

INVESTIGATING NOVEL TRAITS IN SINGLE TRAIT SELECTION FOR THEIR POTENTIAL IN SELECTION INDEXES FOR FEED EFFICIENCY OF CROSSED PIGS

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SUMMARY

Here we considered selection on a single trait only, assuming a selection differential of one genetic standard deviation, to determine which novel traits to include in a multi-trait selection index for feed efficiency in crossbred pigs. The mean feed conversion ratio (FCR) is 2.52 (kg/kg), and a decrease of 5.56%, was observed if selection was based on FCR itself. Selection on other traits also reduced FCR but with a lower response: average daily gain (-2.9%), dry matter digestibility (-1.2%), nitrogen excreted (-0.40%), daily feed intake (-0.37%), group daily feed intake (-0.35%), eating time per day (-0.04%), and growth rate with social effect (-0.01%). Selection for the welfare traits increased FCR: joint lesions (0.2%), and total lesion count (0.06%). Further analysis will include additional traits and use selection index theory with multi-trait selection to determine an optimal selection index for feed efficiency.

INTRODUCTION

Selection for feed efficiency is of high importance for livestock species as it has direct effects on economic factors, reduces water and land requirements, and decreases greenhouse gas footprints (Hayes *et al.* 2013). There is a desire within the pig industry to improve the rate of genetic gain for feed efficiency of crossbred commercial animals, which requires an optimised selection index (Feed-a-Gene 2015). The main objective of this study was to identify indicator traits that make a promising contribution to such an index.

MATERIALS AND METHODS

Feed efficiency is defined as average daily gain (ADG) / daily feed intake (DFI). However, it is standard practice in pig breeding programs to select for a lower feed conversion ratio (FCR), where $FCR = DFI / ADG$. Because one is the reciprocal of the other, we assumed a genetic correlation of one between feed efficiency and FCR. Reported responses to selection are in terms of relative change to the across breed literature mean of 2.52 (kg/kg) (Mrode and Kennedy 1993; Cameron and Curran 1994; Labroue *et al.* 1997; Hoque and Suzuki 2008; Bates and Maechler 2010; Do *et al.* 2013; Saintilan *et al.* 2013; Gilbert *et al.* 2017).

Based on discussions with industry stakeholders we compiled a list of key traits. Production traits currently used in crossbred breeding programs included: FCR, ADG, and DFI. As a preliminary analysis a small number of traits from the list were selected as a representative of broader trait categories. These novel traits included: digestibility of dry matter (DIG), time spent eating per day (BEH), group daily feed intake (GFI), average daily gain with a social effect (GADG) which was selected as an indirect genetic effect (IGE), and nitrogen excreted (BIO). Two traits were selected as indicators of animal welfare including: joint lesions (JOINT) and total skin lesion count (WELF), where the latter represents impaired welfare inflicted by pen mates.

We reviewed the literature for parameter estimates of the indicator traits. Preference was given

to estimates from sources that used crossbreds, had large numbers of progeny with phenotypic information and estimates with smaller standard errors. To determine which traits are likely to benefit the selection of improved feed efficiency, the correlated response to selection in FCR was evaluated for one indicator trait at a time.

For the analysis, genetic standard deviations and genetic correlations with FCR were required (Table 1). For most sources, the genetic variances or the heritability and the phenotypic variance were published, which were then converted to genetic standard deviations ($\sigma_G = \sigma_p * h$). There are no published estimates of genetic standard deviation for digestibility of dry matter, however, the authors of Ouweltjes *et al.* (2018) provided us with unpublished estimates of heritability which we used to estimate a genetic standard deviation.

Table 1. Genetic standard deviations (σ_G), genetic correlation with FCR, and summary of references used in the analysis

Trait	σ_G	Genetic correlation with FCR	σ_G references	Genetic correlation references
FCR	0.14	1.00	(Do <i>et al.</i> 2013)	
ADG	0.07	-0.44	(Do <i>et al.</i> 2013)	(Saintilan <i>et al.</i> 2013)
DFI	0.63	0.36	(Do <i>et al.</i> 2013)	(Saintilan <i>et al.</i> 2013)
DIG	0.41	-0.65	(Ouweltjes <i>et al.</i> 2018)	From broilers (Mignon-Grasteau <i>et al.</i> 2004)
BEH	3.35	0.17	(Do <i>et al.</i> 2013)	(Do <i>et al.</i> 2013)
GFI	0.17	0.12	(Canario <i>et al.</i> 2017; Sánchez <i>et al.</i> 2018)	(Peeters <i>et al.</i> 2013)
GADG	27.94	0.10	(Bergsma <i>et al.</i> 2008; Canario <i>et al.</i> , 2017)	(Canario <i>et al.</i> 2017)
BIO	0.23	0.16	(Saintilan <i>et al.</i> 2013)	(Saintilan <i>et al.</i> 2013)
JOINT	0.16	-0.09	(Luther <i>et al.</i> 2007)	(Luther <i>et al.</i> 2007)
WELF	0.34	-0.08	(Turner <i>et al.</i> 2006)	(Turner <i>et al.</i> 2006)

The response to selection for FCR was calculated as $\mathbf{R} = \mathbf{b}'\mathbf{G}/\sigma_I$, where \mathbf{b} is a vector of weights for each trait, \mathbf{G} is a covariance matrix calculated as a function of the genetic correlations and genetic standard deviations, and σ_I is the standard deviation of the index. As we were only interested in the change of a single trait this could be reduced to $\sigma_{I,R}/\sigma_I = r_{I,R} * \sigma_R$, where I is the indicator trait and R the response trait. The analysis was repeated for each of the traits, with the full weight placed on a single trait each time.

RESULTS AND DISCUSSION

The results showed that selecting for production traits had the largest impact on feed efficiency when included in a selection index (Table 2). Feed conversion ratio decreased (-5.6% relative to the literature mean), from 2.52 (kg/kg) to 2.38 (kg/kg), when 100% of selection was placed on FCR. Other traits reduced FCR in the following descending order: average daily gain (-2.9%), dry matter digestibility (-1.2%), nitrogen excreted (-0.4%), daily feed intake (-0.37%), group daily feed intake (-0.35%), eating time per day (-0.1%), and growth rate with social effect (-0.01%). Selection for joint lesions or total lesion count had the undesirable effect of increasing FCR (0.3% and 0.1%, response to FCR respectively).

Breeding Program Design

Table 2. Response in feed conversion ratio due to a change of one genetic standard deviation (σ_G) in the selected trait

Trait	FCR (kg/kg) with one σ_G change in selected trait	Relative phenotypic change in FCR with one σ_G change in selected trait
Feed conversion ratio (FCR)	2.380 (Originally 2.520)	-5.56%
Average daily gain (ADG)	2.447	-2.90%
Daily feed intake (DFI)	2.511	-0.37%
Dry matter digestibility (DIG)	2.490	-1.20%
Eating time per day (BEH)	2.519	-0.04%
Group daily feed intake (GFI)	2.511	-0.35%
Growth rate with social effect (GADG)	2.520	-0.01%
Nitrogen excreted (BIO)	2.510	-0.40%
Joint lesions (JOINT)	2.525	0.20%
Total lesion count (WELF)	2.522	0.06%

We were interested in the traits that have the largest reduction in FCR and would therefore significantly contribute to a selection index. It is not surprising that the largest improvement to FCR occurred with direct selection, or that selecting for the component traits (ADG and DFI) also resulted in a significant response in FCR. As selection for dry matter digestibility had a reasonable impact on the response to selection for FCR, other digestibility traits such as energy or organic matter digestibility should be investigated further. If faeces are collected to include digestibility, it would be beneficial to also include nitrogen excreted. Unfortunately, there was limited research available on blood biomarkers but these could be worth exploring if they have similar genetic correlations as faecal biomarkers.

The traits that had limited impact on the response to selection of FCR, could still be beneficial. Selection for eating time per day had a limited impact on FCR, but feeding behaviour traits such as time per meal, and number of meals per day, have higher genetic correlations with FCR, have higher heritabilities, but have less accurate parameter estimates (Do *et al.* 2013). Group daily feed intake appears to be a good indicator of individual daily feed intake and had a similar benefit to the selection response of FCR. It is not logically or economically possible to record DFI on crossbred pigs, but GFI would be much easier and cheaper to record, this would benefit a selection index for crossbred feed efficiency. Including an IGE with GADG appears to have limited benefit to selection for FCR but could be important for defining the ADG model used in animal evaluations. The low negative genetic correlation between the welfare traits is unfavourable. However, to address consumer concerns it is important they are added to future selection indexes to limit any negative trends.

For future analysis a genetic covariance matrix will be required, which is to be built with estimates available in the literature. Currently a data set is being analysed which will complete the missing variance components, genetic correlations between traits, and genetic correlations between purebred and crossbred pigs, which Wientjes and Calus (2017) showed to not be equal to one. When the parameter estimation is complete, an optimised multi-trait selection index for feed efficiency in crossbred pigs will be built, and will be based on selection index theory (Hazel 1943). This study used a limited number of traits, future work will include additional traits related to digestibility, i.e. eating behaviour, group records, welfare, biomarkers, perturbations (Putz *et al.* 2018), and microbiota

(Camarinha-Silva *et al.* 2017). Finally, the potential for selection based on variation, heritability, and ease of phenotyping will also be considered.

CONCLUSIONS

The objective of this study was to determine which indicator traits are likely to have a significant contribution to an optimised selection index for feed efficiency in crossbred pigs. From these results production traits are the most promising, but novel traits such as digestibility, group records, and biomarkers could also increase the rate of genetic gain. Before such an index is built genetic correlations between novel traits and FCR need to be estimated.

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REFERENCES

- Bates D. and Maechler, M. (2010) *R*
- Bergsma R., Kanis E., Knol E.F. and Bijma P. (2008) *Genetics* **178**: 1559.
- Camarinha-Silva A., Maushammer, M., Wellmann, R., Vital, M., Preuss, S. and Bennewitz, J. (2017) *Genetics* **206**: 1637.
- Cameron N.D. and Curran M.K. (1994) *Anim. Sci.* **59**: 281.
- Canario L., Lundehheim N. and Bijma P. (2017) *Heredity* **118**: 534.
- Do D.N., Strathe A.B., Jensen J., Mark T. and Kadarmideen H.N. (2013) *J. Anim. Sci.* **91**: 4069.
- Feed-a-Gene. (2015) 'WP5 Use of traits in animal selection (Genetic parameter estimations, genetic model developments & evaluation of breeding schemes).' Available at <https://www.feed-a-gene.eu> [Accessed 10/04/2019].
- Gilbert H., Billon Y., Brossard L., Faure J., Gatellier P., Gondret F., Labussière E., Lebret B., Lefaucheur L. and Le Floch N. (2017) *Animal* **11**: 1427.
- Hayes B.J., Lewin H.A. and Goddard M.E. (2013) *Trends. Genet.* **29**: 206.
- Hazel L.N. (1943) *Genetics* **28**: 476.
- Hoque M.A. and Suzuki K. (2008) *Anim. Sci. J.* **79**: 543.
- Labroue F., Guéblez R. and Sellier P. (1997) *Genet. Sel. Evol.* **29**: 4510.
- Luther H., Schwörer D. and Hofer A. (2007) *Animal* **1**: 1105.
- Mignon-Grasteau S., Muley N., Bastianelli D., Gomez J., Péron A., Sellier N., Millet N., Besnard J., Hallouis J.-M. and Carre B. (2004) *Poultry Sci.* **83**: 860.
- Mrode R. and Kennedy B. (1993) *Anim. Sci.* **56**: 225.
- Ouweltjes W., Verschuren L., Pijlman J., Bergsma R., Schokker D., Knol E., van der Aar P., Molist F. and Calus M. (2018) *Livest. Sci.* **207**: 63.
- Peeters K., Ellen E.D. and Bijma, P. (2013) *Genet. Sel. Evol.* **45**: 27.
- Putz A.M., Harding J.C., Dyck M.K., Fortin F., Plastow G.S., Dekkers J.C. and Canada, P. (2018) *Front. Gent.* **9**
- Saintilan R., Merour I., Brossard L., Tribout T., Dourmad J.-Y., Sellier P., Bidanel J., Van Milgen J. and Gilbert H. (2013) *J. Anim. Sci.* **91**: 2542.
- Sánchez J.P., Piles M., Tulsá M., Reixach J. and Quintanilla R. (2018) *WCGALP* **10**: 574.
- Turner S., White I., Brotherstone S., Farnworth M., Knap P., Penny P., Mendel M. and Lawrence A. (2006) *Anim. Sci.* **82**: 615.
- Wientjes Y. and Calus M. (2017) *J. Anim. Sci.* **95**: 3467.