

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





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





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.



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.

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 multiactor, 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)



August 2018 September 2018

Roadmap for

workshops

demonstrations and

Several demonstrations events and workshops are already planned.

Joint stakeholder session Feed-a-





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 realtime characterisation (WP1)

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

Production of novel feed protein from rapeseed and Europeangrown 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 labscale 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)

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.

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.



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



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



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 postdigestive 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.

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)



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 twophase 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.



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)

Soybean meal BR, crushing in France

- Soybean meal BK, crusning in France
- Soybean meal FR partially deoiled, cooking-pressing
- Soybean meal FR partially deoiled, dehulling cooking-pressing



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



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



Better feeds, better animals

This <u>video</u> 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.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) 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) mathilde.lesciellour@inra.fr

In growing pigs fed on low or high fibre diets during 4 x 3-weekperiods, 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) aira-maye.serviento@inra.fr

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 growerfinisher 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

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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



EPC European Poultry Conference

17-21 September 2018, Dubrovnik, Croatia



Feed Additives Global

26-28 September 2018, Amsterdam, Netherlands

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EuroTier 2018

13-16 November 2018, Hanover, Germany



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Pages 1: Hamlet Protein. 2: Gilles Tran (AFZ). 3: Gilles Tran & Valérie Heuzé (AFZ). 4: Valérie Heuzé (AFZ). 5, 6: Gilles Tran (AFZ). 12: Gilles Tran, Valérie Heuzé, Hélène Thiollet (AFZ). 13: Gilles Tran (AFZ). 14: Valérie Heuzé (AFZ), Mathilde Le Sciellour (INRA). 15: Valérie Heuzé (AFZ), Lisanne Verschuren (Topigs Norsvin). 16: Gilles Tran & Valérie Heuzé (AFZ). 17: Valérie Heuzé (AFZ)

Conception and design

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