertainty, and among-individual variation.
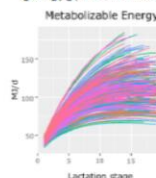
▸ The traits were growth rate, dynamic body composition, metabolic heat production, and energy and protein utilisation efficiency. Except for growth rate, individual traits were estimated through growth models and fitting serial trait observations.

▸ Trait estimates measure real-time individual performance ; population trait distributions inform performance of breeds or treatments; individual-trait scatter plots identify phenotypic clusters.

▸ Metabolic heat production estimates agreed with literature data. Age-varying protein efficiency of pigs was within literature bounds.

Management systems for precision feeding to increase resilience to fluctuating environments (WP4)

Decision Support System development for real-time determination of animal nutritional requirements

Delivery of a Decision Support Tool

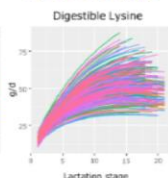▸ A first version of the decision support tool (DSS) was developed. Based on the InraPorc model for growing pigs, it includes a model for energy and protein metabolism, a module for P utilisation, and a spring and damper system used for characterizing the animal's response to perturbation.

▸ In addition to model development, software development includes creating an interactive interface, language localisation and linear multivariable optimization. An open source version of the core model as well as a standalone desktop version for end-users are being developed. The first version of the DSS was shown at the stakeholder meeting held during the 2017 EAAP Annual meeting.

▸ For growing pigs and broilers, a first version of the decision support system (DSS) was implemented using an architecture combining modules for analysing and predicting performance and for estimating the nutritional requirements of animals in real time.

▸ For gestating sows, an Excel procedure was created to implement the DSS.
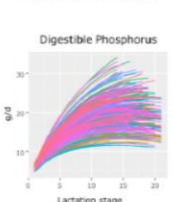
▸ Simulations indicated that compared to classical feeding, precision feeding can reduce protein and amino acid intake and N excretion by 25% in gestating sows and lysine and protein intake by 6.2% in lactating sows.

▸ For broilers, a model implementation is now able to predict daily requirements for metabolizable energy, digestible lysine, and available P.

Controlling module development to support feeder control tasks, real-time measurements

▸ The Controlling Module (CM) integrates all devices and software components involved in precision feeding systems. The CM acts as an intelligent multiple device and DSS integrator, with the capacity to control multitask processes such as monitoring, supervision, and data management.

▸ A language (ACL) was developed to establish the communication between the devices and the CM.

Requirements variability between sows, across the lactating period (Gauthier et al., 2018, INRA)

Precision feeder device development

▸ Enhanced precision feeder prototypes for growing pigs fed ad libitum or restrictively fed are now ready for validation.

▸ For group-housed gestating sows, a precision feeder device has been developed and is now installed in the experimental station of IFIP.
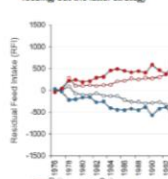
▸ An experimental accelerometer fixed to the sow's ear is available to measure energy expenditure due to physical activity.

▸ For poultry, a complete design of precision feeding system is available.

Building and validation of precision feeding system prototypes

▸ Individual precision feeding of ad libitum-fed growing pigs significantly improved feed conversion and lean meat content of the carcass when compared to two-phase feeding. The total lysine intake tended to be reduced, but to a lower extent than expected.

▸ In restricted feeding conditions, feed efficiency and growth rate were similar for pigs fed a two-phase strategy or with precision feeding, but the latter strategy resulted in a 5% reduction in lysine intake.

▸ The validation tests of ACL communication between feeder devices and CM showed that the communication worked satisfactorily, and that the system reacts in a robust way when working under non-optimal conditions.

Use of new traits in animal selection (WP5)

Genetics of components of feed efficiency and robustness indicators

▸ New traits on behaviour, welfare, and metabolomics indicators have been collected recently and no results are available yet.

▸ In pigs and layers, no deleterious relationships were shown between feed efficiency and responses to challenges, when comparing performance with divergent lines.

▸ In broilers, 116 genomic regions were associated with 16 traits related to digestive efficiency, growth, and faeces composition.

▸ Only preliminary results are available for reproductive females.

In sows, a genetic component of feed intake was found during lactation. In mice, there was a better robustness to stress conditions (restricted feed) for females selected for homogeneity of litter birth weights.

Genetic relationships between the gut microbiota and feed efficiency

▸ Selection on feed efficiency was successful for direct effects, but maternal effects were degraded by the selection (about 1/6 of the direct genetic gain).

▸ Feed, sex, line of feed efficiency, cross fostering, and feeding regimes had significant effects on gut microbiota composition in the different studies.

▸ Some microbiota phyla in rabbits were heritable.

▸ First association studies conducted on the average daily gain of rabbits fed restricted and ad libitum feeding showed four QTL regions on chromosomes 3, 5, and 21.

Statistical-genetic modelling of feed efficiency and robustness features

▸ Pen records of feeding levels can be used to improve genetic evaluation.

▸ Social genetic effects varied over time so it is important to account for them in selection.

▸ The structured antedependence model was validated and showed that the dynamics of feed efficiency over time is affected by selection.

▸ The joint estimations of genetic parameters for variability on multiple traits suggested the existence of a general robustness across traits.

Residual feed intake in 2 feed-efficiency diverging lines of laying hens (Jehl et al., 2018, INRA)

▸ The alternative implementation of a genetic model with indirect genetic effects including feeding behaviour improved model performance.

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

▸ Accuracy and bias of predictions were used as primary criteria to evaluate the tested strategies. They indicated that the separation of additive and dominance components seems to be beneficial for some traits to evaluate purebred candidates to selection for crossbred performance.

▸ Including metafounders did not affect the accuracy and bias of predictions, but improved convergence of the model when the breeds are very distantly related to each other.

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

▸ Currently, approximately 40 million pigs have a breeding value for indirect genetic effects, including Topigs Norsvin animals tested in the different trials of the Feed-a-Gene project.

▸ In rabbits, a selection experiment is being carried out to obtain lines based on two selection criteria: average daily gain under restricted feeding (enhances competition) and residual feed intake with ad libitum feeding. Feed intake data from the first generation have been recorded in five batches of 130-150 rabbits each.

Sustainability assessment of production systems (WP6)

Identification of sustainability indicators for proposed production systems
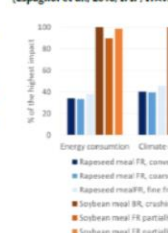
▸ Stakeholders provided 102 usable responses to the Delphi survey. The highest-ranked dimension of sustainability was the Economic dimension, followed by Environmental and Social.

▸ Indicators related to financial viability of farming activities were the highest, reflecting that farming will not continue in the future if farms cannot achieve profitability.

Life Cycle Assessment of proposed management systems

▸ The global feeding strategies to be evaluated through Life Cycle Assessment (LCA) have been set for pigs in conventional crossbred and South European Iberian pigs.

▸ A survey establishing the list of required data has been done among partners. Work on LCA for innovative production systems in poultry production has started.

On-farm evaluation of proposed management systems

▸ Variables required to handle Cost-Benefit Analysis have been set after literature analysis. Corresponding data are collected from farm specialised in pig and poultry production in Denmark, Germany, France, Poland and Spain over the 2010-2015 period.

Evaluation of consumer and farmer attitudes

▸ A literature review has been conducted on the use of choice experiments to explore public preferences and trade-offs for different livestock production attributes. This informed the design of a choice experiment questionnaire that will be used to estimate values for the most important externality attributes (e.g., environmental or animal welfare) associated with the management systems that are being examined.

Anticipated environmental impacts of new protein sources (Espagnol et al., 2018, IFIP, ITAVI)

Dissemination, training and technology transfer (WP7)

Communication

2 intermediary newsletters have been sent since the 2nd newsletter:

- Feed-a-Gene News October 2017
- Feed-a-Gene News January 2018

Two booklets of abstracts have been distributed:

- Book of abstracts 2016-2017
- Book of abstracts 2017 EAAP / EC-PLF

Happy New Year 2018

An animated Greeting card was sent to stakeholders in January 2018.

Stakeholder platform and events

- The stakeholder platform now contains 371 participants.
- A stakeholder session was organised during the EAAP meeting in Tallinn in August 2017.

Events

Many researchers participated in international and national events, particularly:

- EAAP 2017 (Estonia)
- EC-PLF 2017 (France)
- WCGALP 2018 (New-Zealand)

Feed-a-Gene Season 1 ▶ YouTube

Watch researchers talk about Feed-a-Gene and their research on the project's YouTube channel.

Better feeds, better animals

This video made for the general public is in the top 10 of the 300 videos created to showcase H2020 projects!

Join Feed-a-Gene on social media!

- **f** www.facebook/feedagene
- **t** twitter.com/FeedaGene
- **in** www.linkedin.com/company/feed-a-gene
- **YouTube** www.youtube.com/FeedageneEuProject
- **R** www.researchgate.net/project/Feed-a-Gene-3

Stakeholder meeting at the 68th EAAP meeting in Tallinn, August 2017

- Jaap van Milgen (INRA) discussing with the stakeholders
- Masoomeh Taghipoor (INRA)
- Nora Formoso-Rafferty (UCM)
- Veronika Halas (KU) and Valérie Heuzé (AFZ)

Peer-reviewed papers published in 2017-2018

The following 9 peer-reviewed papers are now available.

- Ragab M., Piles M., Quintanilla R., Sánchez J.P., 2018. Indirect genetic effect model using feeding behaviour traits to define the degree of interaction between mates: an implementation in pigs growth rate. Animal, 12 (7): 1-9 doi.org/10.1017/S1751731118001192

- Tallentire C.W., Mackenzie S.G., Kyriazakis, I., 2018. Can novel ingredients replace soybeans and reduce the environmental burdens of European livestock systems in the future? Journal of Cleaner Production, 187: 338-347 doi.org/10.1016/j.jclepro.2018.03.212

- Beauclercq S., Nadal-Desbarats L., Hennequet-Antier C., Gabriel I., Tesseraud S., Calenge F., Le Bihan-Duval E., Mignon-Grasteau S., 2018. Relationships between digestive efficiency and metabolomic profiles of serum and intestinal contents in chickens. Scientific Reports, 8: Article number: 6678 doi.org/10.1038/s41598-018-24978-9

- Verschuren L.M.G., Calus M.P.L., Jansman A.J.M., Bergsma R., Knol E.F., Gilbert H., Zemb O., 2018. Fecal microbial composition associated with variation in feed efficiency in pigs depends on diet and sex. Journal of Animal Science, 96 (4): 1405–1418 doi.org/10.1093/jas/sky060

- Sánchez J.P., Ragab M., Quintanilla R., Rothschild M.F., Piles M., 2017 Genetic parameters and expected responses to selection for components of feed efficiency in a Duroc pig line. Genetics Selection Evolution, 49:86 doi.org/10.1186/s12711-017-0362-x

- Huynh-Tran V.H., Gilbert H., David I., 2017. Genetic structured antedependence and random regression models applied to the longitudinal feed conversion ratio in growing Large White pigs. Journal of Animal Science, 95 (11) : 4752-4763 doi.org/10.2527/jas2017.1864

- Wientjes Y.C.J., Calus M.P.L., 2017. The purebred-crossbred correlation in pigs: a review of theory, estimates and implications. Journal of Animal Science, 95 (8): 3467-3478 doi.org/10.2527/jas.2017.1669

- Piles M., David I., Ramon J., Canario L., Rafel O., Pascual M., Ragab M., Sánchez J.P., 2017. Interaction of direct and social genetic effects with feeding regime in growing rabbits. Genetics Selection Evolution, 49:58 doi.org/10.1186/s12711-017-0333-2

- Tran-Huynh V.H., Gilbert H., David I., 2017. How to improve breeding value prediction for feed conversion ratio in the case of incomplete longitudinal body weights. Journal of Animal Science, 95 (1): 39-48 doi.org/10.2527/jas.2016.0980

Communications

Feed-a-Gene researchers have published about 50 communications and posters. For the whole list, see:

- www.feed-a-gene.eu/media/communications

Nine young researchers in the spotlight

The 3rd annual meeting of Feed-a-Gene included oral presentations from young talented researchers whose work received funding by the H2020 programme.

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

Antonio Diego Brandao Melo (IRTA)
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The effects of high protein rapeseed meal (RSM) combined with enzyme (NSPase or protease) supplementation in 144 growing pig diets have been assessed during 6 weeks. It was shown that high protein RSM had no effect on body weight gain but reduced feed intake and thus improved feed conversion ratio. Fat digestibility was improved by RSM inclusion but DM, N or energy digestibilities were not affected by the diets. Enzymes combined to RSM had no further effect on pig production performance.

Development of models to predict the nutritional value of feedstuffs and feed mixtures by NIR

Samantha Joan Noel (Aarhus University)
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NIR spectral scanning is a cheap and non-destructive way to predict feedstuffs composition provided it can be consistently calibrated with traditionally measured (chemical analysis) reference data. Over 1000 samples of individual feedstuffs and mixed diets were scanned and used to develop calibration models for 11 chemical, 18 amino acid, 10 mineral and 16 biological constituents. NIR predictions were tested with a reference group of samples that were not used to make the calibration models. Most of chemical and amino acid constituent models performed well while the mineral models performed poorly. Though the predictions for the biological constituents were slightly less accurate, they compared very well with the accuracy of the original *in vivo* data.

Relationship between microbiota composition and nutrient digestibility, effect of dietary fibers

Mathilde Le Sciellour (INRA UMR PEGASE)
mathilde.lesciellour@inra.fr

In growing pigs fed on low or high fibre diets during 4 x 3-week-periods, digestibility measurements and faecal collections were done for RNA sequencing and subsequent microbiota characterization. It was possible to discriminate the 2 diets via 31 OTU's. In pigs fed low fibre diets, *Clostridiaceae* and *Turicibacter* were negatively correlated to digestibility coefficients while *Lactobacillus* were positively correlated with protein digestibility and energy digestibility. In pigs fed high fibre diets, no correlation was found and it was not possible to quantitatively predict digestibility with microbiota information.

Short- and long-term effects of DON challenge on the performance and feeding behaviour of finishing pigs

Aira Maye Serviento (INRA)
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One of the most common mycotoxins in swine diets is deoxynivalenol (DON). It is thus important to evaluate the effects of DON challenge as a function of age on growth performance and feed efficiency in finishing pigs. DON challenge reduced feed intake by 25-30%, BW by 40-60% and feed efficiency by 20-34% in a study conducted on 160 pigs. The severity of DON effects depends on the age of the pigs and of the number of challenges occurring: though pigs can recover to some extent, in all cases DON is deleterious to the final weight.

Plasma metabolites related to nitrogen efficiency in grower-finisher pigs

Lisanne Verschuren (Topigs Norsvin)
Lisanne.verschuren@topigsnorsvin.com

Untargeted metabolomics were used to study the effect of birth weight (low or high BtHW) on N metabolism of pigs receiving adequate (100% needs) protein or restricted (70% needs) protein diets at growing-finishing stage. Plasma metabolites differed according to BtHW of pigs but also according to the diet. The metabolites indicating the effects of protein restriction were different between pigs of different BtHW and could be the result of differences in N metabolism in pigs of different BtHW.

On the use of voluntary feed intake for automatic detection and characterization of the response of growing pigs to perturbations

Hieu Nguyen Ba (INRA UMR PEGASE)
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Hypothesizing there is an ideal trajectory of cumulative feed intake in growing pigs, data of feed intake were analysed and compared to the ideal trajectory. It was then possible to develop a generic model of feed intake based on differential equation where deviations from the ideal trajectory of cumulative feed intake reveal periods of perturbation characterized by duration and magnitude. The equation could be characterized by 2 parameters: a first one describes the reduction in daily feed intake and corresponds to resistance to a perturbation (i.e. a "resistance" trait) and the second one describes the capacity of animal to adapt and recover ideal trajectory (i. e. a "resilience" trait). In this model, cumulative feed intake is a valuable proxy for complex and difficult to measure robustness trait (i.e. resistance + resilience traits)

Application of a pig model to predict broiler performance

Galyna Dukhta (Kaposvar University)
galyna.dukhta@ke.hu

Starting from InraPorc model of growth, it was proposed to adapt it to a poultry growth model including 3 submodules:

- a metabolic module which simulates energy and protein partitioning in broilers and individual daily growth performance under ideal conditions,

- a P and Ca module that predicts digestible P and Ca utilization and thus P load of broiler production,

- and a feed intake module that takes environmental conditions into account and modifies actual energy intake as a response to undesired heat losses.

Precision feeding development for lactating sows: nutritional requirements modelling

Raphaël Gauthier (INRA)
raphael.gauthier@inra.fr

The InraPorc lactating model was used to develop a decision support tool for the precision feeding of lactating sows which are often under-optimally fed. Data on sows and their environment were used to determine the optimal supply for each animal. In sows fed in excess, it was possible to reduce average digestible lysine excess by 75%, and, in deficient sows, it was possible to reduce deficiency by 63%. Precision feeding also reduced lysine and P intake.

Genetics component of feed efficiency in layers using DNA-seq and RNA-seq: preliminary results

Frédéric Jehl (INRA)
frederic.jehl@inra.fr

DNA and multi-tissue (fat, blood, hypothalamus and liver) RNA sequencing were used to characterize lines of laying hens diverging for feed efficiency. DNA sequencing found 143,965 bi-allelic SNPs (single nucleotide polymorphism) for which one allele is homozygous in one line and heterozygous in the other line. 4 SNPs were predicted to lead to a premature stop codon and could have a role in the difference of feed efficiency. 98% of the SNPs were out of the coding region. RNA sequencing revealed that, depending on the tissue, 2996 to 6826 genes were differently expressed in the 2 lines. Pathways associated with the coding genes remain to be studied.

Upcoming events

Feed-a-Gene researchers will present communications in the following congresses in 2018.

DPP Digestive Physiology of Pigs

21-24 August 2018, Brisbane, Australia

EAAP 2018

27-31 August 2018, Dubrovnik, Croatia

- **Thursday 30 August: full-day stakeholder session Feed-a-Gene / SAPHIR**

SPACE 2018

11-14 September 2018, Rennes, France

- Joint Feed-a-Gene / SAPHIR conference on 11 September

- Live demonstration of the Decision Support System for precision feeding (INRA booth)

EPC European Poultry Global

17-21 September 2018, Dubrovnik, Croatia

Feed Additives Global

26-28 September 2018, Amsterdam, Netherlands

EuroTier 2018

13-16 November 2018, Hanover, Germany

The unique Feed-a-Gene tie!

www.feed-a-gene.eu

The intermediate newsletters were disseminated in email form.

Intermediate newsletter – October 2017

Feed-a-Gene News - October 2017
Mon, 2017-10-02 15:02

Book of abstracts 2017 EAAP / EC-PLF

This booklet contains 22 abstracts of oral communications and posters presented at the Feed-a-Gene session of the 68th annual meeting of the EAAP in Tallinn, Estonia (30 August 2017) and at the 8th EC-PLF European Conference on Precision Livestock Farming, Nantes, France (12-14 September 2017). These abstracts are enriched with additional tables and figures.

- Click here to download the booklet

Feed-a-Gene Season 1: the series

During the Feed-a-Gene session held during the EAAP meeting in Tallinn, we filmed a series of 10 interviews of researchers associated with the project. In Episode 1, coordinator Jaap van Milgen discusses the rationale, goals and expected impacts of the project.

- Click here to view the Feed-a-Gene Episode 1 on YouTube

In episodes 2-9 (to be released in the following weeks), work package leaders and researchers will present ongoing scientific activities and the results obtained so far. In the season finale, Jaap van Milgen will talk about the importance of stakeholders and about their feedback and input on the project.

Two new Feed-a-Gene peer-reviewed articles

Feed-a-Gene researchers have published 2 peer-reviewed articles in the *Journal of Animal Science* that deal with genetic parameter estimations and contribute to the progress of WP5 Use of traits in animal selection. These articles are in Open Access and can be downloaded by clicking on their title below:

- January 2017: How to improve breeding value prediction for feed conversion ratio in the case of incomplete longitudinal body weights by Tran-Huynh V. H., Gilbert H. and David I. (INRA)
- August 2017: The purebred-crossbred correlation in pigs: a review of theory, estimates and implications by Wientjes Y. and Calus M. (Wageningen University and Research)

Intermediate newsletter – January 2018

Feed-a-Gene News - January 2018
Tue, 2018-01-23 10:30

Editorial by project coordinator Jaap van Milgen

Dear readers,

First, I would like to wish you all the best for 2018 in your professional and personal life. Try to stay healthy and happy; the New Year should bring us plenty of challenging opportunities.

After the first two annual newsletters, sent out in 2016 and 2017, I am pleased to introduce this second Feed-a-Gene intermediate news bulletin. Because the number of project results will increase during the last two years of the project, we plan to publish newsletters more frequently so that you can become more aware of these project results and use them in your day-to-day business.

Please have a look at the videos published on the Feed-a-Gene YouTube channel. You will find several videos of researchers talking about their role in the project, and more videos will be published in the next weeks. We also created a funny video, "Better feeds, better animals" in which we explain the objectives and activities of the Feed-a-Gene project to a broad audience. This video is part of a competition set out by the European Commission to increase public awareness of H2020 projects. We participate in this competition where the winner is determined by the number of "likes". If you like it (and I am sure you do), please click on the "thumbs up" button on YouTube.

2017 last achievements: peer-reviewed papers and communications

A lot has happened in the last quarter of 2017. Two peer-reviewed papers were accepted and published:

- October 2017: Genetic structured antedependence and random regression models applied to the longitudinal feed conversion ratio in growing Large White pigs by Huynh-Tran et al., 2017, in the Journal of Animal Science
- December 2017: Genetic parameters and expected responses to selection for components of feed efficiency in a Duroc pig line by Sanchez et al., 2017, in Genetics Selection Evolution
Both articles are downloadable and present some of the results of the fruitful WP5 Use of traits in animal selection.

4 communications were presented between September and November 2017:

- Emma Fabrega (IRTA): New physiological indicators for welfare assessement: Cromogranin A (11th IVBM International Veterinary Behaviour Meeting, 14-16 September 2017, Samorin, Slovakia)
- Nathalie Quiniou (INRA): Assessment of the dynamic growth of the fattening pigs from body weight measured daily and automatically to elaborate precision feeding strategies (8th EC-PLF European Conference on Precision Livestock Farming 2017, 12-14 September, Nantes, France)

- Ludovic Brossard (INRA): Selection of methods to analyze body weight and feed intake data used as inputs for nutritional models and precision feeding in pigs (EC-PLF)
- Galina Dukhta (Kaposvár University): A growth model to predict body weight and body composition of broilers (A jövo tudósai, a vidék jövoje - Future scientists, Future countryside, Doctoral Conference, 24 November 2017, Debrecen University, Debrecen, Hungary)

In addition, project coordinator Jaap van Milgen presented Feed-a-Gene at the "Climate and Environmental Sustainability" session held at the FOOD2030 conference of the European Commission, on 16 October 2017. During this presentation he discussed feed efficiency and the role of livestock in sustainable food production. The video of the presentation is available here.

Next in 2018!

2 scientific papers have been submitted for peer review.

Feed-a-Gene researchers have already planned 7 presentations for the next 2 months:

- Hervé Garreau, Hélène Gilbert, Loys Bodin (INRA), Mostafa Helal and Juan Pablo Sanchez (IRTA) will present no less than 5 communications at the next WCGALP (World Congress on Genetics Applied to Livestock Production), 11-16 February, Auckland, New Zeland
- Lisanne Verschuren (Topigs) will present 2 communications at the following meetings:
  - WIAS Science Day 2018, Work on your Impact in Animal Sciences and Society, 5 Feburary 2018, Wageningen, The Netherlands
  - AASV (American Association of Swine Veterinarians) annual meeting, 2-6 March 2018, San Diego, California, USA

All materials will be published on the website when they become available.

2.3.2 Contents

The third Feed-a-Gene newsletter contains the following:

- Editorial by Project coordinator Jaap van Milgen (INRA)
- A short report about the 3rd Feed-a-Gene annual meeting in April 2018 in Newcastle
- A tentative roadmap for demonstrations and workshops
- A short note about the stakeholder meeting in Tallinn with notable citations
- Progress reports for the Feed-a-Gene project
- A list of 9 peer-reviewed papers
- Summaries of 9 presentations made by young scientists during the annual meeting
- Upcoming events

The intermediate newsletter of October 2017 contained links to the Book of abstracts disseminated during the Stakeholder meeting, a link to a video of Jaap van Milgen presenting Feed-a-Gene, and links to 2 new peer-reviewed papers.

The intermediate newsletter of January 2018 contained an editorial by Jaap van Milgen, links to videos produced by Feed-a-Gene, links to communications and peer-reviewed papers, and announcements for 2018.

2.3.3 Dissemination

An email informing of the publication of the 3rd annual newsletter was sent to 370 registered stakeholders on 26 June 2018.

The intermediate newsletters were sent to 355 registered stakeholders respectively on 2 October 2017 and January 2018.

The newsletters are available to all visitors on the website (https://www.feed-a-gene.eu/media/newsletter). Information about the newsletters was disseminated on social media (Facebook, Twitter, LinkedIn).

3 Demonstrations events

Two demonstration events were organized in 2017.

3.1 Demonstration of the precision feeding Decision Support System (DSS)

A short demonstration of the precision feeding DSS designed in the WP4 was carried out on 27 April 2017 at the University of Lleida, Spain. It was included in the 2nd annual meeting of Feed-a-Gene. Jesus Haro (from Feed-a-Gene partner Exafan, a Spanish equipment manufacturer), explained the functioning of the feeders, controlling modules, sensors and software. The audience was about 20 people, who were all Feed-a-Gene partners.

The demonstration was filmed and the video uploaded on YouTube on 11 May 2017. It has since been viewed by 331 people. The minutes were recorded and edited by the AFZ team with help of project manager Vincent Troillard.

The minutes of this demonstration are joined in Annex.

3.2 Demonstration of the biological modelling Decision Support System (DSS)

A demonstration of the biological modelling DSS designed in the WP3 took place during the Feed-a-Gene stakeholder meeting held on 30 August 2017 at the 68th EAAP Meeting in Tallinn, Estonia. Masoomeh Taghipoor (INRA) carried out a live demonstration of the software in front of an audience of 120 Feed-a-Gene stakeholders. Masoomeh Taghipoor and WP3 leader Veronika Halas (KU) answered questions from stakeholders and Feed-a-Gene partners about the modelling approaches and the potential users of the model and software.

The minutes were recorded and edited by the AFZ team with help of project coordinator Jaap van Milgen, and work package leader Veronika Halas.

The minutes of this demonstration are joined in Annex.

4 Stakeholder meeting

The 2017 stakeholder meeting was held on 30 August 2017 at the 68th EAAP Meeting in Tallinn, Estonia. The meeting featured 16 oral presentations and 3 posters by Feed-a-Gene researchers, a demonstration of the biological modelling DSS and a general discussion between the Feed-a-Gene partners and stakeholders. A printed booklet containing "enriched" abstracts (abstracts with graphs and tables) of the presentations and posters was distributed to audience members.

The discussion touched many topics, with a focus on the role of the microbiome, its relations with feeds and genetics, the optimal design experiments for studying these effects, and on biomarkers.

A short description of the stakeholder meeting featuring several remarks from Feed-a-Gene partners and stakeholders is included in the 3rd Newsletter.

The minutes were recorded and edited by the AFZ team with help of coordinator Jaap van Milgen and work package leaders Veronika Halas and Hélène Gilbert. The minutes of the stakeholder meeting are joined in Annex.

5 Conclusions

The third newsletter is a dissemination tool meant to inform stakeholders and consortium partners of the current state of the project and of the progress made so far. As the project is now producing results, the newsletter is longer than the previous ones and dedicates 11 pages (out of 17) to progress reports and results.

The demonstrations showed the first practical results of the work done in the WP3 (software) and the WP4 (software and hardware). Likewise, the stakeholder meeting was particularly important due to the significant number or presentations shown that day to a large audience.

6 Partners involved in the work

AFZ, Aarhus University, Exafan, INRA, IRTA, Kaposvár University, Newcastle University, Topigs Norsvin, Universitat de Lleida, and Wageningen UR contributed this deliverable.

7 Annexes

- Third Feed-a-Gene newsletter in PDF format.
- Intermediate newsletters in PDF format
- Minutes of the stakeholder meeting and of the two demonstrations

![Feed-a-Gene]

Newsletter #3
June 2018

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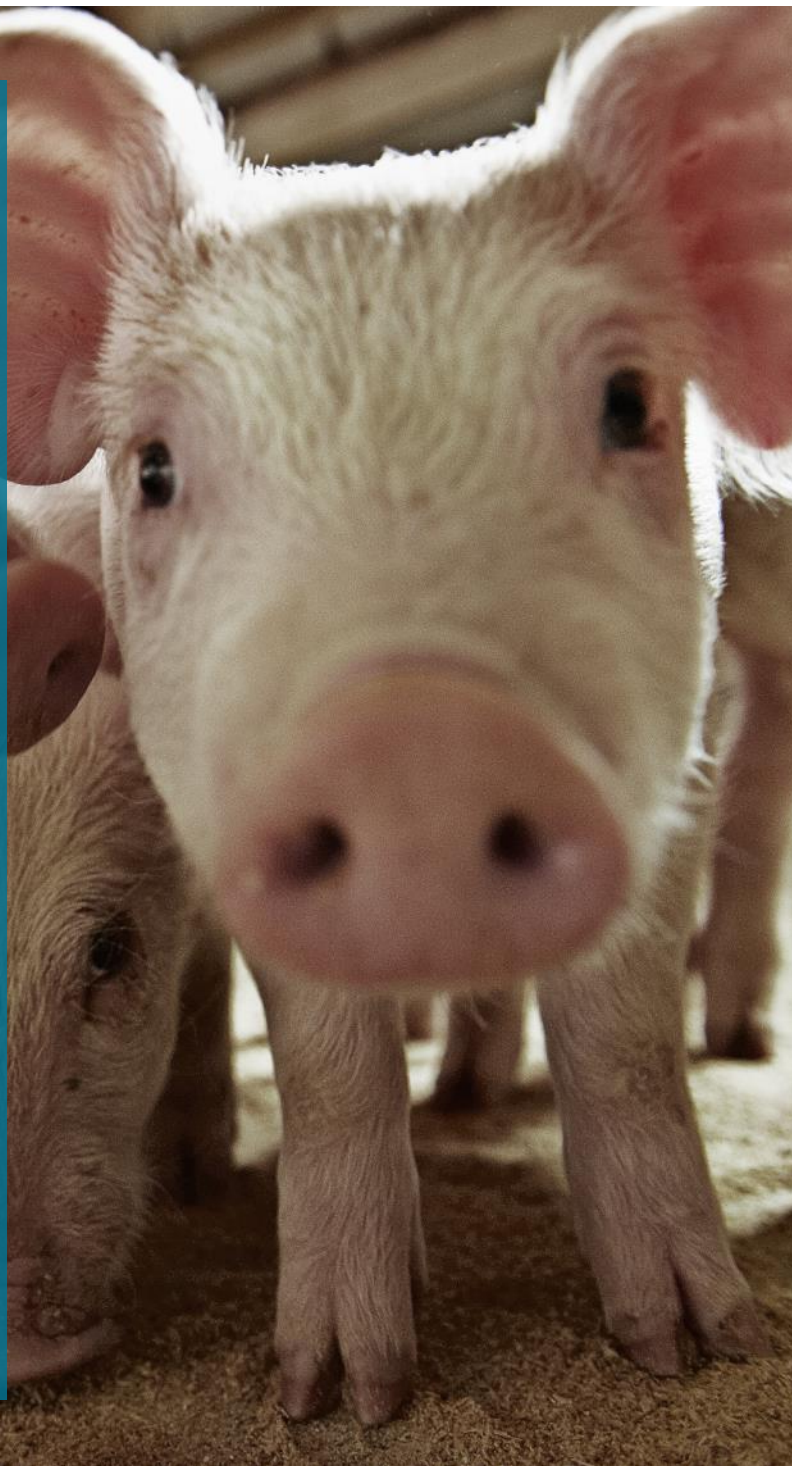
Editorial

Dear readers,

We are proud to present the third newsletter of the Feed-a-Gene project funded through the Horizon 2020 programme of the European Commission. As our project is now three years on its way, it is entering a phase where it produces results on a regular basis, and this newsletter includes a large panel of the works presented during the 3rd annual meeting held on 24-26 April in Newcastle upon Tyne, United Kingdom.

Several demonstrations and workshops targeted at specific groups of stakeholders are being planned and will start in the second half of 2018. Two joint Feed-a-Gene/Saphir sessions are planned: the first one on 30 August at the EAAP meeting in Dubrovnik, Croatia, and the second one on 11 September at the SPACE agricultural show in Rennes, France. A stakeholder meeting dedicated to biological modelling will take place on 11 October in Budapest, Hungary.

We hope that this newsletter will give you a good idea of the progress made in the past three years.

Jaap van Milgen (INRA)
Feed-a-Gene project coordinator

Third Feed-a-Gene Annual meeting

Newcastle upon Tyne, UK

The third annual meeting of the Feed-a-Gene project took place on 24-26 April 2018 in Newcastle upon Tyne, United Kingdom. It was hosted by the Newcastle University, one of the project partners. The meeting was attended by 68 people.

The University of Newcastle hosted the third annual meeting of the Feed-a-Gene programme. During this meeting, Feed-a-Gene partners presented the work done so far, shared their results and planned activities for the next year. All attendees appreciated the organization of the meeting by Prof. Ilias Kyriazakis and his team at University of Newcastle.

Feed-a-Gene project coordinator Jaap van Milgen and project manager Vincent Troillard would like to thank all the people at UNEW who made this meeting possible and enjoyable.

A year of results

During the meeting, young researchers (PhD and post-doc) were put in the spotlight and presented 10 oral communications. Other researchers presented their results during a poster (14 posters) session. These presentations showed the progress done in all work packages since the last scientific event (EAAP meeting in Tallinn in August 2017) for which a book of abstracts had been published. It was stressed that results of dissemination and related communications had substantially increased since 76 documents have been submitted: peer-reviewed papers, communications, posters,

book chapters, PhD dissertations and technical papers. 56 have already been published and among them 9 are peer-reviewed papers.

Prof. Ilias Kyriazakis presented PROHEALTH, a FP7 European animal health project funded to help combat production diseases of pigs and poultry. PROHEALTH aims to increase the understanding of animal pathologies linked to the intensification of production and it helps providing effective control strategies to reduce the impact on animal welfare, including health. The project is in its last year of implementation and many interesting results are already available (www.fp7-prohealth.eu).

Sharing data in the context of Open Science

Following the lectures held in the previous meetings about data management (*FAIR data management* by Richard Finkers/WUR in 2016; *Lightweight data management* by François Moreews/INRA in 2017), Feed-a-Gene coordinator Jaap van Milgen presented the results of a survey carried out this year among Feed-a-Gene researchers.

Out of 66 researchers who answered, 65% had made publications involving data, algorithm, software or prototypes, and 75% of those researchers were willing to make them available. The preferred mode of dissemination was a data repository (45%), followed by making the material available upon request (32%), and by providing the data as supplementary material (25%). No researcher was in favour of making the data available upon payment. The preferred type of repository was that of the researcher's organisation (43%). The preferred condition for making the material available in a public repository was that the authors be cited (42%).

From top to bottom, left to right:

▸ Meeting session at Newcastle University

▸ Ilias Kyriazakis (UNEW)

▸ Florence Gondret (INRA) during the poster session

▸ Jaap van Milgen (INRA) wearing his unique Feed-a-Gene tie

▸ Hélène Gilbert (INRA)

▸ Sandrine Espagnol (IFIP)

▸ At the Blackfriars restaurant in Newcastle: Candido Pomar (AAFC), Jaap van Milgen (INRA), Charlotte Gaillard (INRA), Ludovic Brossard (INRA), Joao Filipe (UNEW)

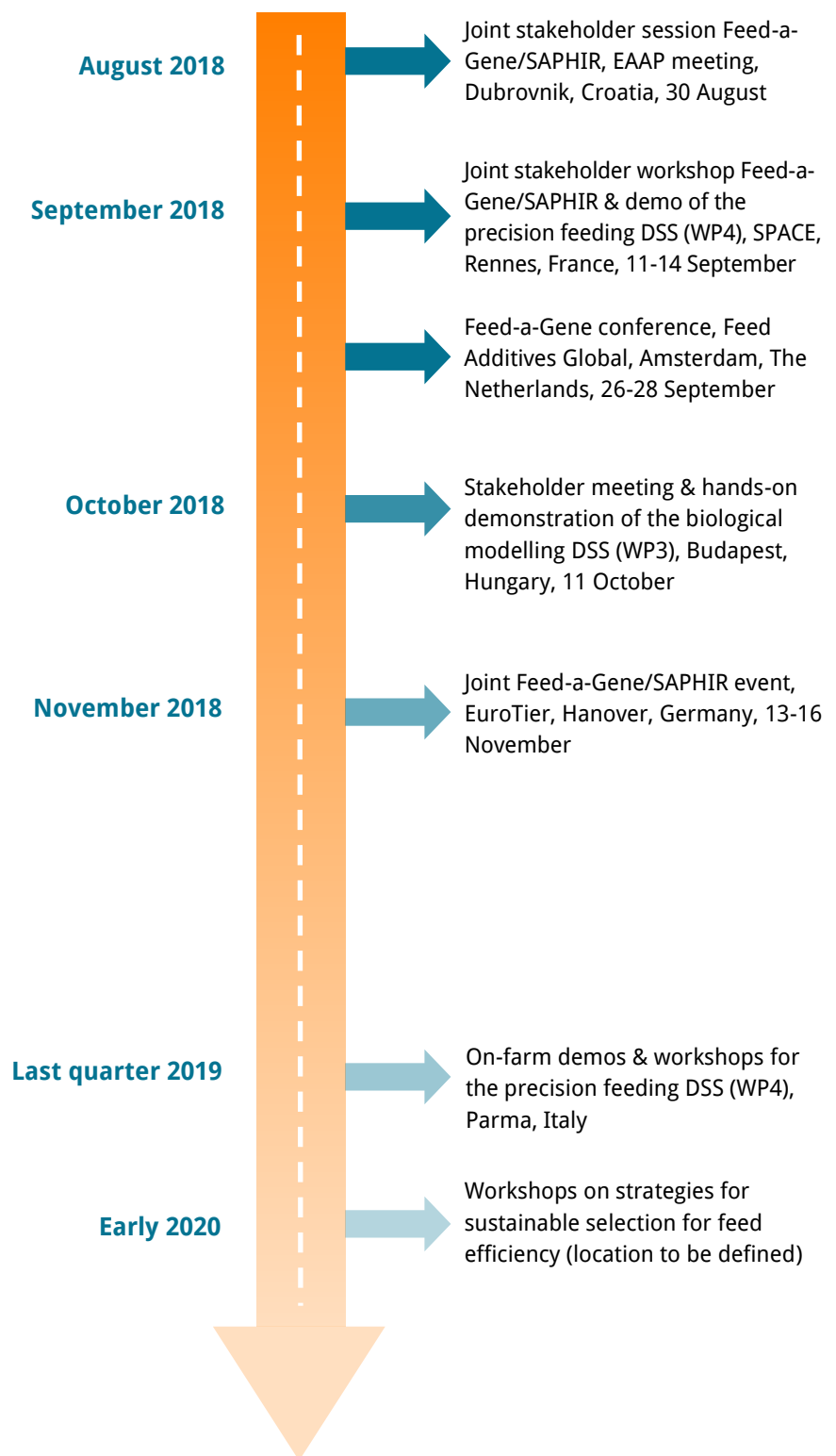## SAB recommendations: keep focusing on stakeholders expectations

The stakeholder advisory board (SAB) attended the 3rd annual meeting and reaffirmed its interest in the programme. Stakeholders highlighted the fact that the multi-actor, multi-approach used in Feed-a-Gene is a challenging experience but also a great opportunity for very positive outcomes such as the integration of breeding and feeding. While science and project management are well done and partners are fully involved in the project, care should be taken to fulfil stakeholders expectations, particularly those of farmers, industry and policy makers. Communication towards stakeholders should be in the form of practical abstracts, policy briefings, and press releases. For higher impact on these categories of stakeholders, Life Cycle Assessment results and answers provided in the consumers questionnaire should be highlighted in all communication materials.

SAB members: Erik Dam Jensen (FEFAC), Jan Venneman (Effab), Leo den Hartog (Trouw Nutrition)

Roadmap for demonstrations and workshops

Several demonstrations events and workshops are already planned.

August 2018 — Joint stakeholder session Feed-a-Gene/SAPHIR, EAAP meeting, Dubrovnik, Croatia, 30 August

September 2018 — Joint stakeholder workshop Feed-a-Gene/SAPHIR & demo of the precision feeding DSS (WP4), SPACE, Rennes, France, 11-14 September

Feed-a-Gene conference, Feed Additives Global, Amsterdam, The Netherlands, 26-28 September

October 2018 — Stakeholder meeting & hands-on demonstration of the biological modelling DSS (WP3), Budapest, Hungary, 11 October

November 2018 — Joint Feed-a-Gene/SAPHIR event, EuroTier, Hanover, Germany, 13-16 November

Last quarter 2019 — On-farm demos & workshops for the precision feeding DSS (WP4), Parma, Italy

Early 2020 — Workshops on strategies for sustainable selection for feed efficiency (location to be defined)

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Stakeholder session
68th EAAP annual meeting, Tallinn, Estonia, 30 August 2017

A stakeholder session was organised during the EAAP meeting in Tallinn in August 2017. It was attended by about 120 people. The session included 16 oral presentations and 3 posters, a demonstration of the biological modelling DSS (WP3) by Masoomeh Taghipoor (INRA) and a discussion with the stakeholders.

Feed for thoughts from the session

If Warren Buffett wanted to invest in microbiota in order to influence animal performance in a positive way, should he put 10 million in feed company or 10 million in genetics or 50/50? Jaap van Milgen, INRA

Is the microbiome a result of an animal, its diet or environment, or does it have causal effect on animal? If it is causal, then the indicators of the microbiome are a good way to control the levers that are working. But, if it is just a consequence, why do we look at the microbiota at all? Jaap van Milgen, INRA

Experimental design is going to be very important to you. People are going to transplant microbiome from an animal to another which seems to be easy to do. If you can set up cross design don't worry. It seems that experimental designs are embryonic at the moment. Wait a couple of years for people to make mistakes that way and learn from that. We do not have enough data to figure out how to do it properly, we need more mistakes. Pieter Knap, Genus-PIC

The main part in these discussions is understanding what is going on and how to approach that. This may be experimental design, this may be increasing data sets, but the main thing about metabolomics is, yes, we can measure everything, but do we know what we are looking at? Lisanne Verschuren, Topigs Norsvin

Maybe we could have a look at human medicine where biomarkers were studied for diagnosis of different pathologies and, in fact, it has been successful only with very large sets of subjects to be analysed... We don't have to understand the mechanisms, we just have to find the biomarkers. We have to dissociate research of biomarkers and the understanding of the phenotypes. Florence Gondret, INRA

▶ Mario Calus (WUR)

▶ Galyna Dukhta (KU)

▶ William Herrera (Univ. Barcelona)

▶ Stéphane Beauclercq (INRA)

▶ Masoomeh Taghipoor (INRA)

Progress reports
for the Feed-a-Gene project

Alternative feed ingredients and real-time characterisation (WP1)

WP leader: Knud Erik Bach Knudsen, knuderik.bachknudsen@anis.au.dk

Production of novel feed protein from rapeseed and European-grown soybeans

◗ European-grown soybean meals (SBM) have been successfully processed by dehulling (or not), extrusion or flaking+cooking (FCP). They were analysed for chemical and antinutritional compounds and tested with piglets and broilers.

◗ The degree of hydrolysis was higher in the SBMs than in intact soybeans. The rate of hydrolysis was higher for the meal from extrusion processing. Dehulling lowered the fibre content and increased the maximum degree of hydrolysis in meal from extrusion processing, but decreased the degree of hydrolysis in meal from flaking cooking. None of the processes caused lysine damage.

◗ *In vitro* laboratory tests were used to select proteases and NSPases for animal studies.

◗ A conventional European rapeseed meal (RSM) has been identified and upgraded at Hamlet Protein for studies with pigs.

Production of novel feed protein from green biomass

◗ 60% of the protein from green biomass extracted from grass and legumes was recovered in pulp and 40% in juice. Proteins in the juice were precipitated to produce a concentrate with 35-45% protein. There was no difference between acid and heat precipitation. Amino acid composition was similar to that of soybean. About 15% of the protein of the plant remained in the residue.

◗ Two large-scale fractionation experiments in a pilot plant were performed in 2016 and 2017 and used for pig trials. Enzyme addition during protein extraction did not improve the protein yield but modified the carbohydrate fraction.

Novel feed-processing technology to upgrade alternative feed ingredients

◗ Large-scale RSM sifting and division into fine and coarse fractions have been carried out. The fine fraction had a higher protein content, while the amino acid composition did not vary between fractions.

◗ Samples of RSM from five different suppliers were divided in a lab-scale experiment into fine and coarse fractions. All fine fractions had lower crude fibre contents than the starting material.

Nutritional evaluation of novel feed ingredients

◗ The green protein concentrates were included at a level of 30% in experimental pig diets without negative impact on feed intake. There was no difference between the sources in standardized ileal digestible (SID) amino acid content, except for methionine and alanine. The SID of crude protein was 22-33%-units lower than that of SBM and SID of amino acids was on

Energy digestibility of cereal grains in pigs: measured *vs* predicted by NIRS (Noel et al., 2018, Aarhus University)

Identification of feed efficiency traits related to individual diversity (WP2)

WP leader: Alfons Jansman
alfons.jansman@wur.nl

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

◗ The development of feeding stations to monitor feed intake and body weight of individual rabbits and broilers in group-housing systems was completed.

◗ Hardware and software were redesigned and modified to create devices, linked data collection software, and tools suitable for experiments carried out to evaluate the effects of dietary and other interventions on individual feed intake in group-housed broilers and rabbits.

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

◗ New knowledge has been generated linking the composition of the intestinal and faecal microbiota to nutrient digestibility and systemic metabolic parameters in pigs, rabbits, and broilers.

◗ A new method using NIR technology to measure nutrient digestibility more easily in a large number of samples is being developed in pigs.

Nutrient metabolism related traits to improve feed efficiency

◗ Absolute N retention at later age is affected by birth weight of pigs.

average 15%-units lower (from -3 to 54).

◗ Pigs had significantly lower body weight and average daily gain, and higher feed conversion ratio when fed with the FCP dehulled SBM compared to control pigs. In line with performance data, amino acid digestibility was lower in the FCP dehulled SBM.

◗ In broilers, SBM processing did not affect any of the tested variables, and all 4 processes resulted in similar performance. Aside from increased carcass yield, hull removal did not confer a significant advantage, possibly due to the adaptive growth of the gizzard and proventriculus in the hulled treatments.

Improvements in nutritive value by use of novel enzymes

◗ Mechanical improvement of RSM increased its protein content, which improved feed efficiency due to a reduction of feed intake. No effect was observed on growth performance. No effect of enzyme inclusion on dry matter, energy or nitrogen digestibility was detected.

New methodologies for characterisation of nutrient composition and value

◗ Predictive calibration models were obtained on NIR scans for 328 cereal samples. Models for chemical data (including amino acids) and biological data from pig trials have been evaluated. In general, NIR calibration models had good predictive ability and robustness, though they were not suitable to predict the mineral composition of cereals.

◗ The removal of anti-nutritional components from RSM and the isolation of a fine fraction both enhanced protein content, but did not substantially affect amino acid pattern. No substantial effects on lysine damage were observed, and lysine damage varied between 0 and 5% of total lysine.

Feed-a-Gene

However, relative N efficiency is not affected by birth weight.

◗ Analysis of the relationship between experimental treatments with metabolome profiles in blood is ongoing.

Behaviour and welfare related traits influencing feed efficiency

◗ A methodology capable of the automatic measurement of a variety of traits at a group level related to feed intake behaviour in pigs has been developed.

◗ A new method was developed to assess interactions between pigs, that uses electronic feed recording information for estimating the ranking of animals within a group as an indicator for behaviour in relation to feed efficiency.

Metabolomics to identify new traits for improvement of feed efficiency

◗ The blood metabolome of pigs and rabbits was shown to be affected by dietary treatment and genotype.

◗ In growing-finishing pigs, blood biomarkers measured at an early stage have been identified as indicators of feed efficiency.

Modelling feed use mechanisms and animal response to nutrient supply and environmental challenges (WP3)

WP leader: Veronika Halas
veronika.halas@ke.hu

Digestive utilisation of feed and nutrients

◗ A mechanistic-dynamic model of transit and digestion for pigs has been developed and improved. Its accuracy was confirmed by a comparison between observed and predicted digestibility values.

◗ This model was transposed to broilers. Inputs are the amount of nutrients ingested (proteins, free amino acids, lipids, starch, sugars, fibre, Ca, P). Equations represent the transit, hydrolysis, fermentation, and absorption of nutrients. Outputs are ileal and faecal nutrient digestibilities. Parameter quantification has been performed but the model needs to be validated.

Metabolic utilisation of feed and nutrients

◗ The initial version of the post-digestive pig model has been improved with a better amino acid and protein model, and by adding models predicting P utilization, P retention and feed intake.

◗ The pig model was transposed to broilers. The broiler model is able to simulate the partitioning of energy and protein and predict P retention and excretion.

◗ A module estimates the body fatty acid composition of pigs and lipid distribution in the different tissues.

Accounting for environmental variability, system disturbance and robustness

◗ Work has been done on the ability to detect perturbations automatically, using the deviation of cumulative feed intake from a targeted trajectory as a response criterion.

◗ In pigs, a mechanistic model was developed to describe the adaptative response to a generic perturbation.

◗ In broilers, Bayesian inference methods were used to estimate perturbations in the performance of birds undergoing intestinal parasitic infection. Results suggest evidence for compensatory growth.
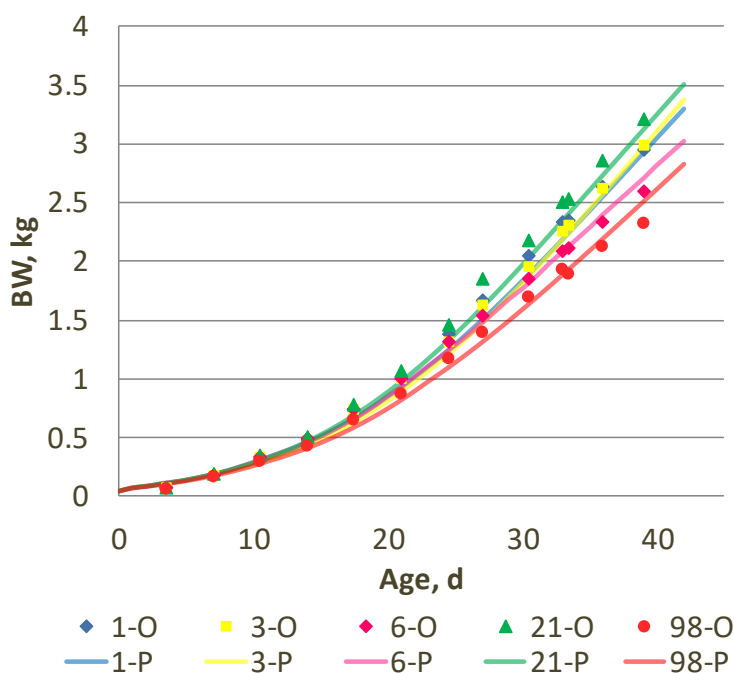
Observed body weight (kg, dots) and predicted body weight (line) from five different datasets of Cobb broilers (Dukhta et al., 2018, Kaposvár University)

Accounting for variation among individuals in nutrient digestion and metabolism processes

◗ A Bayesian inference approach was used in pigs, broilers, and rabbits to obtain posterior distributions of parameters and traits reflecting within-individual variation and data uncertainty, and among-individual variation.

◗ The traits were growth rate, dynamic body composition, metabolic heat production, and energy and protein utilisation efficiency. Except for growth rate, individual traits were estimated through growth models and fitting serial trait observations.

◗ Trait estimates measure real-time individual performance ; population trait distributions inform performance of breeds or treatments; individual-trait scatter plots identify phenotypic clusters.

◗ Metabolic heat production estimates agreed with literature data. Age-varying protein efficiency of pigs was within literature bounds.

Delivery of a Decision Support Tool

◗ A first version of the decision support tool (DSS) was developed. Based on the InraPorc model for growing pigs, it includes a model for energy and protein metabolism, a module for P utilisation, and a spring and damper system used for characterizing the animal's response to perturbation.

◗ In addition to model development, software development includes creating an interactive interface, language localisation and linear multivariable optimization. An open source version of the core model as well as a standalone desktop version for end-users are being developed. The first version of the DSS was shown at the stakeholder meeting held during the 2017 EAAP Annual meeting.

Management systems for precision feeding to increase resilience to fluctuating environments (WP4)

WP leader: Jesús Pomar
pomar@eagrof.udl.es

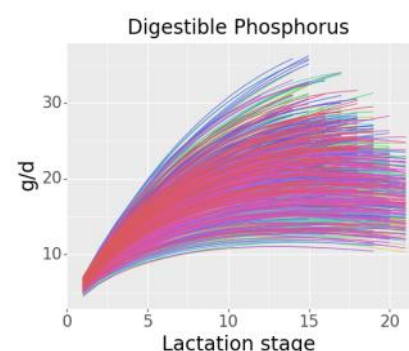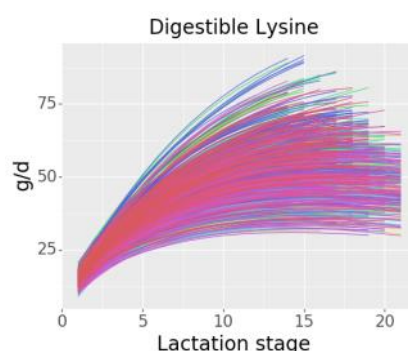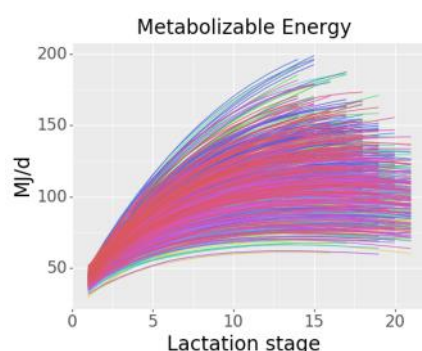## Decision Support System development for real-time determination of animal nutritional requirements

◗ For growing pigs and broilers, a first version of the decision support system (DSS) was implemented using an architecture combining modules for analysing and predicting performance and for estimating the nutritional requirements of animals in real time.

◗ For gestating sows, an Excel procedure was created to implement the DSS.

◗ Simulations indicated that compared to classical feeding, precision feeding can reduce protein and amino acid intake and N excretion by 25% in gestating sows and lysine and protein intake by 6.2% in lactating sows.

◗ For broilers, a model implementation is now able to predict daily requirements for metabolizable energy, digestible lysine, and available P.

Controlling module development to support feeder control tasks, real-time measurements

◗ The Controlling Module (CM) integrates all devices and software components involved in precision feeding systems. The CM acts as an intelligent multiple device and DSS integrator, with the capacity to control multitask processes such as monitoring, supervision, and data management.

◗ A language (ACL) was developed to establish the communication between the devices and the CM.

Requirements variability between sows, across the lactating period (Gauthier et al., 2018, INRA)

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Precision feeder device development

◗ Enhanced precision feeder prototypes for growing pigs fed *ad libitum* or restrictively fed are now ready for validation.

◗ For group-housed gestating sows, a precision feeder device has been developed and is now installed in the experimental station of IFIP.

◗ An experimental accelerometer fixed to the sow's ear is available to measure energy expenditure due to physical activity.

◗ For poultry, a complete design of precision feeding system is available.

Building and validation of precision feeding system prototypes

◗ Individual precision feeding of *ad libitum*-fed growing pigs significantly improved feed conversion and lean meat content of the carcass when compared to two-phase feeding. The total lysine intake tended to be reduced, but to a lower extent than expected.

◗ In restricted feeding conditions, feed efficiency and growth rate were similar for pigs fed a two-phase strategy or with precision feeding, but the latter strategy resulted in a 5% reduction in lysine intake.

◗ The validation tests of ACL communication between feeder devices and CM showed that the communication worked satisfactorily, and that the system reacts in a robust way when working under non-optimal conditions.

Use of new traits in animal selection (WP5)

WP leader: Hélène Gilbert
helene.gilbert@inra.fr

Genetics of components of feed efficiency and robustness indicators

◗ New traits on behaviour, welfare, and metabolomics indicators have been collected recently and no results are available yet.

◗ In pigs and layers, no deleterious relationships were shown between feed efficiency and responses to challenges, when comparing performance with different feeds in divergent lines.

◗ In broilers, 116 genomic regions were associated with 16 traits related to digestive efficiency, growth, and faeces composition.
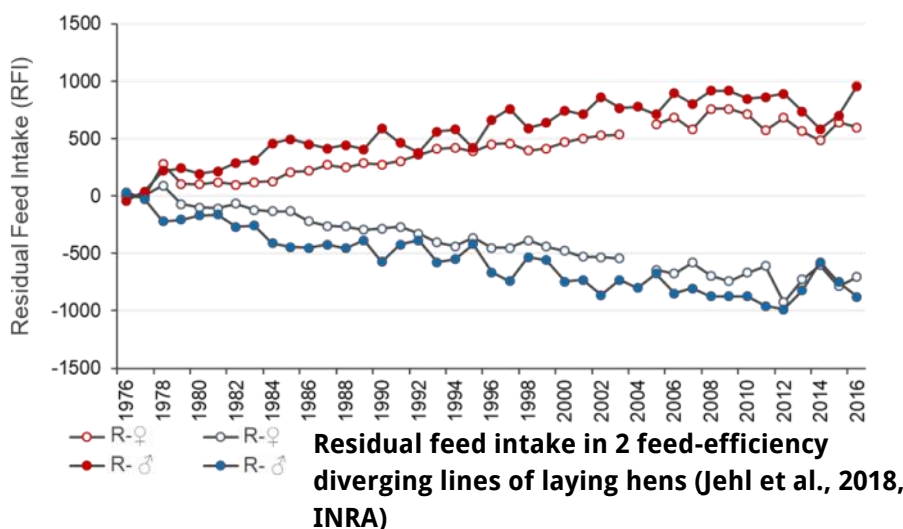
◗ Only preliminary results are available on reproductive females. In sows, a genetic component of feed intake was found during lactation. In mice, there was a better robustness to stress conditions (restricted feed) for females selected for homogeneity of litter birth weights.

Genetic relationships between the gut microbiota and feed efficiency

◗ Selection on feed efficiency was successful for direct effects, but maternal effects were degraded by the selection (about 1/6 of the direct genetic gain).

◗ Feed, sex, line of feed efficiency, cross fostering, and feeding regimes had significant effects on gut microbiota composition in the different studies.

◗ Some microbiota phyla in rabbits were heritable.

◗ First association studies conducted on the average daily gain of rabbits fed restricted and *ad libitum* feeding showed four QTL regions on chromosomes 3, 5, and 21.

Statistical-genetic modelling of feed efficiency and robustness features

◗ Pen records of feeding levels can be used to improve genetic evaluation.

◗ Social genetic effects varied over time so it is important to account for them in selection.

◗ The structured antedependence model was validated and showed that the dynamics of feed efficiency over time is affected by selection.

◗ The joint estimations of genetic parameters for variability on multiple traits suggested the existence of a general robustness across traits.

Residual feed intake in 2 feed-efficiency diverging lines of laying hens (Jehl et al., 2018, INRA)

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◗ The alternative implementation of a genetic model with indirect genetic effects including feeding behaviour improved model performance.

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

◗ Accuracy and bias of predictions were used as primary criteria to evaluate the tested strategies. They indicated that the separation of additive and dominance components seems to be beneficial for some traits to evaluate purebred candidates to selection for crossbred performance.

◗ Including metafounders did not affect the accuracy and bias of predictions, but improved convergence of the model when the breeds were very distantly related to each other.

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

◗ Currently, approximately 40 million pigs have a breeding value for indirect genetic effects, including Topigs Norsvin animals tested in the different trials of the Feed-a-Gene project.

◗ In rabbits, a selection experiment is being carried out to obtain lines based on two selection criteria: average daily gain under restricted feeding (enhances competition) and residual feed intake with *ad libitum* feeding. Feed intake data from the first generation have been recorded in five batches of 130-150 rabbits each.

Sustainability assessment of production systems (WP6)

WP leader: Guy Garrod
guy.garrod@newcastle.ac.uk

Identification of sustainability indicators for proposed production systems

◗ Stakeholders provided 102 usable responses to the Delphi survey. The highest-ranked dimension of sustainability was the Economic dimension, followed by Environmental and Social.

◗ Indicators related to financial viability of farming activities were the highest, reflecting that farming will not continue in the future if farms cannot achieve profitability.

Life Cycle Assessment of proposed management systems

◗ The global feeding strategies to be evaluated through Life Cycle Assessment (LCA) have been set

for pigs in conventional crossbred and South European Iberian pigs.

◗ A survey establishing the list of required data has been done among partners. Work on LCA for innovative production systems in poultry production has started.
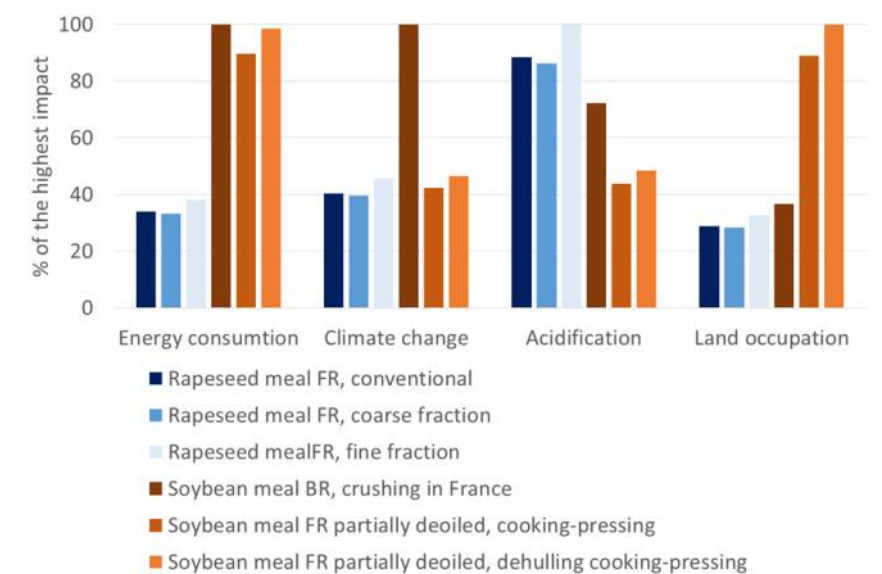
On-farm evaluation of proposed management systems

◗ Variables needed to handle Cost-Benefit Analysis have been set after literature analysis. Data are collected from pig and poultry farms in Denmark, Germany, France, Poland and Spain over the 2010-2015 period.

Evaluation of consumer and farmer attitudes

◗ A literature review has been conducted on the use of choice experiments to explore public preferences and trade-offs for different livestock production attributes. This informed the design of a choice experiment questionnaire that will be used to estimate values for the most important externality attributes (e.g., environmental or animal welfare) associated with the management systems that are being examined.

Anticipated environmental impacts of new protein sources (Espagnol et al., 2018, IFIP, ITAVI)

Legend:
- Rapeseed meal FR, conventional
- Rapeseed meal FR, coarse fraction
- Rapeseed mealFR, fine fraction
- Soybean meal BR, crushing in France
- Soybean meal FR partially deoiled, cooking-pressing
- Soybean meal FR partially deoiled, dehulling cooking-pressing

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Dissemination, training and technology transfer (WP7)

Communication

2 intermediary newsletters have been sent since the 2nd newsletter:

◗ Feed-a-Gene News October 2017

◗ Feed-a-Gene News January 2018

Two booklets of abstracts have been distributed:

◗ Book of abstracts 2016-2017

◗ Book of abstracts 2017 EAAP / EC-PLF

An animated Greeting card was sent to stakeholders in January 2018.

Stakeholder platform and events

◗ The stakeholder platform now contains 371 participants.

◗ A stakeholder session was organised during the EAAP meeting in Tallinn in August 2017.

Events

Many researchers participated in international and national events, particularly:

◗ EAAP 2017 (Estonia)

◗ EC-PLF 2017 (France)

◗ WCGALP 2018 (New-Zealand)

Feed-a-Gene Season 1

▶ YouTube

Watch researchers talk about Feed-a-Gene and their research on the project's YouTube channel.

Better feeds, better animals

This video made for the general public is in the top 10 of the 300 videos created to showcase H2020 projects!

Join Feed-a-Gene on social media!

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www.youtube.com/FeedageneEuProject

www.researchgate.net/project/Feed-a-Gene-3

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Stakeholder meeting at the 68th EAAP meeting in Tallinn, August 2017

◗ Jaap van Milgen (INRA) discussing with the stakeholders

◗ Masoomeh Taghipoor (INRA)

◗ Nora Formoso-Rafferty (UCM)

◗ Veronika Halas (KU) and Valérie Heuzé (AFZ)

Peer-reviewed papers published in 2017-2018

The following 9 peer-reviewed papers are now available.

◗ Ragab M., Piles M., Quintanilla R., Sánchez J.P., 2018. Indirect genetic effect model using feeding behaviour traits to define the degree of interaction between mates: an implementation in pigs growth rate. Animal, 12 (7): 1-9 doi.org/10.1017/S1751731118001192

◗ Tallentire C.W., Mackenzie S.G., Kyriazakis, I., 2018. Can novel ingredients replace soybeans and reduce the environmental burdens of European livestock systems in the future? Journal of Cleaner Production, 187: 338-347 doi.org/10.1016/j.jclepro.2018.03.212

◗ Beauclercq S., Nadal-Desbarats L., Hennequet-Antier C., Gabriel I., Tesseraud S., Calenge F., Le Bihan-Duval E., Mignon-Grasteau S., 2018. Relationships between digestive efficiency and metabolomic profiles of serum and intestinal contents in chickens. Scientific Reports, 8: Article number: 6678 doi.org/10.1038/s41598-018-24978-9

◗ Verschuren L.M.G., Calus M.P.L., Jansman A.J.M., Bergsma R., Knol E.F., Gilbert H., Zemb O., 2018. Fecal microbial composition associated with variation in feed efficiency in pigs depends on diet and sex. Journal of Animal Science, 96 (4): 1405–1418 doi.org/10.1093/jas/sky060

◗ Sánchez J.P., Ragab M., Quintanilla R., Rothschild M.F., Piles M., 2017 Genetic parameters and expected responses to selection for components of feed efficiency in a Duroc pig line. Genetics Selection Evolution, 49:86 doi.org/10.1186/s12711-017-0362-x

◗ Huynh-Tran V.H., Gilbert H., David I., 2017. Genetic structured antedependence and random regression models applied to the longitudinal feed conversion ratio in growing Large White pigs. Journal of Animal Science, 95 (11) : 4752-4763 doi.org/10.2527/jas2017.1864

◗ Wientjes Y.C.J., Calus M.P.L., 2017. The purebred-crossbred correlation in pigs: a review of theory, estimates and implications. Journal of Animal Science, 95 (8): 3467-3478 doi.org/10.2527/jas.2017.1669

◗ Piles M., David I., Ramon J., Canario L., Rafel O., Pascual M., Ragab M., Sánchez J.P., 2017. Interaction of direct and social genetic effects with feeding regime in growing rabbits. Genetics Selection Evolution, 49:58 doi.org/10.1186/s12711-017-0333-2

◗ Tran-Huynh V.H., Gilbert H., David I., 2017. How to improve breeding value prediction for feed conversion ratio in the case of incomplete longitudinal body weights. Journal of Animal Science, 95 (1): 39-48 doi.org/10.2527/jas.2016.0980

Communications

Feed-a-Gene researchers have published about 50 communications and posters. For the whole list, see:

◗ www.feed-a-gene.eu/media/communications

Nine young researchers in the spotlight

The 3rd annual meeting of Feed-a-Gene included oral presentations from young talented researchers whose work received funding by the H2020 programme.

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

Antonio Diego Brandao Melo (IRTA)
antonio.brandao@irta.cat

The effects of high protein rapeseed meal (RSM) combined with enzyme (NSPase or protease) supplementation in 144 growing pig diets have been assessed during 6 weeks. It was shown that high protein RSM had no effect on body weight gain but reduced feed intake and thus improved feed conversion ratio. Fat digestibility was improved by RSM inclusion but DM, N or energy digestibilities were not affected by the diets. Enzymes combined to RSM had no further effect on pig production performance.

Development of models to predict the nutritional value of feedstuffs and feed mixtures by NIR

Samantha Joan Noel (Aarhus University)
Samantha.noel@anis.au.dk

NIR spectral scanning is a cheap and non-destructive way to predict feedstuffs composition provided it can be consistently calibrated with traditionally measured (chemical analysis) reference data. Over 1000 samples of individual feedstuffs and mixed diets were scanned and used to develop calibration models for 11 chemical, 18 amino acid, 10 mineral and 16 biological constituents. NIR predictions were tested with a reference group of samples that were not used to make the calibration models. Most of chemical and amino acid constituent models performed well while the mineral models performed poorly. Though the predictions for the biological constituents were slightly less accurate, they compared very well with the accuracy of the original *in vivo* data.

Relationship between microbiota composition and nutrient digestibility, effect of dietary fibers

Mathilde Le Sciellour (INRA UMR PEGASE)
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In growing pigs fed on low or high fibre diets during 4 x 3-week-periods, digestibility measurements and faecal collections were done for RNA sequencing and subsequent microbiota characterization. It was possible to discriminate the 2 diets via 31 OTU's. In pigs fed low fibre diets, *Clostridiaceae* and *Turicibacter* were negatively correlated to digestibility coefficients while *Lactobacillus* were positively correlated with protein digestibility and energy digestibility. In pigs fed high fibre diets, no correlation was found and it was not possible to quantitatively predict digestibility with microbiota information.

Short- and long-term effects of DON challenge on the performance and feeding behaviour of finishing pigs

Aira Maye Serviento (INRA)
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One of the most common mycotoxins in swine diets is deoxynivalenol (DON). It is thus important to evaluate the effects of DON challenge as a function of age on growth performance and feed efficiency in finishing pigs. DON challenge reduced feed intake by 25-30%, BW by 40-60% and feed efficiency by 20-34% in a study conducted on 160 pigs. The severity of DON effects depends on the age of the pigs and of the number of challenges occurring: though pigs can recover to some extent, in all cases DON is deleterious to the final weight.

Plasma metabolites related to nitrogen efficiency in grower-finisher pigs

Lisanne Verschuren (Topigs Norsvin)
Lisanne.verschuren@topigsnorsvin.com

Untargeted metabolomics were used to study the effect of birth weight (low or high BthW) on N metabolism of pigs receiving adequate (100%) protein or restricted (70%) protein diets during the growing-finishing stage. Plasma metabolites differed between the BthW groups and diets. The metabolites indicating the effects of protein restriction were different between pigs of different BthW and could be the result of differences in N metabolism in pigs of different BthW.

On the use of voluntary feed intake for automatic detection and characterization of the response of growing pigs to perturbations

Hieu Nguyen Ba (INRA UMR PEGASE)
hieu.nguyen-ba@inra.fr

It is hypothesized that there is a targeted trajectory curve of cumulative feed intake which is the optimal amount of feed the pig desires to eat when it faces no perturbation. Deviations of feed intake from this curve are considered as a period of potential perturbation and can be characterized by their duration and magnitude. A model based on differential equations was then developed to characterize the animal's response to perturbations. In the model, a single perturbation can be characterized by two parameters. One parameter describes the immediate reduction in daily feed intake at the start of the perturbation (i.e., a "resistance" trait) while another describes the capacity of the animal to adapt to the perturbation through compensatory feed intake (i.e., a "resilience" trait).

Application of a pig model to predict broiler performance

Galyna Dukhta (Kaposvár University)
galyna.dukhta@ke.hu

Starting from InraPorc model of growth, it was proposed to adapt it to a poultry growth model including 3 submodules:

◗ a metabolic module which simulates energy and protein partitioning in broilers and individual daily growth performance under ideal conditions,

◗ a P and Ca module that predicts digestible P and Ca utilization and thus P load of broiler production,

◗ and a feed intake module that takes environmental conditions into account and modifies actual energy intake as a response to undesired heat losses.

Precision feeding development for lactating sows: nutritional requirements modelling

Raphaël Gauthier (INRA)
raphael.gauthier@inra.fr

The InraPorc lactating model was used to develop a decision support tool for the precision feeding of lactating sows which are often under-optimally fed. Data on sows and their environment were used to determine the optimal supply for each animal. In sows fed in excess, it was possible to reduce average digestible lysine excess by 75%, and, in deficient sows, it was possible to reduce deficiency by 63%. Precision feeding also reduced lysine and P intake.

Genetics component of feed efficiency in layers using DNA-seq and RNA-seq: preliminary results

Frédéric Jehl (INRA)
frederic.jehl@inra.fr

DNA and multi-tissue (fat, blood, hypothalamus and liver) RNA sequencing were used to characterize lines of laying hens diverging for feed efficiency. DNA sequencing found 143,965 bi-allelic SNPs (single nucleotide polymorphism) for which one allele is homozygous in one line and heterozygous in the other line. 4 SNPs were predicted to lead to a premature stop codon and could have a role in the difference of feed efficiency. 98% of the SNPs were out of the coding region. RNA sequencing revealed that, depending on the tissue, 2996 to 6826 genes were differently expressed in the 2 lines. Pathways associated with the coding genes remain to be studied.

Upcoming events

Feed-a-Gene researchers will present communications in the following congresses in 2018.

DPP Digestive Physiology of Pigs

21-24 August 2018, Brisbane, Australia

EAAP 2018

27-31 August 2018, Dubrovnik, Croatia

▶ **Thursday 30 August:**
full-day stakeholder session
Feed-a-Gene / SAPHIR

SPACE 2018

11-14 September 2018, Rennes, France

▶ Joint Feed-a-Gene / SAPHIR
conference on 11 September

▶ Live demonstration of the Decision
Support System for precision feeding (INRA booth)

EPC European Poultry Conference

17-21 September 2018, Dubrovnik, Croatia

Feed Additives Global

26-28 September 2018, Amsterdam, Netherlands

EuroTier 2018

13-16 November 2018,
Hanover, Germany

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Feed-a-Gene News - October 2017

Mon, 2017-10-02 15:02

Book of abstracts 2017 EAAP / EC-PLF

This booklet contains 22 abstracts of oral communications and posters presented at the Feed-a-Gene session of the 68th annual meeting of the EAAP in Tallinn, Estonia (30 August 2017) and at the 8th EC-PLF European Conference on Precision Livestock Farming, Nantes, France (12-14 September 2017). These abstracts are enriched with additional tables and figures.

- [Click here to download the booklet](#)

Feed-a-Gene Season 1: the series

During the Feed-a-Gene session held during the EAAP meeting in Tallinn, we filmed a series of 10 interviews of researchers associated with the project. In Episode 1, coordinator Jaap van Milgen discusses the rationale, goals and expected impacts of the project.

- [Click here to view the Feed-a-Gene Episode 1 on YouTube](#)

In episodes 2-9 (to be released in the following weeks), work package leaders and researchers will present ongoing scientific activities and the results obtained so far. In the season finale, Jaap van Milgen will talk about the importance of stakeholders and about their feedback and input on the project.

Two new Feed-a-Gene peer-reviewed articles

Feed-a-Gene researchers have published 2 peer-reviewed articles in the *Journal of Animal Science* that deal with genetic parameter estimations and contribute to the progress of WP5 Use of traits in animal selection. These articles are in Open Access and can be downloaded by clicking on their title below:

- January 2017: How to improve breeding value prediction for feed conversion ratio in the case of incomplete longitudinal body weights by Tran-Huynh V. H., Gilbert H. and David I. (INRA)
- August 2017: The purebred-crossbred correlation in pigs: a review of theory, estimates and implications by Wientjes Y. and Calus M. (Wageningen University and Research)

Feed-a-Gene News - January 2018
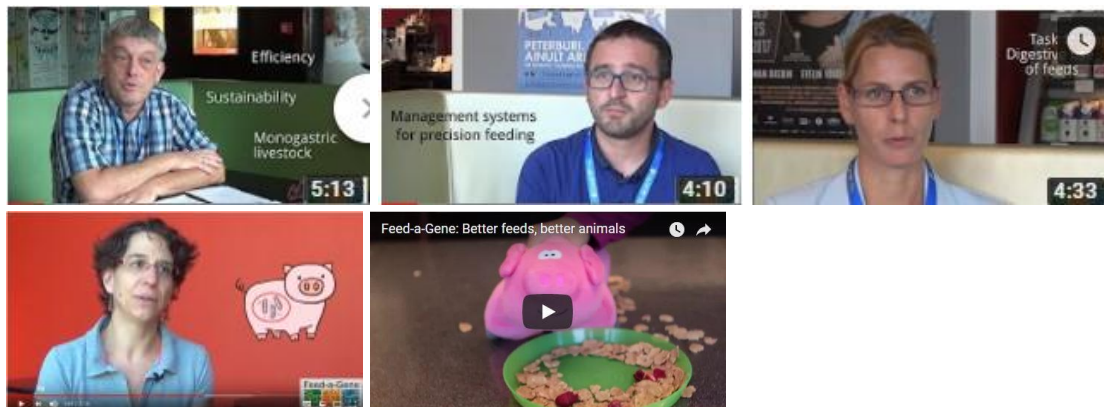
Tue, 2018-01-23 10:30

Editorial by project coordinator Jaap van Milgen

Dear readers,

First, I would like to wish you all the best for 2018 in your professional and personal life. Try to stay healthy and happy; the New Year should bring us plenty of challenging opportunities.

After the first two annual newsletters, sent out in 2016 and 2017, I am pleased to introduce this second Feed-a-Gene intermediate news bulletin. Because the number of project results will increase during the last two years of the project, we plan to publish newsletters more frequently so that you can become aware of these project results and use them in your day-to-day business.

Please have a look at the videos published on the Feed-a-Gene YouTube channel. You will find several videos of researchers talking about their role in the project, and more videos will be published in the next weeks. We also created a funny video, "Better feeds, better animals" in which we explain the objectives and activities of the Feed-a-Gene project to a broad audience. This video is part of a competition set out by the European Commission to increase public awareness of H2020 projects. We participate in this competition where the winner is determined by the number of "likes". If you like it (and I am sure you do), please click on the "thumbs up" button on YouTube.

2017 last achievements: peer-reviewed papers and communications

A lot has happened in the last quarter of 2017. Two peer-reviewed papers were accepted and published:

- October 2017: Genetic structured antedependence and random regression models applied to the longitudinal feed conversion ratio in growing Large White pigs by Huynh-Tran et al., 2017, in the Journal of Animal Science
- December 2017: Genetic parameters and expected responses to selection for components of feed efficiency in a Duroc pig line by Sanchez et al., 2017, in Genetics Selection Evolution

Both articles are downloadable and present some of the results of the fruitful WP5 Use of traits in animal selection.

4 communications were presented between September and November 2017:

- Emma Fabrega (IRTA): New physiological indicators for welfare assessement: Cromogranin A (11th IVBM International Veterinary Behaviour Meeting, 14-16 September 2017, Samorin, Slovakia)
- Nathalie Quiniou (INRA): Assessment of the dynamic growth of the fattening pigs from body weight measured daily and automatically to elaborate precision feeding strategies (8th EC-PLF European Conference on Precision Livestock Farming 2017, 12-14 September, Nantes, France)

- Ludovic Brossard (INRA): Selection of methods to analyze body weight and feed intake data used as inputs for nutritional models and precision feeding in pigs (EC-PLF)
- Galina Dukhta (Kaposvár University): A growth model to predict body weight and body composition of broilers (A jövo tudósai, a vidék jövoje - Future scientists, Future countryside, Doctoral Conference, 24 November 2017, Debrecen University, Debrecen, Hungary)

In addition, project coordinator Jaap van Milgen presented Feed-a-Gene at the "Climate and Environmental Sustainability" session held at the FOOD2030 conference of the European Commission, on 16 October 2017. During this presentation he discussed feed efficiency and the role of livestock in sustainable food production. The video of the presentation is available here.

Next in 2018!

2 scientific papers have been submitted for peer review.

Feed-a-Gene researchers have already planned 7 presentations for the next 2 months:

- Hervé Garreau, Hélène Gilbert, Loys Bodin (INRA), Mostafa Helal and Juan Pablo Sanchez (IRTA) will present no less than 5 communications at the next WCGALP (World Congress on Genetics Applied to Livestock Production), 11-16 February, Auckland, New Zealand
- Lisanne Verschuren (Topigs) will present 2 communications at the following meetings:
  - WIAS Science Day 2018, Work on your Impact in Animal Sciences and Society, 5 Feburary 2018, Wageningen, The Netherlands
  - AASV (American Association of Swine Veterinarians) annual meeting, 2-6 March 2018, San Diego, California, USA

All materials will be published on the website when they become available.

Minutes of the stakeholder meeting and of the two demonstration events

Annex to Deliverable 7.5

Feed-a-Gene, Association française de zootechnie, 15 June 2018

Stakeholder meeting, 30 August 2017, Tallinn, Estonia

Jaap van Milgen (Feed-a-Gene Project coordinator):

There is still a lot to do to put the outcomes on shelves. Our TRL level would be TRL5. What should I advise if Warren Buffett wanted to invest in microbiota in order to influence animal performance in a positive way? Should he put 10 million in feed company (additive probiotics) or 10 million in genetics (have the good animals to have a good microbiota) or 50/50?

Pieter Knap (stakeholder):

Calculate the h^2 of the thing and divide according the h^2. But are you going to be able to calculate the h^2 and h^2 of what? That is the question.

Jaap van Milgen:

Will you be able to calculate h^2 at this stage? The question is regarding efficiency and robustness of animal production systems. We want to make the good use of feeds in a context of having feed less in competition with food.

Mark Saltier (stakeholder):

It is all about integration: everyone has to make money at any level of the chain, genetic companies, feed companies, farmers, supermarket has to make money. Consumers have to pay less. All along the chain…

Jaap van Milgen:

How Warren Buffett should invest in order to get the best ROI. Where is the greatest potential to affect animal performance, efficiency and robustness through the microbiota? What are the best levers? Genetics feeding, combination of these?

Unidentified stakeholder:

It is a good question, but perhaps the time is wrong for that. The question does not come at the right moment since we have heard [this morning] about genetics. Thus, having only heard genetics, I would say invest in genetics and after this afternoon presentation I would say the contrary, maybe.

Hélène Gilbert (WP5 leader):

Maybe you have the feeling we don't have enough indicators to answer a specific question. Part of the question is which type of indicators is missing, and how can we produce them so that they have a value?

Jaap van Milgen:

We do not really know if genotype affects the microbiota or if the microbiota affects the phenotype? How does it work?

Unidentified stakeholder:

I think it was mentioned this morning that we don't know yet whereas the genetics affect the microbiota or the contrary. You should make a company that builds microbiota profiles because everybody is going to work on it.

Jaap van Milgen:

OK.

Unidentified stakeholder:

I think we have to build the basic model. Research on microbiota is turned to know which species are involved, in which circumstances and their conditions of growth, but actually we need the framework model by which you can link the inputs and the outputs of the report performance such as welfare, FCR. Creating the basic model that does not exist.

Jaap van Milgen:

What is missing? The model or the framework model? Model, data, indicators, biomarkers?

Unidentified stakeholder:

The framework model is missing. We don't know if we give a particular under particular environmental circumstances. We don't know what the outcomes are going to pay. Sometimes they work or not, sometimes they are detrimental. It is better to know what to use under specific circumstances. You need a basic model which tells you: « if I am under these circumstances I use this type of additive, under others, I have to do something else ». And then if I know that I feed this I will get this outcome.

Jaap van Milgen:

Other suggestions for Warren?

Juan Pablo Sanchez (WP 5 researcher):

It is a difficult point. The nutritional effects can be considered to be fixed effects. You can test one situation versus another. If you think in this way you can imagine plenty of probiotics and ingredients in the diets. When you approach the issue from an animal perspective, you are thinking of characterizing the variation across all the animal population. We probably need to design a strong experimental design assessing as much as possible treatments jointly with all the animal variability that might exist. From diff experiments it would be difficult to answer this question: the money in the pig studies, in the diet could be strong or in microbiome composition. The experiment will be done under this diet, but why don't they experiment under different diets?

Unidentified stakeholder:

I would start a microbiome company.

Jaap van Milgen:

Let's continue on the microbiome: is the microbiome a result of an animal, its diet or environment or does it have causal effect on animal?

Unidentified stakeholder:

We know that microbiome has lived with animal for ages. They interact in a positive way, sometimes in negative. We have seen it on humans and in cows. It depends on what kind of microbiome you are looking at. It may be small things or big things. Welcome in microbiome world!

Hervé Garreau (WP5 researcher):

Animal genetic variability is partly explained by microbiome, partly by animal. It is tricky to separate what is the real animal effect and the microbiota effect. But whatever it comes from, how will we be able to increase the genetic gain on efficiency and at which cost by the microbiome, is it costly efficient? In what proportion will we increase the genetic gain on feed efficiency taking into account this information?

Hélène Gilbert (WP5 leader):

What information do you need for that? This morning we have seen different models derived from different datasets. Dataset is not yet there. Do we have to produce more data, in which direction? or to use directly those from the breeders so that we will see what happens in the field which is what we need at the end?

Unidentified stakeholder:

In what is cause or consequence, I think the relevant thing is the effect of the bacteria on the animal performance. Because what we take, is the performance of the animal we don't care a lot about the bacteria performance yet. We have to identify the different treatments that could make microbiota composition favourable for animal performance. Also, this can be achieved indirectly by changing the animal that modify all its microbiota, but the relevant thing to do is the effect of the microbiota on the animal

Jaap van Milgen:

To some extent I agree, but at the end we are looking for levers. For things that we can use to change production: genetics, nutrition, whatever… If it is causal, if we know that through the bacteria we can cause an effect on the animal, then the indicators of the microbiome are a good way to control the levers that are working. But, if it is just a consequence, why do I look at the microbiota at all? If the microbiota has an effect on the animal, I build a microbiome company. The issue of cause or consequence is very important. If it is a consequence, it is not worth it!

Pieter Knap (stakeholder):

Experimental design is going to be very important to you. People are going to transplant microbiome from an animal to another which seems to be easy to do. If you can set up cross design don't worry. It seems that experimental designs are embryonic at the moment. Wait a couple of years for people to make mistakes that way and learn from that. We do not have enough data to figure out what to do it properly, we need more mistakes.

Mark Saltier (stakeholder):

In conference on microbiome people show that microbiome has a profound effect on everything. In Australia, they use microbiome in human to cure clostridium infections. Microbiome certainly has profound effects.

Unidentified stakeholder:

When we deal with microbiome we should go to big data because what we learnt is that small dataset of only 6-12000 individuals could not give significant results. So, this is not just big data, but big applications, big proposals, big projects. A new era!

Egbert Knol (WP5 partner):

There were these experiments where you used the embryos and their microbiome under 10 generations. Effects of co-selection of animal and microbiome seem positive.

Jaap van Milgen:

Do we have to look at other microbiome, on the skin for example?

Unidentified stakeholder:

What microbiome the one, the thirty, the 60? probably all of them, bigger, bigger data!

Jaap van Milgen:

What do we sample? It is difficult: we get a lot of data can we transform it into information? Is data really the problem? We measure anything, price go down. What is lacking? Data, concept, or the interaction?

Pieter Knap (stakeholder):

We have the technology, we can do it. Let say how we think it works and then design experiments from there, then measure. And there will be sufficient mistakes and we will learn.

Unidentified stakeholder:

Is it easier to change the genotype, to test microbiome or the contrary? The question is whether antibiotic use really changes the microbiota. Do we understand how that antibiotics use changes the microbiota and

how it impacts the actual feed efficiency of the animal. It seems like trying to make as an extreme difference as possible to start understanding what is going on in the gut would be a start rather than trying to understand little tiny steps.

Jaap van Milgen:
Anyone?

Pieter Knap (stakeholder):
The world is full of data without any useful information behind. Would it be a waste of money to generate data? Useful data is not only big, but also interesting and relevant contrast. If the data get bigger you can have as many data as you want, but you don't get information. The important thing is that you make sure you create big contrast within data of for traits that are actually relevant. We don't know how those traits are, right now, that's why we need to make those mistakes. We need to make experimental designs, we have to think about what we want to measure and find the way to do it. Until you have not found, you make mistakes. It is very important to do that.

Jaap van Milgen:
Is experimental design that simple?

Unidentified stakeholder:
No, it is not that simple. It is the reason why we have 10 million € and that we would need 20! It does not need to be simple, it does not need to be solved in a week. The project is no competition, it is pre-competitive.

Jaap van Milgen:
Coming back to what we need from you. If we could make a design to do together genetics, feeding feeds, what would be the design that could answer the question of relevant causality around 2020.

Hélène Gilbert (WP5 leader):
The design is the best thing we can have at the end? Putting everything together.

Unidentified stakeholder:
If you want your design to be good, you must run it on commercial farms. The biggest problem is that it is almost impossible to measure performance in term of FCR in commercial farms. It is, by far, too difficult to measure real individual performance and to relate them to the microbiome. Unbelievably to do it under commercial conditions.

Unidentified stakeholder:
Understand relations between microbiome and animal then it is moved to manipulating. Microbiome has been manipulated before, using copper, antibiotics… Is it something acceptable by the society? Is this a role that stakeholders can contribute on?

Jaap van Milgen:
Who has the answer? With copper and antibiotics, society is very reluctant to go back to what we did in the past. Probiotics and even fibre, different fibres and again at the end of all, gut is much more than the faeces in terms of microbiome profiles.

Egbert Knol (WP2 partner):
We have seen at least two estimates of 40-50% so If you take more the samples, you get far over 100% it explains. So, if this is true we don't have to go much further, we have quite nice estimates of what is going on…

Jaap van Milgen:
Linking to Mario, using the crossbred performance and information from commercial farms, is it something that you can use, link? From commercial farms in terms of feed efficiency? Is it feasible? Linking it to

intestinal biomarkers, is it possible? Can you link to more fundamental biology? Trying to make the link between crossbred and purebred it is what you see and what you want. You want to have the liveliest mechanism to intervene. We should look more closely at what research we can make on farm, real time, cheap and easy with those mechanisms. We can measure in experimental conditions on which we have some knowledge. Because many indicators we have used this morning are not accessible in a commercial farm. Even a blood sample is difficult to have. Experimental conditions of blood sampling organised in experimental settings with post-prandial curves or whatever you can imagine but take a blood sample in a commercial farm is not that easy. How do we make the link? Is there a link to be made? Or is it 25-50 years from now? Pieter?

Pieter Knap (stakeholder):

It would be better to ask Mario Calus, of course, but you did not!

Mario Calus (WP5 researcher):

I don't know. You need to measure things on individuals. We need to understand why we need to do it as precise as possible, so we want to stay away from commercial farms, for now. But in the future if you want to monitor something you can make pools, some pools per farm and just to monitor how the microbiota evolves over time or something like that and try to link that together. There is a risk that we try to make things too complicated from the start. It's going to be step by step.

Unidentified stakeholder:

But you don't know either…

Another unidentified stakeholder:

As a lot of us…

Unidentified stakeholder:

I think a part of the challenge is really understand what happens in those farms. If we take the example of what the environment is… Is it just a farm, a health status? Is that measurement of different factors? We don't record, we don't report, and we don't analyse. This sounds like a very large complex situation, but I think initially going into individual animal getting a better understanding at that level before you take it out to the commercial farms. Let's say OK, what are those factors, then start coming in the play.

Hélène Gilbert (WP5 leader):

To enlarge it a bit because we have spoken essentially about microbiome. We wanted to know if we had to speak about biomarkers. We have been having talks about metabolomics and transcriptomics. Do we have the same questions about biomarkers? What do we need to do better or more or different so that the molecules that we see associated with something in some of our trials get to have a value for management or selection or whatever? Is it more tools, more trials? Different conditions? Is it the same question as for microbiome and then we can go for lunch?

Lisa Verschuren (WP2 researcher):

I have the feeling that the main part in all these discussions is actually understanding what is going on and how to approach that. This may be experimental design, may be data set increasing but the main thing about metabolomics is, yes, we can measure everything, but do we know what we are looking at? With microbiota do we know what we are looking at? I think understanding what we are looking at is the main part of this discussion, so I think experimental design is necessary to understand the biology and why we have to look at it.

Jaap van Milgen:

Florence, you want to make a remark?

Florence Gondret (WP2 researcher):

If your question is just related to having robust biomarkers, for the traits of interest such as feed efficiency maybe we could have a look at the past years for human medicine where biomarkers were studied for diagnosis of different pathologies and, in fact, it has been successful only with very large sets of subjects to be analysed ... We don't have to understand the mechanisms, just have to find the biomarkers. We have to dissociate research of biomarkers and the understanding of the phenotypes. So, if your question is "Do you need money?" Yes, I need money and time and post-docs to acquire more and more animals and to handle more and more data to release robust biomarkers, but it is quite a different question of research because for that we don't have to understand biological mechanism behind.

Jaap van Milgen:

5 minutes to lunch! Another session this afternoon. We need your feedback. Any specific request?

Pieter Knap (stakeholder):

An hour or half an hour ago, we said that the outcomes of a project like this are 2 things: 1) a proper model which does not exist yet, and 2) a good experimental design to parameterize the model. Suppose that would be the required output of this 5-year program, would you be happy with that? Would it be an acceptable goal in your life to spend 5 years producing a proper experimental design?

Jaap van Milgen:

For me, it would be perfect if we can come up with this question. Even though we have not been able to end up with the question I would be very satisfied.

Hélène Gilbert (WP5 leader):

It depends of the heritability of this trait!

Jaap van Milgen:

Let's come back to precision feeding. What do you think about that? I mean we have certain things we are monitoring continuously. Monitoring is crucial to precision livestock farming (PLF): what are you doing, what do you feed them, will that be a limiting step? How long will it take to take this thing up? What could be the driving factor? Knowing that feed is very costly in pig and poultry production, what would be the driving or the limiting factor? Who wants to share?

Egbert Knol (WP2 partner):

I think that individual feeding of finishing pigs will not be possible. So you would have to do on a pen basis. Sort animals together in a pen and then go for feeding optimum, but that reduces the size of 10-15 or 25. 2 days ago, we had a PLF session here at EAAP. The limiting factor to PLF according to the speaker belonging to the industry is that farmers simply don't want to do it. We have to wait for the next generation of farmers.

Jean-Yves Dourmad (WP4 researcher):

I remember in 1986, I made a presentation on nutrition and I concluded that because of the improvement of performance we would move to a specialized diet for gestating and lactating sows, and most people in the room said it was impossible "this will never occur". About 10-15 years later ago in the West of France when we suggested to move toward finishing diet the answer was the same, but as soon as we considered the effect on N retention in 6 months, most of the farmers moved to this new strategy. It is not often the farmers, but the technicians who stops the changes.

Jaap van Milgen:

Not the economics either?

Jean-Yves Dourmad (WP4 researcher):

And the economics also! Because in some situation you have an increase of costs of investment, but the ROI can be high. I agree that at short term it is not feasible, but at 10-year term, yes, it is.

Jaap van Milgen:

Sometimes people make the comparison with adoption of robots. They have been around for ten years. the adoption has been very slow, but they are coming. It is difficult to predict what make people adopt.

Mark Saltier (stakeholder):

It is difficult to make a financial model. It is almost impossible. There is also an opportunity cost and so does it make more money. If I have million, do I spend it on this or that? In the last months farmers lost money on every pig they produced. The economic is so marginal that it is very difficult to convince to invest a million €. From the feed industry side, we would welcome them, we would be happy to use it, but from the farmers point of view it is not the investment of the moment.

Jaap van Milgen:

Last comment?

Ilias Kyriazakis (WP3 researcher):

Sometimes you have been overtaken by events. Because usual moving to larger units that rely less on less on human intervention, actually the only solution for farmers might be that precision livestock feeding solution. For example, for the cows there is a large number of farmers that rely on automatic oestrus detection. They do not rely on other things.

Jaap van Milgen:

We have to come to an end. We will try to have another session next year in Dubrovnik in common with Saphir.

Demonstration of the decision support system (DSS) for biological modelling, 30 August 2017, Tallinn, Estonia

Hélène Gilbert (WP5 leader):

Masoomeh Taghipoor presented earlier that we can have many perturbations during the growing phase. Then it is possible to parameterize 3 spring-damper in the DSS. How do you think you can use it in a dynamic way? What will we have to feed tomorrow pigs that have suffered from perturbations for few days before?

Masoomeh Taghipoor (WP3 researcher):

For now, as I showed you, we provide data. Our model is based on *a posteriori* analysis of data. But later, we can use this model as a basis in the case of precision feeding to give an idea about how could be the behaviour under these perturbations. But just as a basis we are not going to predict what happens tomorrow.

Juan Pablo Sanchez (WP5 researcher):

What is the format of the file that you are using to feed the program?

Veronika Halas (WP3 leader):

It is written in Delphi so that you can run it easily. In the row data, the basis is only feed intake and body weight. Feed intake on daily basis and body weight not as often

Stakeholder from ILVO:

This is a very nice tool. For which decision is that aimed and who for in terms of end users?

Veronika Halas (WP3 leader):

The target group is nutritionists and farmers to see the results of different scenarios. It might be used by geneticists and also in higher education to demonstrate the principles of animal performance. The goal with that is... I think we can use it for different purposes: we can see what the animal response is if we change the animal profile, what is the response at certain feed composition. I would like to step forward and like to

integrate a function that makes different phases as it is not realistic to have only one diet for the whole growth period. It would be able to predict, or the user can define phases or daily changes in the diet. It is the very beginning: we just want to show how it looks like, what means an interactive interface and we will improve it.

Jaap van Milgen:

The outcomes of many of this work will be published in peer reviews, anyone who is interested in making software will be able to read the publications. The problem with models is that few people actually use models. Who takes the time to rewrite the code? So, we made the decision to provide this tool so that people can understand what has been written. I am very convinced it is the best way to understand what we should write in methodological in mathematical models quite difficult to understand. Models are difficult to understand; the best way is to play with the tool. It is a tool to play to understand also for those people who are about reading the publications: they will see how it feels. I think it is one of the advantages of the DSS. The geneticists will say "I want to make it differently, I need 10000 animals and not 10!". The point is to make publication about modelling a little bit more accessible

Jean-Yves Dourmad (WP4 researcher):

I have a question about the connexion between WP3 and WP4. This modelling approach is to give a model for WP4 to improve the prediction of performance or improve precision feeding. So, until now for WP4 we try to predict the consumption of the pig for the next day and the growth of the pig for the next day according to the pig's own data. We could use other data too, but we don't. Could we use you approach to feed at real-time the parameters of the pigs? You have 5 parameters, is it possible to feed these parameters at real-time? Can we use your model to predict those parameters only from the data of the 10 first days or 20 first days? Do you think it could work?

Masoomeh Taghipoor (WP3 researcher):

The calibration is not a predictive calibration but yes it makes the calibration if we have the dataset. So, the animal performance is defined based on the performance that has been done. But the model simulation that shows you the protein and fat deposition this is the model that we use both of us. Because it is based on InraPorc and we integrate between modules. I think that to predict the profile from an earlier time to further that will be a task for Joao Filipe. So, he can probably do it.

Jean-Yves Dourmad (WP4 researcher):

In all cases you need to have a specific profile for each pig you need to predict your 5 parameters.

Veronika Halas (WP3 leader):

If you have the profile from an earlier data set, then you might adjust it based on the available data, what do you think Joao?

Jaap van Milgen:

If you have only 10 data points, you remain very tricky, 11 would be better. You can do that on real-time probably. I have to think about the procedure to say "now, it's reliable but there may be perturbations that we let start coming on. When do we say if these perturbations are not part of the normal feed intake curve or growth curve? Of course, we only have a small rate of data and if we make smaller it is still feasible but less reliable.

Joao Filipe (WP3 researcher):

For the predictions, the estimates we made from many data depend on the quality of the data. That's why I think that having a distribution gives an idea of the incertitude. If you have very few data points you might have incertitude enough for the actual path of the model to be issued. More data points, more model parameters. I guess what Jaap van Milgen said might be possible, but you might have great uncertainty.

Unidentified stakeholder:

Have you put immune castrates already in your model?

Masoomeh Taghipoor (WP3 researcher):

Not yet… we want to take any perturbation into account. The only thing related to the question of Florence about perturbation who increase feed intake, cumulative feed intake, yes. For now, it is not in the model, but it is possible. With our procedure, we also can take it into account.

Jaap van Milgen:

In that case of immune castration what would be a positive perturbator? What makes animals consume more? Cold stress could be a positive stress, but I cannot think about many others in which animals will increase their cumulative feed intake above and beyond what it would be normally.

Mark Saltier (stakeholder):

From a commercial perspective, from the perspective the model could be used by farmers, and nutritionists have you looked at this around putting financial modelling? Because obviously there are cost implications to increase P Ca and, protein particularly. So actually, if you could put in parts of the model the actual value of the animal or the cost of the weight of the animal at the time where the farmer is intending to sell the animal and also include the cost of the protein and that kind of things then you would really have a chance the farmer gets interested because you could look then and say "as I make, as I change, as I move the protein across , I will increase the value of the product by X but the cost is Y and what is the overall benefit?"

Ourselves in a number of feed companies have looked in precision feeding. There is no doubt of our interest in this product? It is likely that pigs will be fed individually in the long term, but you can make the model, look it and averages it for the pen because feeding the pen is more likely than individual feeding in the next 5-10 years.

Phosphorus model: most of the phosphorus given to the animal is produced by the inclusion of phytase which increases available phosphorus to the diet. If you look at the phosphorus part of the model have you looked for increasing or decreasing phytase as well as putting phosphorus in the diet?

Masoomeh Taghipoor (WP3 researcher)/Veronika Halas (WP3 leader):

The price is a good idea. The farmer should say what is the price of the feed. The phytase: as I told you, there are different modules. In digestion module, the addition of phytase will be integrated. In the metabolic module the digestible nutrients are the input parameter so at the moment in the demo version we fix the digestibility of phosphorus, but that is one of the very important question: if we use or not what is the excretion level and what is needed, which is the optimal unit?

Unidentified stakeholder:

Comment on the financial side. We run very complex financial models for different feedstuffs so that, on nutritionist specifications, they will run the financial models to say which is the best possible cost aligning with the nutritionist recommendations. This sort of model already exists within feed businesses because obviously we are looking at a variety of feedstuffs and at different costs so that cost-benefit can be ran.

Jaap van Milgen:

A last question?

Egbert Knol (WP2 partner):

In the present model can you run 10 000 animals?

Do InraPorc remain to exist?

Jaap van Milgen:

I think Yes.

Egbert Knol (WP2 partner):

I think what you show here helps geneticists to estimate parameters that you need in InraPorc. And one of the major reason that we participate in this project is to get proper estimates which can go into InraPorc. So, I can imagine that there are modules which we develop here which can go into InraPorc. If this go to replace InraPorc, then I have to really, really think how we go to use it.

Jaap van Milgen:

I am not sure we are going to replace InraPorc. InraPorc is not dealing with poultry, this is more demo tool. InraPorc also looks at how nutrients are being utilised by animals. So right now, with InraPorc we do estimates. Ludovic who is there, you have used it with 10 000, is it physical, the same procedure, we use the same agregus, it is very fast, once you have the data on FI, BW you can estimate the parameters and the thing that is newer is that you can have data that are not clean, that are perturbated to some extent. That is something that we can also include.

Unidentified stakeholder:

Perhaps I missed something. I have a question about body composition, description of body composition and protein deposition based on growth precocity, genetics, but how can we associate this model with the case of perturbation where not only nutrient intake will be defined, but also partition of nutrients between lean and fat. Is it in your mind?

Masoomeh Taghipoor (WP3 researcher):

It is a very good question. When we started to take into account perturbations we wondered if we were going to sort with the influence of perturbation on feed intake or in nutrient and energy partition in the animal. As we needed an indicator for the presence of perturbation we said OK let's start with feed intake and if necessary we are going further, and we see how it influences partition of nutrients, but for sure, it also has an impact.

Jaap van Milgen:

OK thank you. If you have further questions, ask Veronika and Masoomeh.

Demonstration of the precision feeding system, 28 April 2017, Lleida, Spain

This demonstration was done at the University of Lleida on 28 April 2017 in front of 20 people. The following text are the minutes of the video that was done during the event. This demonstration was viewed by 329 people on the Feed-a-Gene Youtube channel since this event

Jesus Haro, WP4 partner

My name is Jesus Haro I'm working in Exafan. Exafan and the University of Lerida have designed and developed together intelligent feeders for pigs. Those feeders are used in the Feed-a-Gene project and are part of the Decision Support System to be developed for precision feeding of pigs and poultry. The overall DSS will contain intelligent feeders and other hardware, a controlling module and the core Decision Support Tool (software including database, piloting rules and real-time nutritional model)

This short demonstration is about the feeders. The feeders have a weighing system incorporated at their bottom. When the pigs come to eat, they are weighed and individually identified thanks to their ear tags at the feeder. With the weight of the animal and its identification the feeders release the right food for every animal, so the feeders communicate with the controlling module. The controlling module receives the information from the feeder: the amount of food, the weight, a lot of other information. Moreover, the controlling module can communicate with all the sensors and receive information from the devices like, for example, the climate controller that provides information about temperature, CO_2 values and humidity values, fan speed data.

The controlling module also communicates with another module called the core decision support system that is being developed by another team of the work package 4 in the Feed-a-Gene project together they will integrate a system that will calculate all we need to provide the right food for pigs.