

Book of Abstracts of the 68th Annual Meeting of the European Federation of Animal Science



**Book of abstracts
No. 23 (2017)**

68th ANNUAL MEETING OF
THE EUROPEAN FEDERATION
OF ANIMAL SCIENCE

28 August – 1 September 2017, Tallinn, Estonia

EAN: 9789086863129
e-EAN: 9789086868599
ISBN: 978-90-8686-312-9
e-ISBN: 978-90-8686-859-9
DOI: 10.3920/978-90-8686-859-9

ISSN 1382-6077

First published, 2017

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The Netherlands, 2017



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

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To explore the role of feeding behavior traits (FBt) and social genetic models for genetic evaluation of both FBt and performance traits (Pt), genetic parameters were estimated for daily gain (DG), daily feed consumption (DC), feed conversion ratio (FCR), backfat thickness (BF), feeding rate (FR), feeding frequency (FF), and occupation time (OT). Traits were recorded in 663 Duroc pigs. Two bivariate models were fitted: animal models (AM) and social interaction animal models (SAM). Estimations were done following Bayesian procedures. Heritability (h^2) estimates obtained with AM for all traits were medium-high, due to additional heritable variation captured by social genetic effects (SGE) higher estimates of the ratio of total genetic variance to phenotypic variance (T^2) were obtained with SAM. Only OT direct genetic effects (DGE) seem to be positively correlated with DGE of DG, DC and BF (0.34(0.14), 0.61(0.18) and 0.38(0.09), respectively), when AM was used the respective genetic correlations were not different from zero. With AM, unfavorable genetic correlation between BF and DG (0.64(0.15)) were estimated. With SAM either SGE or DGE correlations remained high and unfavorable, but the correlation between SGE of DG and DGE of BF was negative (-0.80(0.13)), being null that between SGE of BF and DGE of DG. Large estimation errors of within-trait direct-social genetic correlations prevented to properly define their sign, but they seem to be of low magnitude. The role of FBt to improve Pt genetic evaluations is limited, except for OT. Consideration of SAM allows disentangling the social origin of certain unfavorable AM correlations. SAM could be used to explore indexes combining SGE and DGE of different traits to take advantage of favorable genetic correlations that might exist between them. This study is part of Feed-a-Gene project and received funding from the European Union's H2020 program under grant agreement n° 633531.

Acknowledgements: Unión de Entidades Españolas de Ciencia Animal (UEECA) for attending the 2017 EAAP meeting in Tallinn, Estonia.

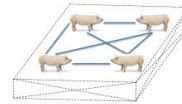
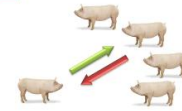
Social genetic effects on productive and feeding behavior traits in growing Duroc pigs

William Herrera, Mohamed Ragab and Juan Pablo Sánchez

INTRODUCTION

Social effects

- ❖ Social interactions among animals
- ❖ Feed efficiency



Animal model with social effects

- Direct Genetic Effect
- Social Genetic Effect

(Gilling, 1967; Muijs, 2005; Bergsma et al., 2008; Bisma, 2010)

INTRODUCTION

Feeding behavior traits

- Feeding rate
- Occupation time to feeder
- Feeding frequency
- Time between consecutive visits



Could be measured with individualized intake systems and is possible to study the feeding behavior of the animals during the fattening period

(Young, 2012; Hoy et al., 2013; Brown Brandt et al., 2013; Morgan et al., 2000; Sari et al., 2015; Greenwood et al., 2016)

OBJECTIVES

To explore alternative selection indexes to improve feed efficiency, either directly or indirectly.

1. Estimate the heritability of productive and feeding behavior traits using animal models and models with social interaction effects.
2. Estimate the genetic correlations between direct genetic effects and social genetic effects for productive and feeding behavior traits and between both groups.

MATERIAL AND METHODS

Database:

	Mean	SD
Start age, days	71.48	7.09
Final age, days	175.3	11.95
Animals/pen	11.9	1.65

2007 **Duroc Line** 2017

- Prolificacy ↑
- Body weight at 180 days of age ↑
- Backfat thickness ↓

Animals	663
Pedigree	5013
Batch	6
Pens	57
Traits	8

Traits	Mean	SD
Average daily gain, ADG (kg)	0.83	0.09
Average daily consumption, ADC (kg)	2.28	0.34
Feed conversion ratio, FCR	2.72	0.23
Backfat thickness, BF (mm)	18.15	5.39
Feeding rate, FR (g/min)	54.45	14.69
Occupation time, OT (min)	63.33	10.49
Feeding frequency, FF (visits)	10.71	3.05
Time between visits, Flnt (h)	3.49	0.98

(Ibañ et al., 1999)

MATERIAL AND METHODS

Models:

- b*: systematic effects (Batch, start age, final age, Number of animals per pen).
- c*: pen random effect, *l*: litter random effect.

1- Animal Model (AM)

$$y = Xb + Z_c c + Z_l l + Z_a a + e$$

a: Additive Genetic Effects (AGE)

$$\text{Var} \begin{bmatrix} a \\ c \\ l \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 & 0 & 0 \\ 0 & I\sigma_c^2 & 0 & 0 \\ 0 & 0 & I\sigma_l^2 & 0 \\ 0 & 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

2- Social Animal Model (SAM)

$$y = Xb + Z_c c + Z_l l + Z_a a_D + Z_s a_S + e$$

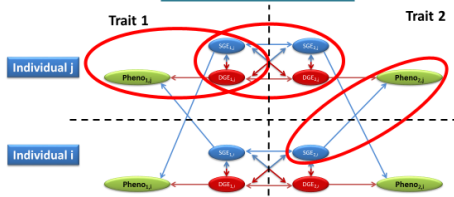
a_D: Direct Genetic Effects (DGE)

a_S: Social Genetic Effects (SGE)

$$\text{Var} \begin{bmatrix} c \\ l \\ a_D \\ a_S \\ e \end{bmatrix} = \begin{bmatrix} I\sigma_c^2 & 0 & 0 & 0 & 0 \\ 0 & I\sigma_l^2 & 0 & 0 & 0 \\ 0 & 0 & A\sigma_{a_D}^2 & A\sigma_{a_D a_S} & 0 \\ 0 & 0 & A\sigma_{a_D a_S} & A\sigma_{a_S}^2 & 0 \\ 0 & 0 & 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

(Bisma, 2005)

MATERIAL AND METHODS



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

MATERIAL AND METHODS

Social Animal Model (SAM)

Total breeding value of an individual

$$TBV_i = a_{D_i} + (n-1)a_{S_i}$$

$$r^2 = \frac{\sigma_{TBV}^2}{\sigma_P^2} \neq AM \Rightarrow h^2 = \frac{\sigma_a^2}{\sigma_P^2}$$

Total breeding variance

$$\sigma_{TBV}^2 = \sigma_{a_D}^2 + 2(n-1)\sigma_{a_D a_S} + (n-1)^2 \sigma_{a_S}^2$$

(σ_{a_D} : Direct genetic variance, σ_{a_S} : Social genetic variance, $\sigma_{a_D a_S}$: Direct-social genetic covariance.)

Phenotypic value of an individual

$$P_i = a_i + \sum_{j=1}^n s_j + e_i$$

(σ_l^2 : Litter variance, σ_c^2 : Pen variance, σ_e^2 : Residual variance, r : Relationship coefficient (0.13))

Total phenotypic variance

$$\sigma_P^2 = \sigma_{a_D}^2 + (n-1)\sigma_{a_S}^2 + 2 * r * (n-1)\sigma_{a_D a_S} + r * (n-1) * (n-2)\sigma_{a_S}^2 + \sigma_l^2 + \sigma_c^2 + \sigma_e^2$$

(Bergsma et al., 2008; Duijvestijn et al., 2012)

MATERIAL AND METHODS

Statistical analysis:

Bayesian procedures

- Characterization of the marginal posterior distributions of the parameters of interest with MCMC.

Gibbs Sampling Algorithm:

Software gibbs290 (Miszta et al., 2002):

- Chain: 1.000.000
- Burn-in: 300.000
- 1 sample / 10 iterations

ADG, ADC, FCR, BF, FR, OT, Flnt FF.

AM - SAM

- Univariate analyses
- Bivariate analyses

- DIC criterion (Spiegelhalter et al., 2002).

RESULTS

Heritabilities of the productive and feeding behavior traits

Traits	AM	SAM		DIC diff.
	h^2	$T^2 = \sigma_{TBV}^2 / \sigma_P^2$	$cor(\sigma_{a_D})$	
Average daily gain, ADG	0.08(0.07)	0.36(0.26)	-0.23(0.67)	15.7
Average daily consumption, ADC	0.17(0.11)	0.66(0.40)	0.14(0.63)	21.61
Feed conversion ratio, FCR	0.15(0.09)	1.12(0.53)	0.52(0.48)	11.42
Backfat thickness, BF	0.27(0.14)	0.60(0.32)	0.15(0.59)	34.29
Feeding rate, FR	0.40(0.10)	0.73(0.30)	0.19(0.53)	11.7
Occupation time, OT	0.29(0.12)	0.30(0.24)	-0.80(0.26)*	33.2
Feeding frequency, FF	0.38(0.11)	1.26(0.57)	0.14(0.50)	29.3
Interval time between visits, Flnt	0.36(0.10)	0.44(0.31)	-0.51(0.43)	33.0

RESULTS

Genetic correlations among productive traits

AM				[DGE of SAM]				
	ADC	BF	FCR	ADG	ADC	BF	FCR	
ADG	0.85(0.24)*	0.49(0.51)	0.40(0.54)	0.83(0.12)*	0.22(0.36)	0.07(0.35)		
ADC		0.69(0.36)	0.82(0.23)*	0.81(0.16)*	0.63(0.22)*	0.69(0.21)*		
BF			0.73(0.31)*	0.67(0.24)*	0.82(0.15)*	0.48(0.26)		
				0.37(0.32)	0.94(0.05)*	0.31(0.36)		

[SGE of SAM]					
	DGE_ADG	DGE_ADC	DGE_BF	DGE_FCR	
SGE_ADG	0.22(0.42)	0.13(0.4)	0.39(0.37)		
SGE_ADC	-0.16(0.4)	-0.19(0.38)	0.41(0.35)		
SGE_BF	-0.07(0.44)	-0.48(0.3)	-0.59(0.24)*		
SGE_FCR	-0.65(0.23)*	0.04(0.4)	0.01(0.37)		

DGE: Direct genetic effect; SGE: Social genetic effect; ADG: Average daily gain; ADC: Average daily consumption; BF: Backfat thickness; FCR: Feed conversion ratio; *Probability of being greater than 0.05 or <0.05.

RESULTS

Genetic correlations between productive and feeding behavior traits:

AM	Production BV – Behavior BV	→	✗
	Production DGE – Behavior DGE	→	✗
SAM	Production SGE – Behavior SGE	→	FCR – FF -0.83(0.13)
	Production DGE – Behavior SGE	→	DGE_ADG – SGE_FR -0.61(0.29)
	Production SGE – Behavior DGE	→	✗

CONCLUSIONS

- SGE play an important role in most of productive and feeding behavior traits.
- The genetic relationships between production traits considering AM are similar to those for both DGE and SGE in the SAM.
- Selection indexes combining SGE and DGE could allow to jointly act on traits for which unfavorable relationships exist under traditional AM.
- Only SGE of some behavior traits are correlated with genetic components of production traits. But, in general, the relationships between behavior and production traits are weak.

ACKNOWLEDGMENTS

Thanks to CAP people from IRTA and Selección Batallé enterprise. This project was financed by Feed-a-Gene (H2020) and RTA2014-00015-C2-01 projects. Data generated by RTA2011-00064-00-00 project were used.



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

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Abstract

To explore the role of feeding behavior traits (FBt) and social genetic models for genetic evaluation of both FBt and performance traits (Pt), genetic parameters were estimated for daily gain (ADG), daily feed consumption (ADC), feed conversion ratio (FCR), backfat thickness (BF), feeding rate (FR), feeding frequency (FF), and occupation time (OT). Traits were recorded in 663 Duroc pigs. Two bivariate models were fitted: animal models (AM) and social interaction animal models (SAM). Estimations were done following Bayesian procedures. Heritability (h^2) estimates obtained with AM for all traits were medium-high, due to additional heritable variation captured by social genetic effects (SGE) higher estimates of the ratio of total genetic variance to phenotypic variance (T^2) were obtained with SAM. Anything correlation was observed between FBt and Pt with SAM, the errors were high for all studied traits, when AM was used the respective genetic correlations were not different from zero. With AM, genetic correlation between BF and FCR (0.73(0.31)) were estimated. With SAM between SGE and DGE correlations remained negative and favorable in order to reduce BF (-0.59(0.24)), but the correlation between DGE of ADG and SGE of FCR was negative (-0.65(0.23)), being favorable to increase ADG. Large estimation errors of within-trait direct-social genetic correlations prevented to properly define their sign, but they seem to be of low magnitude. The role of FBt to improve Pt genetic evaluations is limited. Consideration of SAM allows disentangling the social origin of certain unfavorable AM correlations. SAM could be used to explore indexes combining SGE and DGE of different traits to take advantage of favorable genetic correlations that might exist between them.

Introduction

Animal breeding programs in pigs is difficult when they are bred sharing a pen as usually happens in swine. The interaction between each animal can influence on productive traits of pen mates and genetic evaluations in the same way. To solve this problem, social interaction models have been proposed to allow estimation of genetic parameters with higher accuracy but result is unsafe (Muir, 2005; Bergsma et al., 2008). On the other hand, the feeding behavior traits collected with individual control systems intake allow study traits related to alimentary efficiency (Eissen et al., 1998; Chen et al., 2007; Young, 2012). These two groups of traits are not usually used together in genetic evaluations, so the objective of this study is to use both groups of traits to know if they could increase accuracy of genetic evaluations in swine when these are raised in groups. This study proposes two different models for determinate if feeding behavior traits offers relevant information for improves accuracy genetic evaluations moreover correlations between genetic effects including social interactions were also estimated.

Materials and Methods

The experimental procedures were approved by the ethical committee of the IRTA institution (Institut de Recerca I Tecnologia Agroalimentaries).

Field Data: Using Duroc pigs come from the company Batalle, that was reproductively closed since 1991 (Tibau et al., 1999). From its foundation until 2007 the line was selected using index including Weight at off test, approximately 180 days, (BW180), Backfat thickness (BF180), Intramuscular fat (IMF), number born alive (NBA) and number of functional teats (NT). The IVOG feeders collected the information (Table 1) shows the description of the necessary data for this study.

Table 1 Data structure and description of population

Duroc line pigs

663

Pedigree	5013
Batch	6
Pens	57
Initial age of the test, days	71,48 ± 7,09
Final age of the test, days	175,3 ± 11,95
ADG, kg	0,83 ± 0,09
ADC, kg	2,28 ± 0,34
FCR	2,72 ± 0,23
BF, mm	18,15 ± 5,39
FR, g/min	54,45 ± 14,69
OT, min/day	63,33 ± 10,49
FF, visits/day	10,71 ± 3,05
FInt, h/day	3,49 ± 0,98

ADG: average daily gain, ADC: average daily consumption, FCR: feed conversion ratio, BF: backfat thickness, FR: feeding rate, OT: Occupation time, FF: feeding frequency, FInt: time between consecutive visits.

Feeding Behavior Traits: Behavior traits from databases generated by consumption control system were calculated. This system generates daily data collected by periods of one hour for each animal keeping the number of visits, time spent eating to feeder, consumption and feeding rate. With time spent to feeder, the average daily time between each visit to feeder (FInt) was calculated. With these tables, the average daily hourly was calculated during the test period for each animal and finally were summed or averaged the 24 hours depending on the variable considered. Feeding rate (FR) and average daily time between each visit to feeder (FInt) were calculated as the daily average of 24 hours of the day. Total time spent eating per day (OT) and numbers of visits to feeder per day (FF) as the sum of 24 hours of the day were calculated (table 1).

Production Traits: Productive traits from the databases generated by the consumption control system were calculated. Average daily gain (ADG) by linear regression of body weight on age was calculated, where were available from 4 to 10 weight measurements per animal during the fattening. Average daily consumption (ADC) was calculated by dividing the kilograms of feed consumed during the fattening on the days of the growth period. Feed conversion ratio (FCR) by dividing ADC on ADG was calculated. The millimeters of Backfat thickness with ultrasonic procedure was measured (PIGLOG 105 SFK-Technology) at the growth period end (table 1).

Model of Analysis: Two models, with the same systematic effects (batch number (6 levels), initial age (covariate), final age (covariate) and number of piglets per pen (covariate)), were compared to estimate genetic parameters for production and behavior traits (table 1). The models were:

Animal Model (AM)

$$y = Xb + Z_g g + Z_l l + Z_a a + e,$$

where y is a vector of observations; X is incidence matrix of systematic effects which presented in vector b ; g is the vector of random pen effects with the incidence matrix Z_g relating data to pen effects; l is the vector of random litter effects with the incidence matrix Z_l relating data to litter effects; Z_a is the incidence matrix linking additive genetic effects to data, a is vector of additive genetic effects and e is the vector of residuals. The assumed (co)variance structure between the different random effects in the model was as follows: $var [a] = A\sigma_a^2$; $var [g] = I\sigma_p^2$; $var [l] = I\sigma_l^2$ and $var [e] = I\sigma_e^2$, where A is the additive relationship matrix, I is the identity matrix, σ_a^2 is the additive genetic variance, σ_p^2 is pen effects variance, σ_l^2 is litter effects variance and σ_e^2 is the error variance. Random factors were assumed independent among them. In AM model the $h^2 = \frac{\sigma_a^2}{\sigma_p^2}$, where σ_p^2 is the phenotypic variance and $\sigma_p^2 = \sigma_a^2 + \sigma_g^2 + \sigma_l^2 + \sigma_e^2$.

Social Animal Model (SAM)

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}_g\mathbf{g} + \mathbf{Z}_l\mathbf{l} + \mathbf{Z}_a\mathbf{a}_D + \mathbf{Z}_s\mathbf{a}_S + \mathbf{e},$$

where, \mathbf{y} , \mathbf{X} , \mathbf{b} , \mathbf{Z}_g , \mathbf{Z}_l , \mathbf{g} , \mathbf{l} and \mathbf{e} as defined previously in AM. \mathbf{a}_D is a vector of direct genetic effect (DGE), with incidence matrix \mathbf{Z}_a relating observed data of individual to their direct breeding value; \mathbf{a}_S is the vector of social genetic effects (SGE) and \mathbf{Z}_s is the incidence matrix linking the observed data to the associative breeding values of their group members. With this model, it is assumed that the animals sharing the same pen interact equally between them (Muir, 2005; Cantet and Cappa, 2008; Chen et al., 2008) and elements of \mathbf{Z}_s are 1 for each animal sharing the same pen and 0 if is not sharing. Random factors were assumed to be independent among them except between direct genetic effects and social genetic effects and the (co)variance between them

is $\begin{bmatrix} \mathbf{a}_D \\ \mathbf{a}_S \end{bmatrix} = \mathbf{G}\mathbf{A}$, where \otimes indicates the Kronecker product $\mathbf{G} = \begin{bmatrix} \sigma_{a_D}^2 & \sigma_{a_D, a_S} \\ \sigma_{a_D, a_S} & \sigma_{a_S}^2 \end{bmatrix}$, and where $\sigma_{a_D}^2$

is the direct genetic variance; σ_{a_D, a_S} is the covariance between direct and social genetic effects and $\sigma_{a_S}^2$ is the social genetic effect. Under SAM model each individual interact with $n-1$ of its group members where n is the size of the group, the total breeding value of an individual i (TBV_i) = $a_{Di} + (n-1)a_{Si}$. The total breeding values variation among individuals (σ_{TBV}^2) = $\sigma_{a_D}^2 + 2(n-1)\sigma_{a_D, a_S} + (n-1)^2\sigma_{a_S}^2$. The total heritable variance (T^2) is equal to $T^2 = \frac{\sigma_{TBV}^2}{\sigma_p^2}$ which may exceed one, where the total phenotypic variation is $\sigma_p^2 = \sigma_{a_D}^2 + (n-1)\sigma_{a_S}^2 + 2 * r * (n-1)\sigma_{a_D, a_S} + r * (n-1)(n-2)\sigma_{a_S}^2 + \sigma_g^2 + \sigma_l^2 + \sigma_e^2$ (Duijvesteijn et al., 2012), where, r is the coefficient of familiar relationship between group members of the same pen.

These models using Bayesian resolved by techniques and procedures MCMC marginal posterior distributions of the parameters of interest were characterized. Marginal statistical distributions unknown values were obtained by Gibbs Sampling algorithm using the software gibbsf90 (Misztal et al., 2002). Chains for these analyzes were run samples 1,000,000 discarding the first 300,000 iterations and keeping one sample for each 10 iterations in order to avoid high correlations between consecutive samples. The Deviance Information Criterion (DIC) was used to know the quality of fit of different models for explaining the obtained data (Spiegelhalter et al., 2002).

Results and Discussions

Table 2 shows the estimates of heritability presented for production and behavior traits using univariate models. For AM it can be seen that the estimates of the heritability are smaller for production than feeding behavior traits. The sign and magnitude of correlations between direct and social genetic effects in other studies (Bergsma et al, 2008; Chen et al, 2009; Bouwman et al, 2010; Hsu et al, 2010) were very variable as happens in our case, mistakes are always very important. Another study similar the ratios of the total genetic variation to phenotypic variance (T^2) for ADC and ADG traits were obtained (Bergsma et al., 2008). For Chen et al. (2009), ADG trait T^2 value above 1 were obtained, as in our case for FCR and FF traits, this indicates that the population of Chen et al. (2009), the social effects play about ADG a more important role than ours and that of Bergsma et al. (2008). Other studies (Hall, 1997; Young, 2012) corroborate the results obtained in our population for FR, OT and FF traits. SAM has an extra genetic component, the social genetic effect, correlated with the direct genetic effect into model was higher for all studied traits except for OT whose T^2 was lower than rest of traits due to higher and negative direct-social correlation. The heritability ratios among both models were different, but the ratio of the total genetic variation to phenotypic variance (T^2) does show very different values than heritability from AM, this is due on one hand to the social genetic variation effect and on the other hand to the correlation between direct and social genetic effects. The DIC shows a reduction which SAM than AM for all studied traits; this demonstrates the importance of social genetics effects. SAM model is not usually used in previous studies for feeding behavior traits.

Table 2 Heritabilities of the production and feeding behavior traits

Traits	AM h^2	SAM T^2	Cor (DGE-SGE)	Dif. DIC
Average daily gain, ADG	0.08(0.08)	0.36(0.26)	-0.23(0.67)	15.7
Average daily consumption, ADC	0.17(0.11)	0.66(0.40)	0.14(0.63)	21.61
Feed conversion ratio, FCR	0.15(0.09)	1.12(0.53)	0.52(0.48)	11.42
Backfat thickness, BF	0.27(0.14)	0.60(0.32)	0.15(0.59)	34.29
Feeding rate, FR	0.40(0.1)	0.73(0.30)	0.19(0.53)	11.73
Occupation time, OT	0.29(0.12)	0.30(0.24)	-0.8(0.26)*	33.19
Feeding frequency, FF	0.38(0.11)	1.26(0.57)	0.14(0.50)	29.26
Time between visits, FInt	0.36(0.10)	0.44(0.31)	-0.51(0.43)	33.01

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

Genetic correlations: The sign and magnitude of correlations between direct genetic effects of production traits with SAM (above diagonal table 3) are similar to those offered for additive effects obtained with AM. However of direct genetic effects shows slight decrease in magnitude of correlations obtained with AM. The sign and magnitude of correlations between social genetic effects with SAM (below diagonal Table 3) show generally similar to direct genetic correlations (SAM).

Table 3 Genetic correlations between productive traits using AM, correlations between direct genetic effects (Above diagonal) and correlations between social genetic effects (Below diagonal) between productive traits using SAM

	Animal Model			ADG	Social Animal Model		
	ADC	BF	FCR		ADC	BF	FCR
ADG	0.85(0.24)*	0.49(0.51)	0.40(0.54)		0.83(0.12)*	0.22(0.36)	0.07(0.35)
ADC		0.69(0.36)	0.82(0.23)*	0.81(0.16)*		0.63(0.22)*	0.69(0.2)*
BF			0.73(0.31)*	0.67(0.24)*	0.82(0.15)*		0.48(0.26)
FCR				0.37(0.32)	0.94(0.05)*	0.31(0.36)	

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

Correlations between direct and social genetic effects between production traits (Table 4) reflect association between the effects of the genes of an individual to a certain trait that influence it themselves for a trait and the effects of their genes in other traits of its pen mates. The negative correlation between direct genetic effect ADG and social genetic effect FCR (-0.65) indicates that those animals with favorable genes to increase their ADG have genes that reduce the ADC of its pen mates. Equivalently estimated between social genetic effect BF and direct genetic effect FCR was negative (-0.59). This implies that individuals with favorable genes to decrease their own FCR will also have favorable genes to increase BF of its pen mates.

Table 4 Genetic correlations between DGE and SGE between productive traits using SAM

	DGE_ADG	DGE_ADC	DGE_BF	DGE_FCR
SGE_ADG		0.22(0.42)	0.13(0.4)	0.39(0.37)
SGE_ADC	-0.16(0.4)		-0.19(0.38)	0.41(0.35)
SGE_BF	-0.07(0.44)	-0.48(0.3)		-0.59(0.24)*
SGE_FCR	-0.65(0.23)*	0.04(0.4)	0.01(0.37)	

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

The consideration of social effects on models favorable correlations between components of traits may appear to be complex initially their joint consideration in selection. With the correlations of SAM between both effects, opens the possibility to propose new selection indexes where could have more importance to components correlated favorably.

Conclusions: The social genetic effect play an important role in most of production and feeding behavior traits and could be used to explore indexes combining social and direct genetic effects of the production traits to take advantage of favorable genetic correlations that might exist between them. Selection indexes combining social and direct genetic effects of social animal model could allow to jointly act on traits for which unfavorable relationships exist under traditional animal model. On the other hand, the relationships between behavior and production traits were weak.

Acknowledgments: Unión de Entidades Españolas de Ciencia Animal (UEECA) for attending the 2017 EAAP meeting in Tallinn, Estonia.

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