New methodologies to account for repeated measurements, social effects, and variability in performance in genetic evaluations

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FEED-A-GENE

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

Deliverable D5.3

New methodologies to account for repeated measurements, social effects, and variability in performance in genetic evaluations

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1. Summary

Objectives

The general objective of this task was to develop statistical models and procedures as well as new software for selection on feed efficiency and robustness.

Specifically we have worked on three main topics of research:

1. Improvement of models and procedures for selection on feed efficiency taking into account the characteristics and structure of the data
2. Definition of models and procedures to account for indirect genetic (IGE) and environmental effects (i.e., social interaction effects) on growth and feed efficiency
3. Selection for the individual's environmental sensitivity (robustness) and interaction between the genotype and feeding regimen

Rationale

Pig and rabbit data originating from task 5.1 and task 5.2 were used to implement the proposed models and procedures in task 5.3, which were developed following a frequentist or a Bayesian approach. The implementation of the statistical methodologies were developed from existing software and their details are available in the published papers. Models were compared in terms of goodness of fit, predictive ability, and response to selection on real and simulated data. In addition, a freely available software module was developed that allows multiple-trait analyses.

Regarding the first topic of research, we have developed and implemented the structured antedependence model (SAD) for the analysis of longitudinal records of feed conversion ratio (FCR). This model fits the covariance structure of the data with few parameters better than other models and provides unbiased estimates of the correlation between distant measurements of the trait. A selection criterion combining the weekly breeding values using the eigen-decomposition of the genetic covariance matrix was proposed to summarize the individual estimated breeding value (EBV) trajectory into a reduced number of parameters for practical applications to selection. We have also assessed the impact of missing records of body weight on the prediction of breeding values and estimation of genetic parameters of FCR and have proposed a procedure to impute them. The potential of genomic information to improve the accuracy of breeding value predictions for residual feed intake, applying single step genomic approaches to the random regression and SAD models was also assessed. We proposed a procedure to estimate breeding values and genetic and environmental parameters of feed efficiency from group records of feed intake and individual records of body weight gain and metabolic weight at fattening. In this procedure, feed efficiency is defined as a conditional trait derived from elements of genetic and environmental covariance matrices. These measurements of feed efficiency are genetically and phenotypically uncorrelated with production traits. Thus, selection for this trait does not lead to unfavourable correlated responses on production traits.

Models and procedures to account for the genetic and environmental social interaction effects (also known as indirect genetic effects, IGE) on growth and feed efficiency were proposed. A specific degree of interaction between each pair of animals sharing the same pen/cage was defined by the correlation between each pair of pen/cage mates for different feeding behaviour variables obtained from electronic feeder data. This information alleviates collinearity and improves the model performance and led to a more accurate genetic evaluation of traits affected by IGE. We also have investigated how IGEs vary over time implementing a structured antedependence (SAD) model that includes IGEs. We have evaluated, by simulation, the response to selection on longitudinal average daily gain (ADG) using different selection strategies. We have also estimated the effect of the interaction between the genotype and feeding regimen and we have elucidated the origin of such an interaction.

Finally, we have developed a software module for genetic analysis of multiple-traits heteroscedastic models. This software allows to estimate the magnitude of animal genetic sensitivity to express a specific trait in different environments or for different traits. Thus, it allows knowing the genetic determinism of a definition of global robustness as the genetic correlation between the sensitivities of different traits to environmental variations. The software is implemented in ASReml-4.

Teams involved

Institut National de la Recherche Agronomique (INRA – GenPhySE), France

Institut de Recerca i Tecnologia Agroalimentàries (IRTA), Spain

TOPIGS NORSVIN, The Netherlands

Stichting DLO, Wageningen University & Research Centre (DLO), The Netherlands.

Species and production systems considered:

The results of this deliverable can be applied to any farm animal species. Tests and demonstrations were run on pig and rabbit datasets.

2. Introduction

The general objective of this task was to develop and implement models and software for direct selection for feed efficiency and robustness, which take into account the characteristics and structure of the data coming from different species and the existence of several factors generating genetic variability that can be used to improve this important trait.

Specifically, we have worked on the following topics:

1. **Improvement of models and procedures for selection on feed efficiency taking into account the characteristics and structure of the data**

   With the development of electronic feeders, it is possible to individually record feed intake throughout the production period in species such as pigs. This information can lead to more accurate estimates of genetic parameters and breeding values than using single measurements. However, to analyze longitudinal data it is necessary to implement appropriate models with few parameters that account for the covariance structure of the repeated records. A common measurement of feed efficiency is feed conversion ratio (FCR), which corresponds to the ratio of feed intake (FI) to body weight (BW) gain. The analysis of individual patterns of FCR requires the availability of longitudinal records of the two traits. However, these two traits are not usually measured at the same time or with the same frequency. While there are daily records of FI obtained from the electronic feeders, BW is measured weekly or even monthly. Thus, there can be missing records of BW for substantial parts of the growing period. This can have an impact on the estimation of genetic parameters of FCR. In addition, a method for imputation of missing BW that minimizes this impact must be found.

   Electronic feeders are expensive equipment that are not available for all the species hitherto. Measurement of FI at the group level is feasible and cheaper than individual recording but the use of this kind of information for selection requires appropriate models and definitions of feed efficiency.

   With current definitions of feed efficiency such as residual feed intake (RFI), there is no phenotypic correlation between residuals and the explanatory variables representing the animal’s requirements, but this does not guaranty having null genetic correlations. In fact, unfavorable genetic response on growth has been observed after selection for RFI calculated from phenotypic regressions (Gilbert et al., 2007; Cai et al., 2008). To avoid these undesired effects, it is necessary to base the correction of FI not on the phenotypic regression, but on the genetic regression of FI on production traits, as proposed by Kennedy et al. (1993), who defined this as “restricted residual feed intake” (RRFI), because of its equivalence to a restricted selection index in which production traits are held constant. This definition of RRFI guarantees null genetic correlation with performance traits, and thus null correlated responses among them. Implementation of this or of similar definitions of feed efficiency has been previously performed using multiple-trait models for individual records (Strathe et al., 2014; Shirali et al., 2018) but not for records for group-housed animals.

2. **Definition of models and procedures to account for indirect genetic (IGE) and environmental effects (i.e., social interaction effects) on growth and feed efficiency**

Social interaction effects are the effects that an individual has on the phenotype of its group partners and are of both genetic and environmental nature. They can induce positive (cooperation) or negative (aggressive or competition) effects on animal welfare, productivity, and health. Ignoring these effects when selecting traits that might be affected by the interaction between pen mates may lead to negative consequences on the magnitude and sign of response to selection, which depends on the genetic parameters for direct and social genetic effects. Thus, selection for individual performance may lead to strong competition when the covariance between direct and social effects is negative. The response to selection, which is determined by the sign of the covariance between an individual’s phenotypic trait value and its total breeding value, could take the opposite direction of what is desired. This is particularly true for rabbits, when feed restriction is applied during fattening, which is a common practice in production farms to reduce mortality associated to digestive disorders. If animals are housed collectively in cages, as it is the case on commercial rabbit farms, it elicits competition for feed intake between cage mates. The importance of these kinds of effects has been previously evaluated in several species (e.g., pig, quail, and mink) but not in rabbits.

Social interaction effects are also very important in pigs even when they are fed ad libitum. However, estimating those effects is difficult or not possible because of problems derived from collinearity both between direct and indirect genetic effects and between pen effects and indirect genetic effects. It is therefore necessary to find appropriate models to avoid this problem.

The intensity of social interactions between animals may vary with time. For example, several studies recording the behaviour of animals in group-housed conditions have shown that aggressive behaviour is generally stronger at mixing and tends to decrease with time. However, it is necessary to define models to analyse longitudinal records of traits affected by IGE, and to evaluate different selection strategies based on those models in terms of potential response to selection.

Feeding regimen and housing conditions regarding the number of individuals sharing the cage can lead to a genotype by environment interaction on growth and feed efficiency traits due to the impact of indirect genetic effects among cage mates (Bijma, 2011). It is necessary to assess the existence and magnitude of this interaction effect to define adequate selection strategies.

3. **Selection for the animal's individual environmental sensitivity (robustness) and interaction between the genotype and feeding regimen**

Specific and global robustness of animals are both strategic issues for animal breeders. The specific robustness of a particular trait, which can be defined as the genetic ability of animals to perform a homogenous production of this trait under different environmental conditions, can be quantified via statistical models that rely on the hypothesis that the residual or environmental variance of the trait is partially under genetic control (San Cristobal et al., 1998). According to this heteroscedastic model, the genetic component of the residual variance is then interpreted as a genetic sensitivity to the uncontrolled variations of the environment, providing a measure of the specific robustness of the given trait. In contrast, global robustness can be viewed as the ability of an individual to cope with adversities while maintaining its production levels for different traits, as well as a good expression of its functional traits. This global robustness can be assessed by the correlation between the genetic sensitivities of different traits to environmental variations.

Although several methods to estimate the magnitude of animal genetic sensitivity to express a specific trait in different environments have been developed, these methods have never been applied to several traits together, and the existence of a global robustness concept is still questionable. It was necessary to extend and improve the existing models to allow for the analysis of multiple traits. Consequently, the interaction between the genotype and feeding regimen at fattening could be evaluated, and ultimately some direct indicators of robustness in reproductive females and growing animals (i.e., health, mortality and longevity) could be compared.

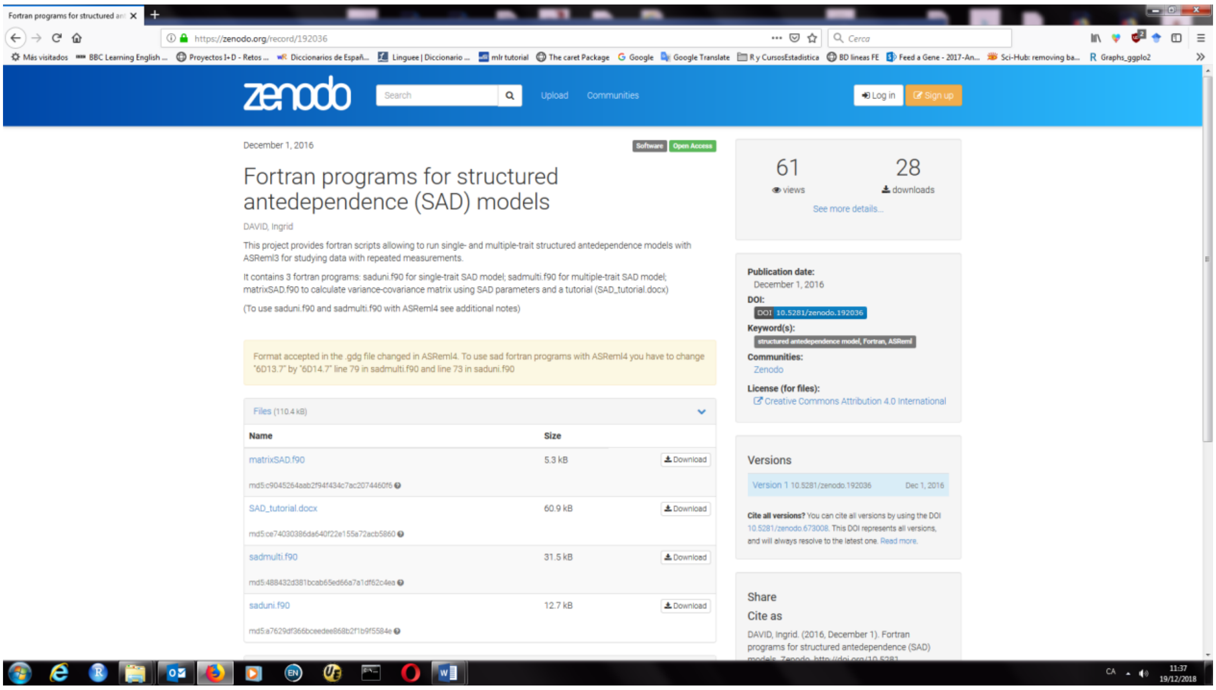
The new statistical methodologies have been implemented in existing software. Details can be found in the published papers. In the following section, we indicate their main overall characteristics.

3. Results

3.1 Results on models to select for feed efficiency taking into account the characteristics and structure of the data

We developed and implemented the structured antedependence model (SAD) for the analysis of longitudinal records of FCR. This model fits the covariance structure of the data better than random regression models, as has been shown by others (Jaffrézic and Pletcher, 2000; Jaffrézic et al., 2004; David et al., 2017), and it requires fewer parameters to fit the covariance matrices than the random regression model. In addition, unlike the random regression models, it provides unbiased estimates of the correlation between distant measurements of the trait. However, it has been less often used in genetic analyses because of the lack of user-friendly software. Therefore, software for the analysis of longitudinal records using a SAD model has been developed by one of the members involved in the task, which is freely available at https://zenodo.org/record/1228058 (Figure 1). It allows the use of multiple-trait SAD models for the analysis of several correlated longitudinal traits such as growth and feed intake.

Figure 1. Access to Fortran programs for structured antedependence (SAD) models



December 1, 2016

Fortran programs for structured antedependence (SAD) models

DAVID, Ingrid

This project provides fortran scripts allowing to run single- and multiple-trait structured antedependence models with ASReml3 for studying data with repeated measurements.

It contains 3 fortran programs: saduni.f90 for single-trait SAD model; sadmulti.f90 for multiple-trait SAD model; matrixSAD.f90 to calculate variance-covariance matrix using SAD parameters and a tutorial (SAD_tutorial.docx)

(To use saduni.f90 and sadmulti.f90 with ASReml4 see additional notes)

Format accepted in the .gdg file changed in ASReml4. To use sad fortran programs with ASReml4 you have to change "6D13.7" by "6D14.7" line 79 in sadmulti.f90 and line 73 in saduni.f90

Files (110.4 kB)

Name	Size
matrixSAD.f90 md5:c9045264aab2f94f434c7ac2074460f6	5.3 kB
SAD_tutorial.docx md5:ce74030386da640f22e155a72acb5860	60.9 kB
sadmulti.f90 md5:488432d381bcab65ed66a7a1df62c4ea	31.5 kB
saduni.f90 md5:a7629df366bceedee868b2f1b9f5584e	12.7 kB

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Publication date: December 1, 2016

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DAVID, Ingrid. (2016, December 1). Fortran programs for structured antedependence (SAD)

Using this software, we evaluated the benefit of using such model for the genetic analysis of longitudinal feed efficiency using data from 2435 growing Large White pigs from a divergent selection experiment for RFI.

We first assessed the impact of missing body weight records on the prediction of breeding values and estimation of genetic parameters for FCR. Then, different approaches were investigated to predict missing weekly BW. For the tested period, a quasi-linear interpolation based on the adjacent weeks was the best approach to deal with missing BW in our dataset, which consolidated the genetic parameter estimations compared to a data structure with missing BW (Huynh-Tran et al., 2017a). In a second step, different longitudinal models, such as random regression models, SAD and character process models were compared. The comparison focused on best-fit to the data criteria (e.g., Loglikelihood, Bayesian Information Criterion), on variance components estimations (e.g., heritability estimates, genetic variances and genetic correlations between weeks), and on the model's predictive ability (i.e., Vonesh concordance coefficients). The results showed that SAD was the most parsimonious model for FCR and RFI. The SAD model also provided similar predictive abilities as the other models. A selection criterion combining the weekly breeding values using the eigen-decomposition of the genetic covariance matrix was proposed to summarize the individual estimated breeding value (EBV) trajectory into a reduced number of parameters for practical applications to selection (Huynh-Tran et al., 2017b). In addition, we evaluated the potential of genomic information to improve the accuracy of breeding value predictions for residual feed intake, applying single step genomic approaches to the random regression and SAD models. In our dataset, prediction accuracies were low and were not improved much by genomic information. Finally, we showed that divergent selection for RFI had a major impact on the FCR and RFI profile trajectories in each line (Huynh-Tran, 2018). In conclusion, the work performed showed that selection for trajectories of feed efficiency is feasible with the current available information.

We also proposed a procedure to estimate breeding values and genetic and environmental parameters of feed efficiency from group records of feed intake and individual records of body weight gain during fattening. In this procedure, feed efficiency is defined as a conditional trait derived from elements of genetic and environmental covariance matrices. Thus, RFI (Koch et al., 1963), i.e., the difference between actual FI and that predicted on the basis of requirements for production and maintenance of body weight, would be defined as feed intake conditioned on growth and metabolic body weight (ADFI | ADG, MBW). Residual growth (Crowley et al., 2010), i.e., the difference between actual growth and that expected on the basis of maintenance energy requirements (determined from the metabolic BW) and actual feed intake, would be defined as growth conditioned on feed intake and metabolic body weight at the genetic and environmental level (ADG | ADFI, MBW). These measurements of feed efficiency are genetically and phenotypically uncorrelated with production traits. Thus, selection for some of these conditional traits does not lead to unfavourable correlated responses on production traits. The procedure has been implemented to estimate the genetic correlation between these measurements of feed efficiency and growth rate of animals on restricted feeding (which is also a measurement of feed efficiency) to know the importance of the interaction effect between the genotype and the feeding regimen on this trait. Results suggest that different genes would be involved in feed efficiency of animals fed ad libitum or restricted.

3.2 Results on models for the analysis of social interaction effects

We have developed and implemented models for the estimation of genetic and environmental parameters of direct and social effects, and estimation of the interaction between the genotype and an environmental factor (the feeding regimen in our case). Results suggest that selection of rabbits for ADG under ad libitum access to feed may completely fail to improve ADG in rabbits that are restrictively fed. This comes from the fact that social genetic effects contribute substantially to estimated total breeding values of rabbits on restricted feeding, but not situations of ad libitum feeding. This result can be seen in the plot of the distribution of the ratio of classical definition of heritability and proportion of total heritable variance relative to phenotypic variance for which the posterior mean is around 1 for ADG on ad libitum feeding and 0.5 on restricted feeding (Figure 2). Also, the genetic correlation between direct and social genetic effects for animals is negative and moderate on restricted feeding but null on ad libitum feeding (Figure 2). Therefore, selection for ADG should be performed under production conditions regarding the feeding regimen, by accounting for IGE if the amount of feed is limited.

Figure 2. Results from Piles et al. (2017)

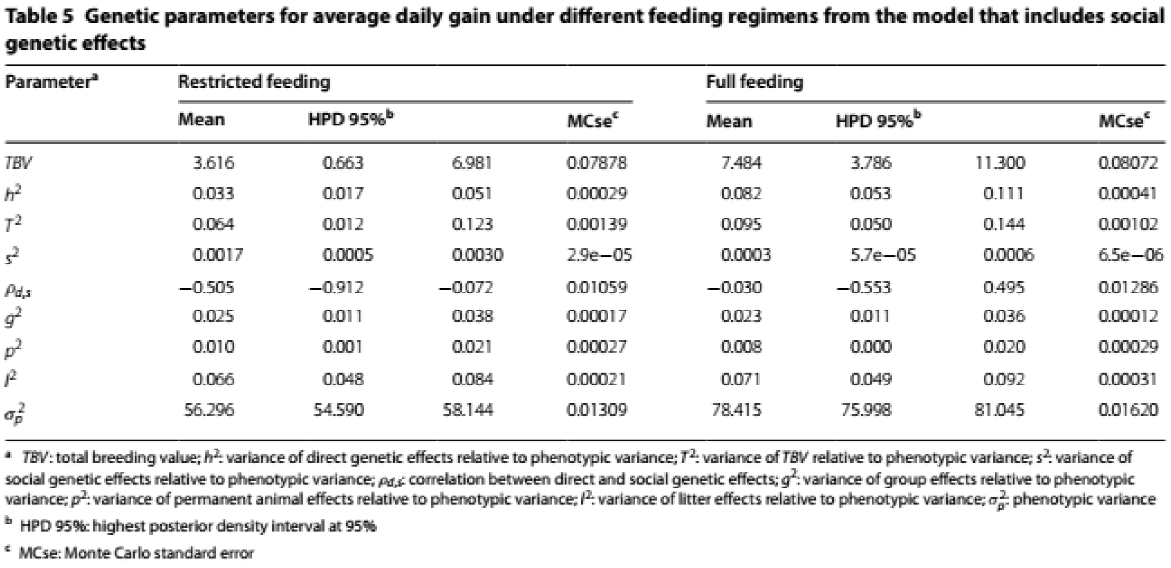

Table 5 Genetic parameters for average daily gain under different feeding regimens from the model that includes social genetic effects

Parameter[a]	Restricted feeding				Full feeding			
	Mean	HPD 95%[b]		MCse[c]	Mean	HPD 95%[b]		MCse[c]
TBV	3.616	0.663	6.981	0.07878	7.484	3.786	11.300	0.08072
h^2	0.033	0.017	0.051	0.00029	0.082	0.053	0.111	0.00041
T^2	0.064	0.012	0.123	0.00139	0.095	0.050	0.144	0.00102
s^2	0.0017	0.0005	0.0030	2.9e−05	0.0003	5.7e−05	0.0006	6.5e−06
$\rho_{d,s}$	−0.505	−0.912	−0.072	0.01059	−0.030	−0.553	0.495	0.01286
g^2	0.025	0.011	0.038	0.00017	0.023	0.011	0.036	0.00012
p^2	0.010	0.001	0.021	0.00027	0.008	0.000	0.020	0.00029
l^2	0.066	0.048	0.084	0.00021	0.071	0.049	0.092	0.00031
σ_p^2	56.296	54.590	58.144	0.01309	78.415	75.998	81.045	0.01620

[a] *TBV*: total breeding value; h^2: variance of direct genetic effects relative to phenotypic variance; T^2: variance of *TBV* relative to phenotypic variance; s^2: variance of social genetic effects relative to phenotypic variance; $\rho_{d,s}$: correlation between direct and social genetic effects; g^2: variance of group effects relative to phenotypic variance; p^2: variance of permanent animal effects relative to phenotypic variance; l^2: variance of litter effects relative to phenotypic variance; σ_p^2: phenotypic variance

[b] HPD 95%: highest posterior density interval at 95%

[c] MCse: Monte Carlo standard error

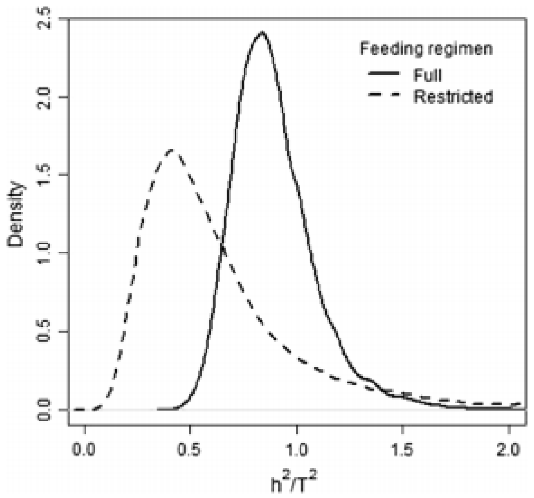

Fig. 2 Marginal posterior distribution for the ratio of classical definition of heritability (h^2) and proportion of total heritable variance relative to phenotypic variance (T^2) of average daily gain of growing rabbits on full (*F*) and restricted (*R*) feeding regimen (Model 2)

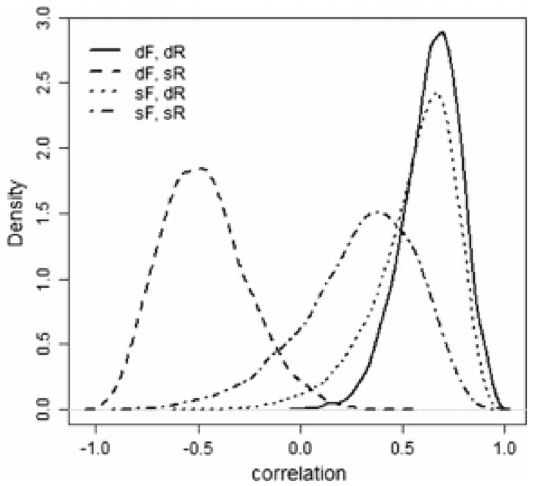

Fig. 3 Marginal posterior distribution of the genetic correlations between direct (*d*) and social (*s*) effects for average daily gain of growing rabbits on full (*F*) or restricted (*R*) feeding regimen

We have also proposed an alternative implementation of the animal models including indirect genetic effects, aiming to alleviate collinearity through the use of feeding behaviour traits, to approach a specific degree of interaction between each pair of pen mates. The feeding behaviour traits of animals housed in groups can be obtained from electronic feeder data (as available in pigs). We have evaluated the use of feeding rate (g/min), feeding frequency (min/d), time between consecutive visits to feeder (min/d), occupation time (min/d), and an index considering all these traits to define a pair-mate specific degree of interaction. Assuming that each individual interacts differently with its mates improved the performance of models fitting indirect genetic effects and led to more accurate genetic evaluation of traits affected by indirect genetic effects, such as growth. This can be seen in the lower deviance information criteria and lower posterior standard deviations of the posterior distributions of genetic parameters obtained from those models compared with those of the classical IGE model (Figure 3).

Figure 3. Results from Ragab et al. (2018)

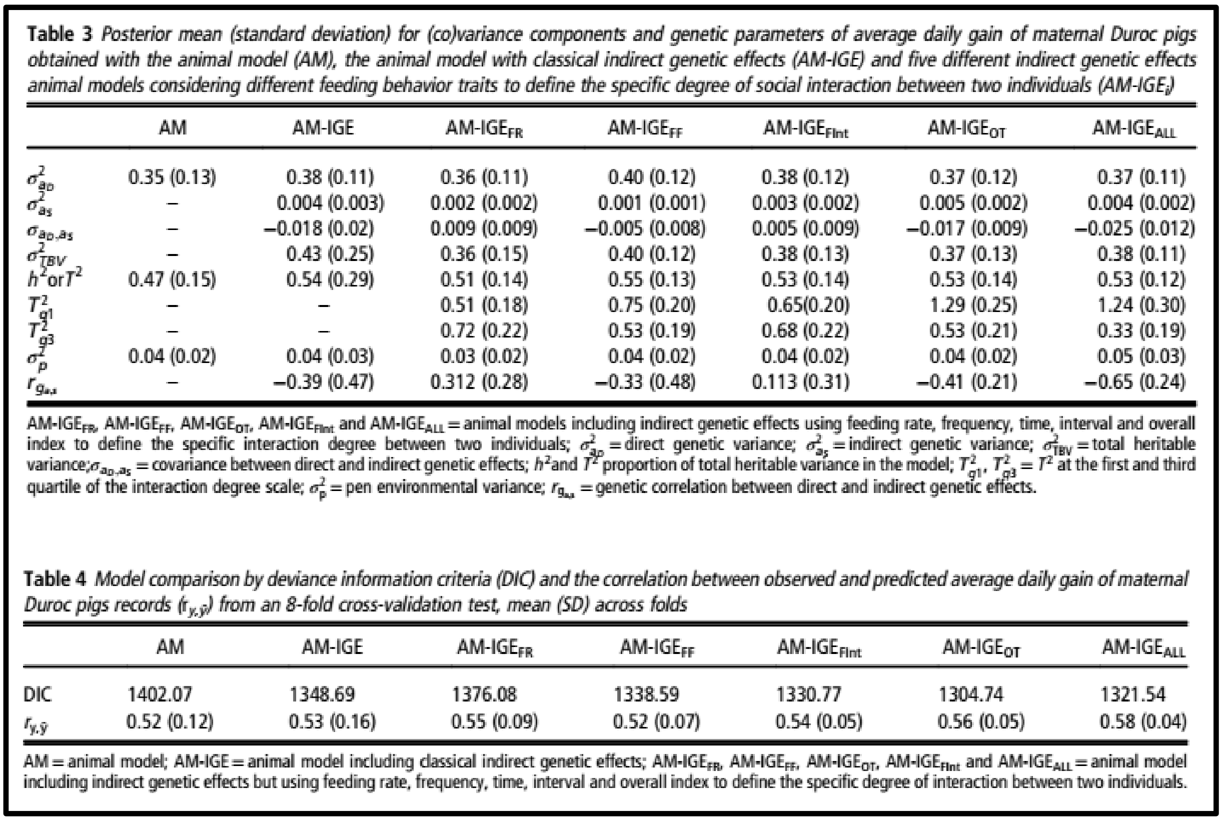

Table 3 *Posterior mean (standard deviation) for (co)variance components and genetic parameters of average daily gain of maternal Duroc pigs obtained with the animal model (AM), the animal model with classical indirect genetic effects (AM-IGE) and five different indirect genetic effects animal models considering different feeding behavior traits to define the specific degree of social interaction between two individuals (AM-IGE$_i$)*

	AM	AM-IGE	AM-IGE$_{FR}$	AM-IGE$_{FF}$	AM-IGE$_{FInt}$	AM-IGE$_{OT}$	AM-IGE$_{ALL}$
$\sigma^2_{a_D}$	0.35 (0.13)	0.38 (0.11)	0.36 (0.11)	0.40 (0.12)	0.38 (0.12)	0.37 (0.12)	0.37 (0.11)
$\sigma^2_{a_S}$	–	0.004 (0.003)	0.002 (0.002)	0.001 (0.001)	0.003 (0.002)	0.005 (0.002)	0.004 (0.002)
σ_{a_D,a_S}	–	−0.018 (0.02)	0.009 (0.009)	−0.005 (0.008)	0.005 (0.009)	−0.017 (0.009)	−0.025 (0.012)
σ^2_{TBV}	–	0.43 (0.25)	0.36 (0.15)	0.40 (0.12)	0.38 (0.13)	0.37 (0.13)	0.38 (0.11)
h^2orT^2	0.47 (0.15)	0.54 (0.29)	0.51 (0.14)	0.55 (0.13)	0.53 (0.14)	0.53 (0.14)	0.53 (0.12)
T^2_{g1}	–	–	0.51 (0.18)	0.75 (0.20)	0.65(0.20)	1.29 (0.25)	1.24 (0.30)
T^2_{g3}	–	–	0.72 (0.22)	0.53 (0.19)	0.68 (0.22)	0.53 (0.21)	0.33 (0.19)
σ^2_p	0.04 (0.02)	0.04 (0.03)	0.03 (0.02)	0.04 (0.02)	0.04 (0.02)	0.04 (0.02)	0.05 (0.03)
$r_{g_{a,s}}$	–	−0.39 (0.47)	0.312 (0.28)	−0.33 (0.48)	0.113 (0.31)	−0.41 (0.21)	−0.65 (0.24)

AM-IGE$_{FR}$, AM-IGE$_{FF}$, AM-IGE$_{OT}$, AM-IGE$_{FInt}$ and AM-IGE$_{ALL}$ = animal models including indirect genetic effects using feeding rate, frequency, time, interval and overall index to define the specific interaction degree between two individuals; $\sigma^2_{a_D}$ = direct genetic variance; $\sigma^2_{a_S}$ = indirect genetic variance; σ^2_{TBV} = total heritable variance;σ_{a_D,a_S} = covariance between direct and indirect genetic effects; $h^2$and T^2 proportion of total heritable variance in the model; T^2_{g1}, T^2_{g3} = T^2 at the first and third quartile of the interaction degree scale; σ^2_p = pen environmental variance; $r_{g_{a,s}}$ = genetic correlation between direct and indirect genetic effects.

Table 4 *Model comparison by deviance information criteria (DIC) and the correlation between observed and predicted average daily gain of maternal Duroc pigs records ($r_{y,\hat{y}}$) from an 8-fold cross-validation test, mean (SD) across folds*

	AM	AM-IGE	AM-IGE$_{FR}$	AM-IGE$_{FF}$	AM-IGE$_{FInt}$	AM-IGE$_{OT}$	AM-IGE$_{ALL}$
DIC	1402.07	1348.69	1376.08	1338.59	1330.77	1304.74	1321.54
$r_{y,\hat{y}}$	0.52 (0.12)	0.53 (0.16)	0.55 (0.09)	0.52 (0.07)	0.54 (0.05)	0.56 (0.05)	0.58 (0.04)

AM = animal model; AM-IGE = animal model including classical indirect genetic effects; AM-IGE$_{FR}$, AM-IGE$_{FF}$, AM-IGE$_{OT}$, AM-IGE$_{FInt}$ and AM-IGE$_{ALL}$ = animal model including indirect genetic effects but using feeding rate, frequency, time, interval and overall index to define the specific degree of interaction between two individuals.

Finally, we also have investigated how IGEs vary over time for traits under selection such as ADG on restricted feeding used to improve feed efficiency in pigs and rabbits. With this aim, we implemented a structured antedependence model that includes IGEs and we evaluated, by simulation, the response to selection on longitudinal ADG using different selection strategies. We have shown that IGE that act on ADG vary over time and that IGE have bigger magnitude during the first week after mixing. In Figure 4 it can be seen that genetic variance of IGE at week 1 was almost double than the corresponding to all other weeks.

Figure 4. Results from David et al. (2018): Genetic parameters

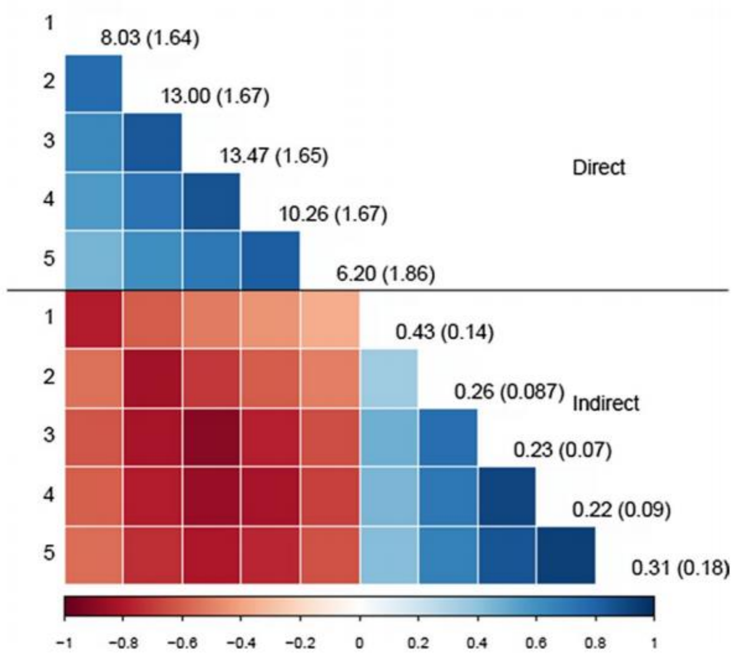

Fig. 4 Estimates of genetic variances for each week (on the diagonal, SE in brackets) and of correlations between weeks and between direct and indirect genetic effects (below the diagonal)

Table 2 Heritability estimates for average daily gain across weeks

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

Combining total estimated breeding values (TEBV) obtained from a SAD model that includes IGE in a selection index would thus be the most effective strategy to improve longitudinal ADG when IGE occur, as can be seen in Figure 5.

Figure 5. Results from David et al. (2018): Response to selection

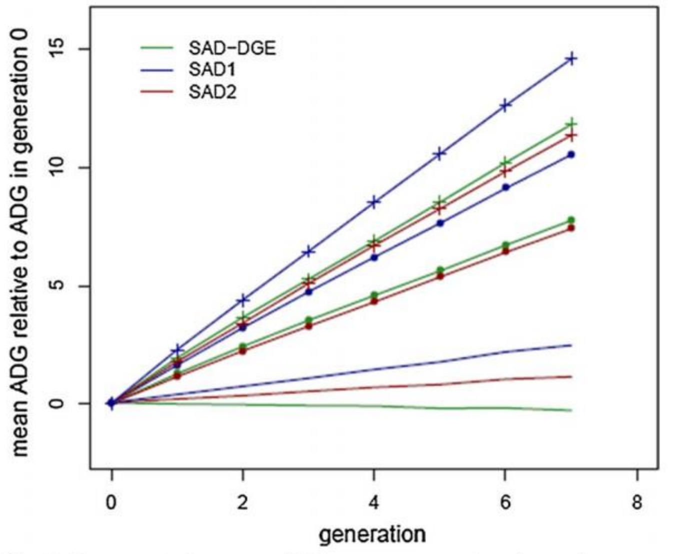

Fig. 5 Changes in the mean ADG across generations for each selection strategy. SAD–DGE-selection criterion: sum of the weekly direct EBV obtained with a SAD model without IGE; SAD1-selection criterion: sum of the weekly TEBV obtained with a SAD model with IGE; SAD2-selection criterion: TEBV of the first week obtained with a SAD model with IGE. Straight line, line with (dot) and line with + represent strong, moderate and weak simulated genetic antagonism between direct and indirect effects, respectively

3.3 Results of the analysis of genetic determinism of environmental variance

We developed a software module for the genetic analysis of bivariate heteroscedastic models. It uses the univariate DHGLM module developed by Felleki et al. (2012), and already implemented in ASReml-4 (Gilmour et al., 2014). It is then possible to jointly estimate the parameters which affect the mean level (location parameter) and the environmental variability (dispersion parameter) of two or more traits, as well as all the cross parameters, such as the genetic correlation between the environmental sensitivities, which provides one measurement of the global robustness.

We applied this module to jointly estimate the genetic parameters for the mean and for the environmental variability of RFI and ADG in Large White pigs using data from a divergent selection experiment for RFI. We found a low negative genetic correlation between the location and dispersion parameters of RFI in these lines. This indicates that the most efficient animals (low RFI) also presented higher genetic sensitivity to micro-environmental variations for that trait. Moreover, an associated significant increase of the environmental variance of RFI was estimated in the LRFI line in response to selection, whereas no clear trend could be identified for the HRFI line, or on ADG for both lines. Finally, we highlighted a low positive genetic correlation between dispersion parameters of RFI and ADG, which suggested that a low global robustness could exist.

The same software was used to study the relationship between genetic parameters of litter size jointly with those of BW in pig and in mice. In contrast with the previous study on RFI and ADG, the data distribution for the litter size was very different to that on BW, but the bivariate DHGLM module can cope with this issue. Most results were similar for both species and, notably, the genetic correlation between the litter size and BW dispersion was low, which comforted the suggestion of the existence of a low but significant global robustness.

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5. Conclusions

New models and procedures for the genetic evaluation of feed efficiency and robustness have been proposed and tested on different datasets. These models take into account the constraints of different livestock species, resulting in specific characteristics and structure of the data regarding the presence of missing values, the correlation between repeated measures of the same trait, and the existence of genetic and environmental effects of cage/pen mates on the individual trait. The estimations obtained showed that the developments give access to breeding values for feed efficiency in cases when they were not available before (group-housed animals), or refined their estimations by accounting for the data structure. Newly developed software or routines in existing software have been developed and made publicly available for the implementation of such models for selection on growth and feed efficiency.

Within the Feed-a-Gene project some of the developments will be further evaluated to provide recommendations for their use in routine evaluation (i.e., user-friendliness and speed of computation are major requirements) or their use to refine the understanding of the genetic architecture of the traits in R&D projects, based on the models properties, and the potential of their optimization. Part of these models are also tested in the project for a practical demonstration of their advantages in rabbits and pigs.

6. Publication list

- Huynh-Tran V.H., Gilbert H., David I. (2017a). Genetic structured antedependence and random regression models applied to the longitudinal feed conversion ratio in growing Large White pigs. Journal of Animal Science 95: 4752-4763.
- Huynh-Tran V.H., Gilbert H., David I. (2017b). How to improve breeding value prediction for feed conversion ratio in the case of incomplete longitudinal body weights. Journal of Animal Science 95:39-48.
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