

# Feed-a-Gene



## Book of abstracts 2016 – 2017

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

Abstracts of scientific articles, communications, posters and book chapters published by Feed-a-Gene researchers up to April 2017

- ▶ Using collective feed intake data to select for feed efficiency on full or restricted feeding regimen
- ▶ Alternative consideration of social genetic effects models in Duroc pigs
- ▶ Unravelling the effects of restricted and *ad libitum* diets on intestinal microbiota in rabbits
- ▶ Mejora de la eficiencia alimentaria de gazapos criados en grupos e interacción entre el genotipo y el régimen alimentario en estas condiciones de alojamiento
- ▶ The quantitative principles of animal growth
- ▶ Conceptual model of digestion for pigs and poultry and its factors of variation
- ▶ Application of models in precision livestock farming
- ▶ Characterization of growing pigs' adaptive response when faced with environmental perturbations
- ▶ Gompertz model improves breeding value prediction for feed conversion ratio for incomplete weights
- ▶ How to improve breeding value prediction for feed conversion ratio in the case of incomplete longitudinal body weights



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

## Feed-a-Gene



Sánchez J.P.<sup>1</sup>, Ramon J.<sup>1</sup>, Rafel, O.<sup>1</sup>, Ragab M.<sup>1,2</sup>, Piles M.<sup>1,\*</sup>

<sup>1</sup>Institut de Recerca i Tecnologia Agroalimentàries, Torre Marimon s/n, 08140, Caldes de Montbui, Barcelona, Spain

<sup>2</sup>Poultry Production Department, Kafer El-Sheikh Univ., Kafer El-Sheikh, 33516, Egypt

\*Corresponding author: miriam.piles@irta.es

### Communication

11th World Rabbit Congress, 15-18 June 2016, Qingdao, China

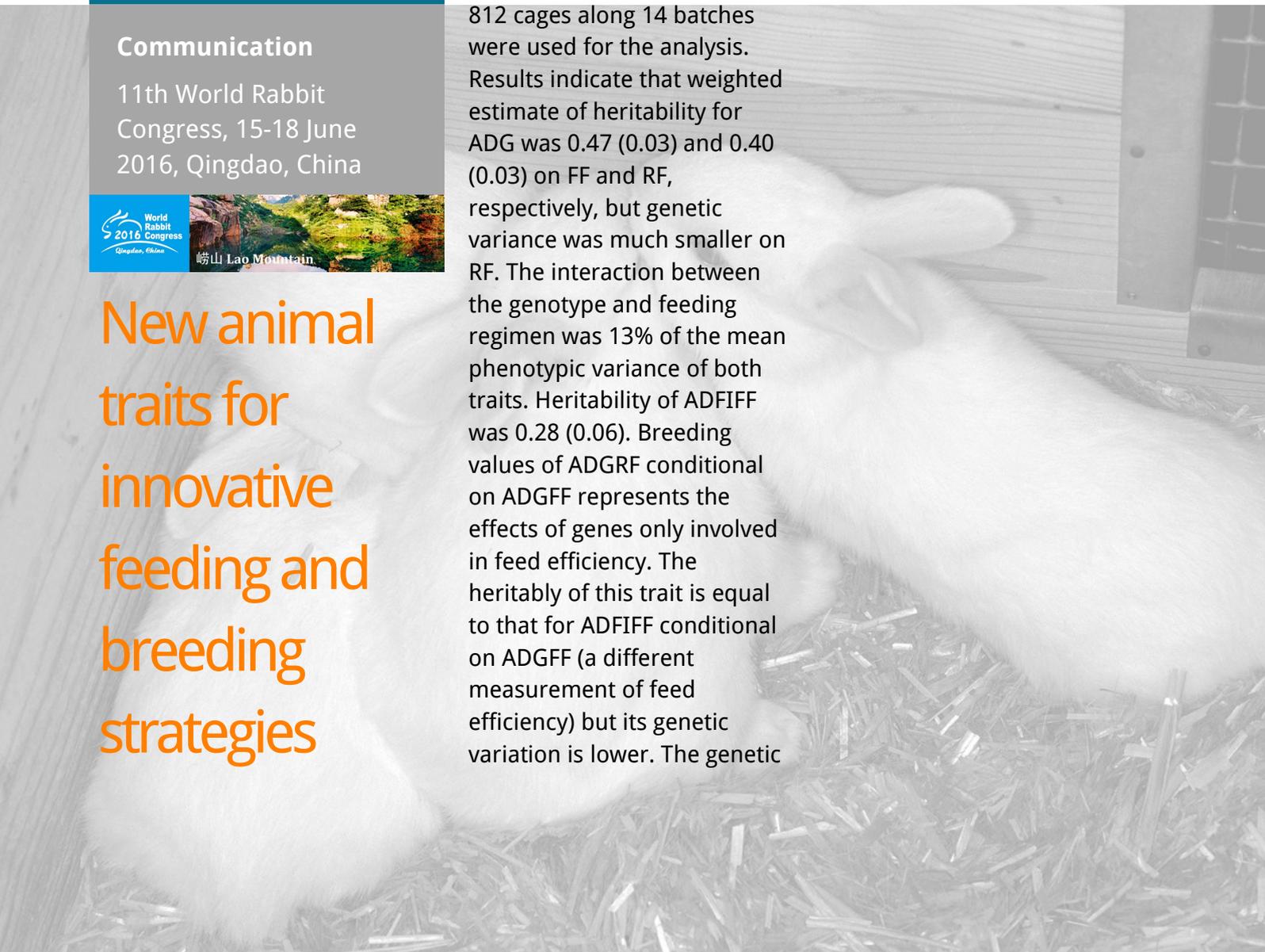


New animal traits for innovative feeding and breeding strategies

## Using collective feed intake data to select for feed efficiency on full or restricted feeding regimen

Variance components of average daily gain (ADG) on both full and restricted feeding regimen (FF and RF), and average daily feed intake (ADFI) on FF of kits raised in collective cages were estimated for each week of the fattening period by using a multiple-trait model analysis. Data from a total of 6,264 kits from 1,317 litters housed in 812 cages along 14 batches were used for the analysis. Results indicate that weighted estimate of heritability for ADG was 0.47 (0.03) and 0.40 (0.03) on FF and RF, respectively, but genetic variance was much smaller on RF. The interaction between the genotype and feeding regimen was 13% of the mean phenotypic variance of both traits. Heritability of ADFIFF was 0.28 (0.06). Breeding values of ADGRF conditional on ADGFF represents the effects of genes only involved in feed efficiency. The heritability of this trait is equal to that for ADFIFF conditional on ADGFF (a different measurement of feed efficiency) but its genetic variation is lower. The genetic

correlation between them was nearly null which indicates that these traits are related to different components of feed efficiency.



# Alternative consideration of social genetic effects models in Duroc pigs



Important statistical difficulties are associated to social interaction models, basically derived from the collinearity between direct and social interaction effects. We present an alternative implementation of these models to alleviate these problems. Bi-weekly average daily gain records (ADG) were recorded on 663 animals between 105 and 182 d of age. The animals were reared in pens with between 10 and 14 mates. Three types of models were fitted: i) repeatability animal model (RAM), ii) repeatability animal model with traditional social interaction effect (RSM) and iii) repeatability animal model with a social interaction effect function of the degree of competition between each pair of mates (RS1M). All the proposed models included the fixed effects of batch, pen size and age, and the interaction between batch and age, and also the random effect of pen. In RS1M pair specific competitions were defined as standardized Euclidean distance between each pair of animals based on two alternative feeding behavior

traits: feeding rate (FR) and time between two consecutive feeding (FT). Estimated total heritability was 0.34 (0.09) and 0.42 (0.17) using RAM and RSM, respectively, under RS1M at the average distance (0) the estimated total heritability was 0.38 (0.09) regardless the behavior trait considered for defining distance. Estimated social interaction heritability for RSM was 0.004 (0.003), this parameter under RS1M reached 0.06 (0.09) when FT was used to define the distance between competitors and the parameter was evaluated at the 3rd quartile of the distance distribution. Using feeding behavior traits to account for variability in the intensity of competition between animals generated parameter estimates with lower errors than the traditional social interaction model, which would be expected to yield higher accuracies in the predictions derived from such models.

Ragab M.<sup>1,2</sup>, Piles M.<sup>1,\*</sup>, Sánchez J.P.<sup>1</sup>

<sup>1</sup>Institut de Recerca i Tecnologia Agroalimentàries, Torre Marimon s/n, 08140, Caldes de Montbui, Barcelona, Spain

<sup>2</sup>Poultry Production Department, Kafer El-Sheikh Univ., Kafer El-Sheikh, 33516, Egypt

\*Corresponding author: miriam.piles@irta.es

## Communication

67th EAAP meeting, 29 August to 2 September 2016, Belfast, United Kingdom



New animal traits for innovative feeding and breeding strategies

## Feed-a-Gene



Velasco M., Viñas M.,  
Piles M. \*, Sánchez J.P.

Institut de Recerca i Tecnologia  
Agroalimentàries, Torre Marimon  
s/n, 08140, Caldes de Montbui,  
Barcelona, Spain

\*Corresponding author:  
miriam.piles@irta.es

### Communication

4th World Congress on  
Targeting Microbiota, 17-  
19 October 2016, Institut  
Pasteur, Paris,  
France



New animal  
traits for  
innovative  
feeding and  
breeding  
strategies

## Unravelling the effects of restricted and *ad libitum* diets on intestinal microbiota in rabbits

**A**iming to assess the effect of restricted and *ad libitum* diets on intestinal microbiota diversity (eubacteria and archaea) in rabbits, a 16S rDNA-based metabarcoding assessment through MiSeq platform was performed. Caecum and faeces samples from 11 adult animals (66-days-old) fed *ad libitum* and 13 fed under restricted (75%) standard diet were assessed. Growth rate was individually recorded and the association between this trait and microbiome compositions was studied as well. Globally, a total of 1823 OTUs without singletons were clustered from 2.195.158 contigs. Taxonomic assignment (Greengenes database gg\_13\_5\_otus) revealed that intestinal microbiota was dominated by Firmicutes (76.3%), followed by Bacteroidetes (7.5%) and Tenericutes (7.5%). No overall differences between diets and faeces-caecum were detected based on Unifrac distances and PCoA analysis. However 7 OTUs were differentially represented between samples of caecum and faeces. It is

noteworthy that 19 OTUs were overrepresented in samples from animals fed *ad libitum*, and 2 (order YS2 (Cyanobacteria)) were overrepresented in animals fed under restriction. OTU richness was positively (pFDR=0.012) associated to daily growth rate. The present study provides evidences of bacterial taxa and microbiome diversity associated to different diets and growth rate in rabbits.

## Mejora de la eficiencia alimentaria de gazapos criados en grupos e interacción entre el genotipo y el régimen alimentario en estas condiciones de alojamiento



**E**n la mayoría de los programas de mejora genética de conejo, la selección directa por eficiencia alimentaria (FE) no se practica debido al elevado coste que supone el registro individual del consumo (FI) implícito en su definición. Una alternativa, propuesta recientemente, es la selección para aumentar la ganancia diaria de peso (ADG) restringiendo el consumo (ADGRF) ya que la variación de este carácter está directamente relacionada con la variación en FE y, al ser constante el consumo, se evita la necesidad de su registro. Este tipo de selección tiene además la ventaja de que se practicaría en las mismas condiciones de producción, ya que la restricción del consumo en el engorde se está generalizando en las granjas de producción de carne de conejo porque reduce la incidencia de enfermedades digestivas que causan una elevada mortalidad. En la actualidad hay dos experimentos de selección en conejo para mejorar la FE de manera directa. Estos utilizan como criterio de selección el incremento en ADGRF y la reducción del consumo de pienso residual (RFI), respectivamente (Drouilhet et al., 2016). En ambos los

animales se alojan en jaulas individuales mientras que, en condiciones comerciales, los gazapos son criados en jaulas colectivas. En estas condiciones, la conducta en la alimentación es diferente debido a las interacciones sociales entre individuos que comparten la jaula, que a su vez afectarían a FI y ADG, especialmente cuando los animales son racionados. Por tanto, en animales en grupo podría existir un efecto de interacción entre el genotipo y el régimen alimentario (GxFR) en la FE, que no se ha observado en animales alojados en jaulas individuales (Drouilhet et al., 2016).

En este trabajo se propone un modelo para el análisis conjunto del crecimiento (ADG; registro individual) y el consumo medio diario (ADFI; promedio del total de la jaula), cuando los datos provienen de gazapos criados en jaulas colectivas tanto en alimentación restringida (RF) como a voluntad (FF). El objetivo es estimar la interacción GxFR y otros parámetros genéticos de diferentes definiciones de la FE que se pueden obtener a partir de componentes de la varianza de los caracteres analizados (Strathe y col., 2014).

Piles M.<sup>1,\*</sup>, Ramon J.<sup>1</sup>,  
Rafel O.<sup>1</sup>, Ragab M.<sup>1,2</sup>,  
Sánchez J.P.<sup>1</sup>

<sup>1</sup>IRTA, Torre Marimon s/n, 08140, Caldes de Montbui, Barcelona, Spain

<sup>2</sup>Poultry Production Department, Kafer El-Sheikh Univ., Kafer El-Sheikh, 33516, Egypt

\*Corresponding author:  
miriam.piles@irta.es

### Poster

XVIII Reunión Nacional de Mejora Genética Animal, 2-3 June 2016, Valencia, Spain

Click on the link below to read the rest of the paper

<http://www.feed-a-gene.eu/node/171>

**New animal  
traits for  
innovative  
feeding and  
breeding**

## Feed-a-Gene



# The quantitative principles of animal growth

Filipe J.A.N.\* , Leinonen I., Kyriazakis I.

Agriculture Building, Newcastle University, Newcastle upon Tyne NE1 7RU, United Kingdom

\*Corresponding author:  
Joao.Filipe@newcastle.ac.uk

### Book chapter

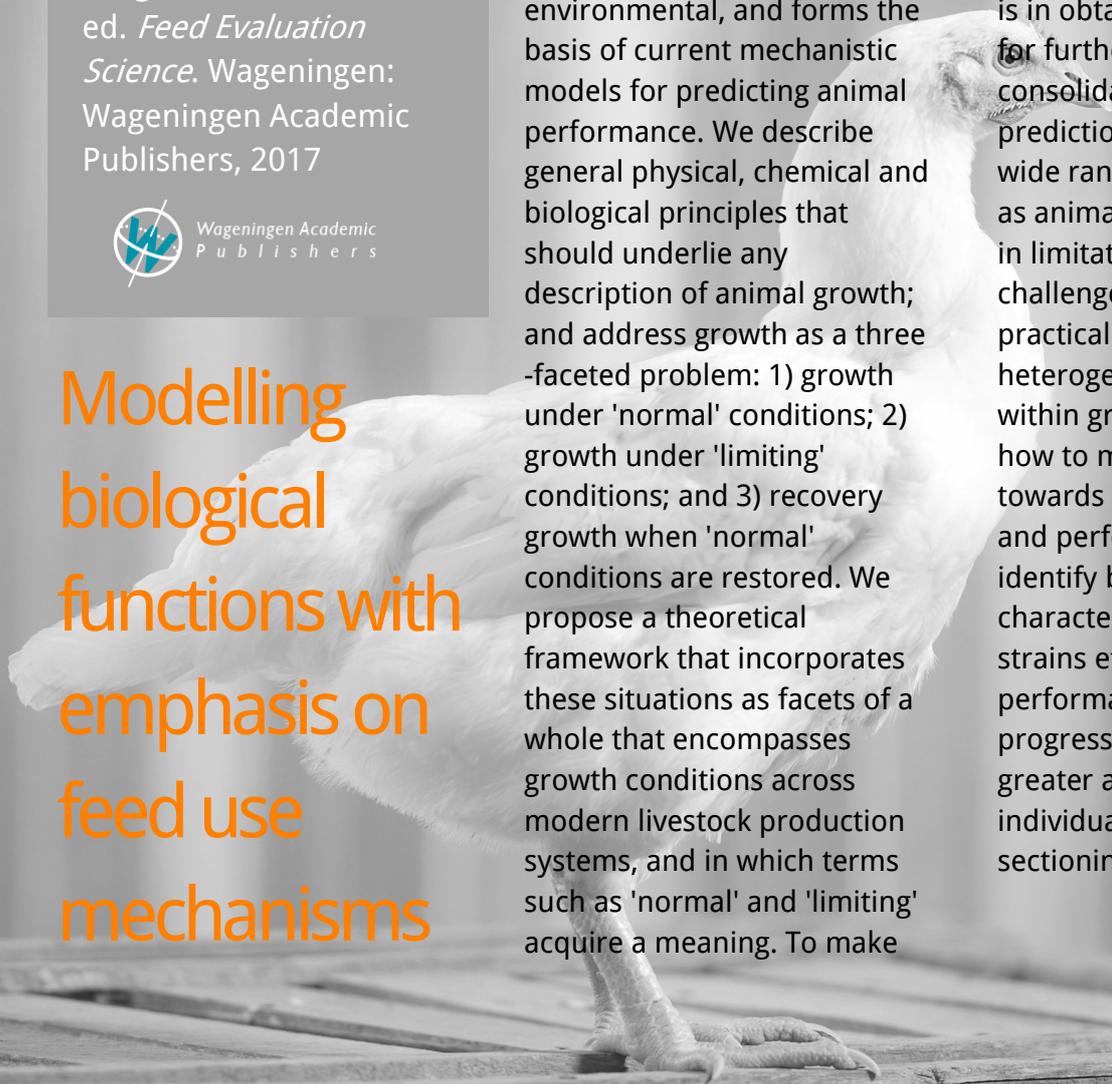
Paul Moughan, Kees de Lange, Wouter Hendriks, ed. *Feed Evaluation Science*. Wageningen: Wageningen Academic Publishers, 2017



Modelling biological functions with emphasis on feed use mechanisms

The principles and a quantitative theory of growth for monogastric livestock animals are described here, focusing on the period from birth to slaughter. The theory helps to understand key relationships between the outcomes that may be desired in a production system and their influencing factors, e.g. nutritional, genetic, and environmental, and forms the basis of current mechanistic models for predicting animal performance. We describe general physical, chemical and biological principles that should underlie any description of animal growth; and address growth as a three-faceted problem: 1) growth under 'normal' conditions; 2) growth under 'limiting' conditions; and 3) recovery growth when 'normal' conditions are restored. We propose a theoretical framework that incorporates these situations as facets of a whole that encompasses growth conditions across modern livestock production systems, and in which terms such as 'normal' and 'limiting' acquire a meaning. To make

this framework quantitative, we apply a body of theoretical and empirical principles in the derivation of mathematical models of growth. The usefulness of existing theories and mathematical models depends on the availability of data for testing hypotheses and parameterising models under a range of conditions. A challenge ahead, therefore, is in obtaining extensive data for further testing and consolidating modelling prediction of growth under a wide range of conditions, or as animals respond to change in limitations. Another challenge lies in addressing practical problems posed by heterogeneity in performance within groups of animals: i.e. how to manage groups towards optimal resource use and performance, and how to identify best phenotypical characteristics within breeds, strains etc. and predict their performance. Further progress will require much greater availability of rich individual data cross-sectioning herds and breeds.



# Conceptual model of digestion for pigs and poultry and its factors of variation



Improving the efficiency of pig and poultry husbandry systems requires a better understanding of nutrient digestion. Mechanistic modelling is a useful tool to identify and quantify the impact of different factors affecting the digestion. Up to now, despite the genericity of physiological processes, models of digestion developed for monogastrics have been species-specific or focused on individual nutrients. In addition, practical nutrition has been mostly based on table values but ignores interactions among nutrients and among nutrients and the animal. The aim of this study was to develop a conceptual model of digestion for pigs and poultry while accounting for different factors of variation (e.g., species, sex, and physiological stage). The digestive tract of the animal is considered as a system where inputs correspond to the ingested nutrients, the compartments are the stomach, the small and large intestine, and outputs are the quantity of absorbed and excreted nutrients. For each compartment, the input and output kinetics were

determined using literature knowledge. Preliminary results suggest that the output of the stomach was represented by a decreasing exponential function. For the small and large intestines, inputs of nutrients depended on outputs of the stomach and the small intestine, respectively, and outputs were formalized with decreasing sigmoid functions. The mathematical formalism is generic but model parameters will be modulated to account for differences related to factors of variation, while factors related to the feed (e.g., composition, technological processes) also need to be considered. This conceptual model is a first step towards the development of a generic predictive tool to determine absorption and excretion of nutrients and to explore how each factor of variation impacts the digestion process and how they interact. This knowledge could contribute to improve the efficiency of animal production and the sustainability of animal production.

Roger S.<sup>1,\*</sup>, Narcy A.<sup>1</sup>, van Milgen J.<sup>2</sup>, Duclos M.J.<sup>1</sup>, Recoules E.<sup>1</sup>

<sup>1</sup>INRA, UR0083, 37380 Nouzilly, France

<sup>2</sup>INRA, UMR1348, 35590 Saint-Gilles, France

\*Corresponding author: [sonia.roger@inra.fr](mailto:sonia.roger@inra.fr)

## Communication

67th EAAP meeting, 29 August to 2 September 2016, Belfast, United Kingdom



Modelling  
biological  
functions with  
emphasis on  
feed use  
mechanisms

Feed-a-Gene



## Application of models in precision livestock farming

Halas V.

Kaposvár University, Kaposvár,  
Guba Sándor u. 40, 7400 Hungary

Corresponding author:  
halas.veronika@ke.hu

### Communication

PREGA 2017 Precíziós  
Gazdálkodás és  
Agrárinformatika, 22  
February 2017, Budapest,  
Hungary



**P**recision livestock farming adopt information technologies to develop a system that improves the efficiency of the food production compared to the classical animal farming systems. The basis of the precision farming is the continuous data collection regarding the environment, the animals, and the feed. The dataset is processed and evaluated by various mathematical models. The presentation is focusing on the nutritional models that are used in precision swine production, and it aims to introduce trends on the directions of model development.

Modelling  
biological  
functions with  
emphasis on  
feed use  
mechanisms



# Characterization of growing pigs' adaptive response when faced with environmental perturbations

Feed-a-Gene



**T**he main objective of this work is to develop a mechanistic model to describe the influence of a generic and unknown perturbation on the feed intake of growing pigs. This latter is considered as a reliable indicator of stress in the environment, its representation by a model is useful to better understand the influence of the stress on the growth kinetics of pigs. Moreover, with novel monitoring technologies, it is now possible to evaluate the impact of these perturbations on animal performance in real time and with a high frequency. The proposed model is based on two sub-models: InraPorc, a model to describe growing pigs' performance in standard conditions, and a well-known model in physics (spring and damper system) to describe the behavior of a system in the presence of external perturbations. Coupling these two models made it possible to represent the influence of environmental perturbations on the feed intake of growing pigs. In this new model, we introduced two parameters to

characterize the response of animals when faced with perturbations. The main interest of this characterization is to define new standards to rank animals based on their performance and on their capacity to recover normal growth after perturbation. The results show that unlike animals with a slow growth, animals with rapid growth are less robust when faced with perturbations and take longer time to regain their standard growth trajectory. Currently, the model is able to simulate the performance of animals facing a given stress; future development of the model will adapt it to the automatic detection and simulation of several perturbations with known or unknown origins.

Taghipoor M. \*,  
Brossard L., van  
Milgen J.

PEGASE, INRA, AgroCampus  
Ouest, 35590 Saint-Gilles, France

\*Corresponding author:  
masoomeh.taghipoor@inra.fr

## Communication

49<sup>èmes</sup> Journées de la  
recherche porcine, 31  
January to 1 February  
2017, Paris, France



Use of traits in  
animal  
selection



## How to improve breeding value prediction for feed conversion ratio in the case of incomplete longitudinal body weights

Tran-Huynh V. H. \*,  
Gilbert H., David I.

UMR INRA / INPT ENSAT / INPT  
ENVT, Génétique, Physiologie et  
Systèmes d'élevage, Chemin de  
Borde Rouge, 31326 Castanet-  
Tolosan, France

\*Corresponding author:  
van-hung.tran@inra.fr

### Scientific article

*Journal of Animal Science*,  
95 (1): 39-48, January 2017

DOI: 10.2527/jas.2016.0980



With the development of automatic self-feeders, repeated measurements of feed intake are becoming easier in an increasing number of species. However, the corresponding BW are not always recorded, and these missing values complicate the longitudinal analysis of the feed conversion ratio (FCR). Our aim was to evaluate the impact of missing BW data on estimations of the genetic parameters of FCR and ways to improve the estimations. On the basis of the missing BW profile in French Large White pigs (male pigs weighed weekly, females and castrated males weighed monthly), we compared 2 different ways of predicting missing BW, 1 using a Gompertz model and 1 using a linear interpolation. For the first part of the study, we used 17,398 weekly records of BW and feed intake recorded over 16 consecutive weeks in 1,222 growing male pigs. We performed a simulation study on this data set to mimic missing BW values according to the pattern of weekly proportions of incomplete BW data in females and castrated males. The FCR was then computed for each week using observed data (obser\_FCR), data with missing BW (miss\_FCR), data with BW predicted using a Gompertz model (Gomp\_FCR), and data with BW predicted by linear interpolation (interp\_FCR). Heritability ( $h^2$ ) was estimated,

and the EBV was predicted for each repeated FCR using a random regression model. In the second part of the study, the full data set (males with their complete BW records, castrated males and females with missing BW) was analyzed using the same methods (miss\_FCR, Gomp\_FCR, and interp\_FCR). Results of the simulation study showed that  $h^2$  were overestimated in the case of missing BW and that predicting BW using a linear interpolation provided a more accurate estimation of  $h^2$  and of EBV than a Gompertz model. Over 100 simulations, the correlation between obser\_EBV and interp\_EBV, Gomp\_EBV, and miss\_EBV was  $0.93 \pm 0.02$ ,  $0.91 \pm 0.01$ , and  $0.79 \pm 0.04$ , respectively. The heritabilities obtained with the full data set were quite similar for miss\_FCR, Gomp\_FCR, and interp\_FCR. In conclusion, when the proportion of missing BW is high, genetic parameters of FCR are not well estimated. In French Large White pigs, in the growing period extending from d 65 to 168, prediction of missing BW using a Gompertz growth model slightly improved the estimations, but the linear interpolation improved the estimation to a greater extent. This result is due to the linear rather than sigmoidal increase in BW over the study period.

Use of traits in  
animal  
selection

## Gompertz model improves breeding value prediction for feed conversion ratio for incomplete weights

**W**ith the development of automatic self-feeders, repeated measurements of feed intake are becoming available in more species. However, corresponding weights are not always recorded which complicate the longitudinal analysis of feed efficiency due to missing values. In our study, male pigs were weekly weighted while females and castrated males were monthly weighted. Our aim is thus to evaluate whether the use of Gompertz model in predicting the missing weights could improve the estimation of breeding values of Feed Conversion Ratio (FCR). For this study, we used 18,387 weekly records of weight and feed intake which were recorded over 18 consecutive weeks for 1,286 male growing pigs. A simulation study was carried out on this dataset to mimic weight missing values according to the pattern of weekly-proportions of incomplete weights observed in females and castrated males. Next, Gompertz model was applied to the data with mimic missing weights and the

estimates were used to predict missing records. Then FCR was computed for each week using observed data (FCRo), data with missing weight (FCRm) and data with predicted weight using the Gompertz model (FCRg). Finally, breeding values for FCRo, FCRg and FCRm (EBVo, EBVg and EBVm, respectively) were estimated using Random regression models. We compared the EBV using Pearson correlation coefficient ( $R^2$ ). Over 100 simulations, the mean of  $R^2$  between EBVo and EBVg was  $0.87 \pm 0.01$  and  $0.84 \pm 0.02$  between EBVo and EBVm. Thus predicting missing weight records using a Gompertz model improved the genetic evaluation of FCR.

### Feed-a-Gene



Tran-Huynh V. H.<sup>\*</sup>,  
Gilbert H., David I.

UMR INRA / INPT ENSAT / INPT  
ENVT, Génétique, Physiologie et  
Systèmes d'élevage, Chemin de  
Borde Rouge, 31326 Castanet-  
Tolosan, France

\*Corresponding author:  
van-hung.tran@inra.fr

#### Communication

67th EAAP meeting, 29  
August to 2 September  
2016, Belfast, United  
Kingdom



Use of traits in  
animal  
selection

# Feed-a-Gene at the 68th EAAP meeting

## Communications

23 communications and posters will be presented by researchers from Feed-a-Gene Consortium partners at the 68th EAAP meeting.

## Feed-a-Gene session

A 1-day session will be dedicated to Feed-a-Gene on 31 August 2017, during which stakeholders will be able to interact with researchers.



28 August – 1 September  
2017

Tallinn, Estonia  
[eaap2017.org](http://eaap2017.org)

## Upcoming events

### 2017 Annual Feed-a-Gene meeting

25-27 April 2017, Lleida, Spain

### XVII Jornadas sobre producción animal

30-31 May 2017, Zaragoza, Spain

### 68th EAAP Annual meeting

28 August - 1 September 2017, Tallinn, Estonia

### 8th European Conference on Precision Livestock Farming (EC-PLF)

12-14 September 2017, Nantes, France

### 11th International Veterinary Behaviour Meeting

14-16 September 2017, Samorin, Slovakia

## Feed-a-Gene Book of abstracts 2016 – 2017

### Photographic credits

Page 1, 2, 8: INRA  
Page 6: Cobb

### Conception and design

Association Française de Zootechnie, April 2017

### Feed-a-Gene project coordinator

Jaap van Milgen  
INRA  
[jaap.vanmilgen@inra.fr](mailto:jaap.vanmilgen@inra.fr)

### Feed-a-Gene project manager

Vincent Troillard  
INRA Transfert  
[vincent.troillard@inra.fr](mailto:vincent.troillard@inra.fr)

[www.feed-a-gene.eu](http://www.feed-a-gene.eu)

