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# Robustness scores in fattening pigs based on routinely collected phenotypes: determination and genetic parameters

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## Abstract

The objective was to determine operational proxies for robustness based on data collected routinely on farm that allow phenotyping of these traits in fattening pigs, and to estimate their genetic parameters. A total of 7,256 pigs, from two Piétrain paternal lines (Pie and Pie NN), were tested at the AXIOM boar testing station (Azay-sur-Indre, France) from 2019 to 2021. During the fattening period (from 75 to 150 d of age), individual performance indicators were recorded (growth, backfat, loin depth, feed intake, and feed conversion ratio [**FCR**]) together with indicators such as insufficient growth, observable defect, symptoms of diseases, and antibiotic and anti-inflammatory injections. These indicators were combined into three categorical robustness scores: R1, R2, and R3. Genetic parameters were estimated using an animal linear model. The robustness score R2 (selectable or not selectable animal) that combined information from status at testing and mortality had the highest heritability estimates of 0.08 ± 0.03 for Pie NN line and a value of 0.09 ± 0.02 for Pie line, compared with traits R1 and R3. The score R3 that combines information from the score R2 with antibiotic and anti-inflammatory injections presented slightly lower heritability estimates (0.05 ± 0.02 to 0.07 ± 0.03). Genetic correlations between R2 and R3 were high and favorable (0.93 ± 0.04 to 0.95 ± 0.03) and R2 and R3 can be considered identical with regard to the confidence interval. These two robustness scores were also highly and favorably genetically correlated with initial body weight and average daily gain, and unfavorably correlated with daily feed intake (ranging from 0.73 ± 0.06 to 0.90 ± 0.08). Estimates of genetic correlations of R2 and R3 with backfat depth and raw FCR (not standardized between starting and finishing weights) were moderate and unfavorable (0.20 ± 0.13 to 0.46 ± 0.20). A part of these genetic correlations, that are of low precision due to the number of data available, have to be confirmed on larger datasets. The results showed the interest of using routine phenotypes collected on farm to build simple robustness indicators that can be applied in breeding.

## Lay Summary

The objective was to determine operational proxies for robustness based on data collected routinely on farm that allow phenotyping of these traits in fattening pigs (from approximately 75 to 150 d of age), and to estimate their genetic parameters. A total of 7,256 pigs, from two Piétrain paternal lines (Pie and Pie NN), were tested. Individual performance indicators were recorded together with indicators such as insufficient growth, observable defects, symptoms of diseases, and antibiotic and anti-inflammatory injections. These indicators were combined into three categorical robustness scores: R1, R2, and R3. The robustness score R2 (selectable or not selectable animal) that combined information from status at testing and mortality had the highest heritability of 0.08 ± 0.03 for Pie NN line and a value of 0.09 ± 0.02 for Pie line. This robustness score was also highly and favorably genetically correlated with initial body weight and average daily gain, and unfavorably correlated with daily feed intake in both lines (ranging from 0.73 ± 0.06 to 0.90 ± 0.08). Estimates of genetic correlations of R2 with backfat depth and feed conversion ratio were moderate and unfavorable (0.20 ± 0.13 to 0.46 ± 0.20). The results showed the interest of using routine phenotypes collected on farm to build simple robustness indicators that can be applied in breeding.

**Key words:** genetic parameters, pig, robustness

**Abbreviations:** ABC, area between curves;ADG, average daily growth;AFS, automatic feeding system;AMW, average metabolic weight;BF, backfat thickness;BF100, backfat thickness estimated at 100 kg live weight;BW, body weight;DFI, daily feed intake;FCR, feed conversion ratio;FI, feed intake;IBW, initial body weight;LD, longissimus dorsi thickness;LD100, longissimus dorsi thickness estimated at 100 kg live weight;PDFI, potential average daily feed intake;Pie, Piétrain Français;Pie NN, Piétrain NN Français free from halothane-sensitivity;RFI, residual feed intake;TBW, body weight at individual testing

## Introduction

In Europe, livestock farming faces new challenges related to a rapidly changing economic, societal, and environmental context. Societal pressure to "eat healthier" is changing the way pigs are raised and, in particular, leads to a decrease in the use of antibiotics. In France, for example, the level of exposure of pigs to antimicrobials (ALEA) decreased by 41% from 2012 to 2016 (Hémonic et al., 2019). In this context, there will be a greater reliance on the innate robustness of farmed animals. The more general context of global warming implies an increase in the frequency of extreme events, such as heatwaves or droughts (Hansen et al., 2012)

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having direct (temperature) and indirect impacts (availability of raw materials for feed production) on animals' rearing environments. All these challenges require having animals able to adapt to these new conditions, which implies an improvement of robustness while maintaining a high level of production. In parallel, improving animal robustness meets the economic expectations of the operators, especially by increasing the viability and reducing treatment costs (Phocas et al., 2016).

There is no real consensus on the definition of robustness as well as on the ways to phenotype it. It is not the aim of the present study to add to the list of definitions but rather to evaluate potential proxies of robustness. Nevertheless, our approach is informed by the definition of robustness adapted to the context of artificial selection of Knap (2005). He defined robustness as "the ability to combine a high production potential with resilience to stressors, allowing for unproblematic expression of a high production potential in a wide variety of environmental conditions." Generally, the production potential is associated with a phenotype of interest, such as growth, feed conversion ratio (**FCR**), etc.

Today, traits included in breeding goals that may be associated with robustness are mainly related to the health status of animals, including resistance to diseases and mortality during a specific period, or to the longevity of reproductive animals (Knap, 2005; Berghof et al., 2019; Knap and Doeschl-Wilson, 2020). Incorporating one or more operational proxies to evaluate the robustness of growing pigs in genetic selection would therefore be of value for the development of more sustainable breeding goals (Berghof et al., 2019). At first sight, animals that have the best performance in a given environment, compared with their contemporaries reared in the same environment, could be considered to be the most robust because they perform well and thus seem to be most adapted to this environment. However, this approach is too narrow as it does not include the costs of achieving this "robustness," which may be hidden in good and stable environments. It seems important to include more direct measures of other robustness components. Studies have already approached this subject but mainly focused on health-related traits that reflect disease resistance. For example, in rabbits, nonspecific disease resistance traits, based on routinely collected phenotypes, show nonzero heritabilities from 0.04 to 0.11 (Gunia et al., 2018), but without simultaneously incorporating other robustness components.

The objective of this study was to determine a set of operational proxies of robustness for fattening pigs (from 75 to 150 d of age) combining aspects of growth, survival, health, and medication; based on phenotypes commonly available on farm; and to evaluate their genetic determinism. In this context, these proxies should reflect the ability of an animal to express or adapt its production potential in the face of changes in the environment relative to other animals that have been raised under the same conditions.

## Materials and Methods

Specific Experimental Animal Care and Use Committee approval was not needed because all the data used in this study were obtained from preexisting databases provided by AXIOM. The data used were from animals raised under commercial conditions that were cared for according to EU-Council directive 2008/120/EC of 18 December 2008 laying down minimum standards for the protection of pigs (http://data.europa.eu/eli/dir/2008/120/oj).

### Populations

Animals from two paternal lines of the Axiom company were used in this study: Piétrain Français (Pie) and Piétrain NN Français free from halothane-sensitivity (Pie NN). These lines are selected on paternal traits for more than 10 generations. In both cases, the objective is to improve the average daily growth (**ADG**) while reducing FCR during the fattening period. The selection objective is also to meet European market requirements for carcass qualities at 100 kg by reducing the backfat thickness (**BF**) and improving loin thickness.

The animals considered in this study were all males (5,116 Pie and 2,140 Pie NN) raised from January 2019 to April 2021 at the boar testing station of the breeding company AXIOM Genetics (Azay-sur-Indre, France).

The station consisted of 2 quarantine rooms, 2 postweaning rooms, and 10 fattening rooms with 12 identical pens each, housing a maximum of 14 pigs per pen, leading to a total capacity of 2,638 places. Each group, from the same week of introduction in the station, was divided into two fattening rooms (24 pens with 14 pigs). Sick pigs were treated with individual medication according to veterinary requirements. The station was not equipped with an air-cooling system.

The studied males were born in six different farms (four farms for Pie and two farms for Pie NN) integrated into the AXIOM breeding scheme and that comply with AXIOM's biosafety and health requirements (monitoring, vaccination plan, etc.), that are negative for monitored diseases (Porcine Reproductive and Respiratory Syndrome, Brucellosis, Classical Swine Fever, Aujesky's disease, major serotypes of *Actinobacillus pleuropneumonia*, Porcine Epidemic Diarrhea, Transmissible gastroenteritis, and Swine dysentery) and vaccinated for *Mycoplasma pneumoniae* and PCV2.

These animals came from 1,462 litters in Pie line (3.5 ± 1.8 piglets per litter) and from 951 litters in Pie NN line (2.3 ± 1.3 piglets per litter). They were born from 182 sires in Pie line (28.1 ± 31.8 piglets per sire) and 88 sires in Pie NN line (25.2 ± 16.5 piglets per sire). The pedigrees contained 11,325 animals across 22 generations for Pie and 3,944 animals across 24 generations for Pie NN. To limit the risk of confounding between environmental (i.e., fattening group) and genetic effects, the sires from the two lines were used at least in two mating groups in each farm and in two different farms. Each fattening group consists of animals sourced from one and three farrowing farms in the Pie line and from one or two farrowing farms in the Pie NN line.

Pigs from both lines entered the boar testing station at an average age of 27.3 ± 2.2 d with an average body weight (BW) of 8.5 ± 1.7 kg for the two lines at the rate of one group of 336 piglets every 3 wk. They were raised in air-filtered quarantine rooms for 5 wk in pens of 14 animals from the same line and birth farm. These groups of 14 pigs were never modified at the different stages of breeding. During this quarantine period, corresponding to the time required for seroconversion control, animals were controlled for monitored diseases: serological control and observation of symptoms. In the case of positive animals for monitored diseases, the whole group was excluded from the farm. Then, animals were raised in postweaning rooms for 2 wk and transferred to fattening rooms when they were 75.3 ± 3.4 d of age (34.5 ± 6.2 kg BW). Pigs were raised in fattening rooms for 74.8 ± 4.0

d until the individual testing at around 149.7 ± 4.1 d of age (108.9 ± 11.5 kg BW). Fattening rooms were equipped with an automatic feeding system (**AFS**): Nedap pig performance testing feeding station (Nedap N.V., Groenlo, the Netherlands). Each pen had one water nipple available for the animals. Animals were fed ad libitum with commercial diets adapted to their physiological needs. The provided diets were nonlimiting in amino acids.

## Information recorded during the fattening period

Each animal was individually weighted on arrival in the fattening room (initial body weight, **IBW**). During the fattening period, BW and feed intake (**FI**) were recorded each time the animal went into the AFS. In addition, each treatment received by the animal and associated symptoms were recorded, as well as the date of death, if necessary. When the average weight of the group was approximately 100 kg, individual tests were performed. Measurements made during the test were: body weight (**TBW**), average ultrasonic BF (= mean of three measurements in mm), and ultrasonic longissimus dorsi thickness (**LD** = one measurement in mm). The BF and LD measures were transformed to correspond to their values at 100 kg live weight (BF100 and LD100, respectively) to compare animals at the equivalent weight. This transformation was done by applying linear coefficients that multiply by the difference between 100 kg and TBW. Coefficients used are 0.04 mm/kg for BF100 and 0.27 mm/kg for LD100 (Sourdioux et al., 2009). Visual observation of the animals was then carried out by the technician in charge of the measurements in order to note the morphological defects, anomalies, and clinical signs of disease according to a frame of reference (Supplementary Appendix 1; Institut Technique du Porc, 2004), noted as "observable defects." These observations were made by the same person within any given fattening group, and by a total of four technicians over the studied period. To avoid deviations in notations, they used the same reference and were trained together each year. Any systematic differences between technicians would be absorbed in the fattening group effect in the statistical model. Part of these observations was used to construct the robustness traits. Animals weighing less than 70 kg were considered to have too poor growth and these were excluded from the test. This threshold was defined by the French Pork and Pig Institute in their specifications for on-farm testing (Institut Technique du Porc, 2004). These animals were only noted with the observation: "Out of test" and the various performance traits were not recorded for them. The ADG was estimated only for animals with TBW greater than or equal to 70 kg, and calculated as the difference between TBW and IBW divided by the number of days elapsed between the two weighings. The FCR was calculated as the ratio between the total FI during the fattening period and the weight gain (TBW – IBW), expressed in kg/kg. The average daily feed intake (**DFI**) was calculated as the total FI during the period divided by the number of days elapsed. The residual feed intake (**RFI**) was also estimated for each animal as the deviation between the recorded DFI and the potential average daily feed intake (**PDFI**) predicted from requirements for maintenance and production. Based on the method proposed by Labroue et al. (1999), the PDFI was estimated by linear regression, with the lm function in R (R Core Team, 2018), of DFI on average metabolic weight (**AMW**), ADG, and BF100. The AMW was estimated for each animal using the formula proposed by Noblet et al. (1991):

$$\mathrm{AMW} = \frac{(\mathrm{TBW}^{1.6} - \mathrm{IBW}^{1.6})}{1.6(\mathrm{TBW} - \mathrm{IBW})}.$$

The estimation of PDFI was computed separately for each line and without including fixed effects.

## Robustness traits

Three synthetic phenotypes to characterize the robustness of the candidates were defined from the measurements performed during the individual test, and from the medical treatments recorded during the testing period (Table 1). The objectives of these synthetic traits were to describe the ability of the animal to be measured at the end of the individual testing present, that is, to be alive and weighing at least 70 kg, and to be in good health without observable defects. The trait R1 corresponded to the distinction used at present in the AXIOM testing protocol to differentiate candidates that can be tested (Note = 1) from those that are dead or weighing less than 70 kg on the day of the individual test (Note = 0). Individual mortality was not available in the database. Consequently, it was not possible to analyze directly this trait. The trait R2 differentiated animals that were selectable, tested, and without any observable defect on the day of testing (Note = 1), from those that were not tested or tested and had an observable defect (Note = 0). We considered it as an observable defect on the day of testing, factors such as weak development and similar, were estimated to relate to the robustness of the animal (see Supplementary Appendix 1 for full description). The trait R3 was a decomposition of the trait R2 in which the category of "selectable" animals was differentiated into those pigs that received at least one antibiotic or anti-inflammatory injection during the testing period (Note = 1) and those that did not receive any injection (Note = 2). For R3, we considered the levels as equidistant as has been commonly done (Varona et

**Table 1.** Description of robustness traits studied

| Variable | Modality | Entitled | Comment |
|---|---|---|---|
| R1 | 0 | Absent | Animal alive but weighing less than 70 kg (not controlled) or dead. |
| | 1 | Present | Animal alive and weighing 70 kg or more (controlled). |
| R2 | 0 | Not selectable | Animal « Absent (R1) » or « Present (R1) » with a negative observation (body condition, health status (abscess, respiratory problem, diarrhea, etc.), cannibalism, poor body development) |
| | 1 | Selectable | Animal « Present (R1) » without negative observation |
| R3 | 0 | Not selectable | Animal « Not selectable (R2) » |
| | 1 | Selectable with medicine | Animal « Selectable (R2) » with at least one antibiotic or anti-inflammatory injection during the fattening period |
| | 2 | Selectable without medicine | Animal « Selectable (R2) » without any medicine injection during the fattening period |

al., 1999; Pérez-Cabal and Charfeddine, 2015). We did not include symptoms in the trait definition due to the subjectivity of the observations.

In addition, the area between curves (**ABC**) index estimated during fattening period, developed by Revilla et al. (2022) which the authors called a resilience phenotype, was also calculated using weight measured by AFS for each animal alive at the end of the fattening period. The datasets analyzed by Revilla et al. (2022) were collected on the same farm from September 2015 to July 2019. The trait ABC was the accumulated difference of area between the unperturbed growth curve and the perturbed curve. The ABC index had no unit. The unperturbed growth curve of each animal was modeled using the Gompertz equation. The perturbed curve was constructed using linear interpolation of body weight measurements recorded by AFS. In comparison to the method proposed by Revilla et al. (2022), some modifications have been made to the data pretreatment when analyzing all data from each AFS within fattening group. This was done to detect inconsistencies linked to the AFS machine. A linear regression of weight on the number of days of test was applied. The standard deviation of the residual value was calculated for each day for each AFS within fattening group. If more than 20% of the weights measured on AFS in a fattening group were greater or less than 4 standard deviations, then records of the AFS within the fattening group were removed from the data set. Animals with less than 20 d of measurements in total were removed from the analysis. The ratio of the number of animals after cleaning procedure and the raw dataset was 0.93 in Pie line and 0.92 in Pie NN line.

### Statistical analysis

Differences in the phenotypic means between the lines were tested using analysis of variance on R software (R Core Team, 2018). To compare the differences and frequencies in the three robustness scores among the two lines, a Chi-square on R was performed. Statistical significance was set a priori at $P \leq 0.05$.

### Genetic parameters estimation

Each trait was analyzed with ASREML 3.0 software (Gilmour et al., 2009), using the restricted maximum likelihood (**REML**) method. Each line was analyzed separately. Firstly, to select fixed and random effects, all traits were analyzed using a single trait model. The global linear mixed model was defined as:

$$\mathbf{y} = \mu + \mathbf{X}\beta + \mathbf{Vb} + \mathbf{Wl} + \mathbf{Zu} + \mathbf{e}$$

where $\mathbf{y}$ was the vector of phenotypes for the considered trait (R1, R2, and R3 considered as continuous phenotypes, IBW, ADG, LD100, BF100, FCR, DFI, and ABC); $\mu$ is the overall mean, $\beta$ was the vector of fixed effects; $\mathbf{b}$ was the vector of random fattening group effect, with $\sim N(0, \mathbf{I_b}\sigma_b^2)$, where $\mathbf{I}$was the identity matrix of appropriate size; $\mathbf{l}$ was a vector of the common litter random effects with $\sim N(0, \mathbf{I_l}\sigma_l^2)$; $\mathbf{u}$ was the vector of additive genetic random effects with $\sim N(0, \mathbf{A}\sigma_u^2)$, where $\mathbf{A}$ was the pedigree-based relationship matrix; $\mathbf{X}$, $\mathbf{V}$, $\mathbf{W}$, and $\mathbf{Z}$ were the known incidence matrices for fixed, fattening group effects, litter effect, and animal genetic, respectively; and $\mathbf{e}$ is the vector of residual random effects with $\sim N(0, \mathbf{I_e}\sigma_e^2)$. For all estimated traits, the fixed effects tested at an $\alpha$-risk of 5% using the Wald F statistic of ASReml (Gilmour et al., 2009) were the birth farm for Pie and Pie NN and halothane-sensitivity gene status for Pie line. The significance of common litter random effect was tested by using likelihood ratio test with R statistical software (R Core Team, 2018) from log-likelihood values estimated on ASReml software (Gilmour et al., 2009). In the two lines, the fattening group effect and common litter effect were significant ($P < 0.05$) for all tested traits expected for traits ABC, FCR, and RFI with the common litter effect in Pie NN line.

In the second step of the analysis, to follow the assumption of the BLUP method, which should be applied to a nonselected base population, and to estimate the covariance between traits, a series of multi-traits models including the four traits under selection (ADG, BF100, LD100, and FCR) and the nonselected traits to be estimated (R1, R2, R3, IBW, DFI, RFI, and ABC) were applied to the data. First, variance and covariance components were estimated with a four-trait linear animal model including ADG, FCR, BF100, and LD100 traits, to estimate heritabilities and genetic correlations of traits under selection. Second, to estimate heritability for each nonselected trait (R1, R2, R3, IBW, DFI, RFI, and ABC) and their genetic correlations with the traits under selection, five-trait linear animal models including the four traits under selection and one trait to be estimated were used. Third, to estimate genetic correlations between the nonselected traits (R1, R2, R3, ABC, IBW, DFI, and RFI), six-trait linear animal models including the four traits under selection as well as the two traits for which the genetic correlation is estimated were performed.

Heritability ($h^2$) was calculated as the ratio of animal genetic variance to the total phenotypic variance, that is, the sum of the genetic additive variance, environmental variances (fattening group, litter if necessary), and the residual variance, estimated with the four-trait model for the traits under selection and with the five-trait models for the nonselected traits.

## Results

### Phenotypic means and distributions

Means of TBW were similar between the two lines (Table 2). The Pie NN animals had significantly lower average values ($P < 0.05$) for IBW (–0.4 kg), ADG (–17 g/d), DFI (–23 g/d), and LD100 (–4.8 mm) and significantly higher average values for BF100 (+0.6 mm) and FCR (+0.01 kg/kg) than Pie. The mean and SD for ABC values were significantly higher for Pie NN animals compared with Pie (+5,223, i.e., +20.5% of ABC), indicating more important deviations between unperturbed and perturbed growth in line Pie NN, suggesting that these are average less robust animals compared with the Pie line. The distributions of the traits R1 and R2 were similar ($P > 0.1$) between Pie and Pie NN (Figure 1). Approximately 95% of the animals introduced in fattening rooms were "Present" (Trait R1—Note = 1), on the day of individual testing and around 80% were "Selectable" (Trait R2—Note = 1). The mortality rate over the fattening period for Pie pigs (3.75%) was significantly higher than for Pie NN pigs (2.42%). Proportions of animals with observable defects at individual testing were 13.6% and 15.5% in Pie and Pie NN lines, respectively. For the trait R3, the Pie line had a significantly higher proportion ($P < 0.001$) of animals "Selectable with medicine" (Trait R3—Note = 1) than the Pie NN line (32.2% vs. 19.7%, respectively).

## Variance–Covariance components

The heritability estimates for robustness traits R1, R2, and R3 were low and in the same range for the two lines, ranging from 0.03 ± 0.01 to 0.09 ± 0.02 (Table 3). Heritability estimates for R2 and R3 tended to be slightly higher than for R1 in each line. Heritability estimates for the ABC index were low for both Pie (0.09 ± 0.03) and Pie NN (0.06 ± 0.03). Heritability estimates were low to moderate in the Pie and Pie NN lines for the traits under selection (ADG, FCR, BF100, and LD100), and also for IBW, DFI, and RFI, ranging from 0.13 ± 0.03 to 0.34 ± 0.05. The higher standard errors in Pie NN were due to the smaller dataset for this line. The fattening group effect ranged from 0.02 ± 0.01 to 0.38 ± 0.07 for the studied traits, with the highest estimates being for LD100 in both lines. The proportion of variance due to common litter effects was similar for all traits, ranging from 0.03 ± 0.01 to 0.08 ± 0.03, except for IBW in the two lines and ABC in Pie line that had the highest proportion of phenotypic variance explained by litter effect.

Genetic correlations between R1 and the two other robustness traits were low to moderate in Pie NN line, ranging from 0.25 ± 0.32 to 0.41 ± 0.30 (Table 5), and higher in Pie line, ranging from 0.42 ± 0.28 to 0.57 ± 0.36 (Table 4). Several estimates of genetic correlations had large standard errors and should be interpreted with caution. In both paternal lines, the genetic correlation between R2 and R3 was high (0.95 ± 0.04 and 0.92 ± 0.06, for Pie NN and Pie lines, respectively). The genetic correlation between ABC and the robustness traits tended to be negative in the Pie NN line, ranging from −0.03 ± 0.33 to −0.21 ± 0.38, and in the Pie line, ranging from −0.08 ± 0.26 to −0.22 ± 0.22, none of these correlations were significantly different from 0. In both lines, the traits R2 and R3 were highly correlated with ADG (correlations higher than 0.76), and moderately correlated with FCR, ranging from 0.32 ± 0.18 to 0.51 ± 0.25. The trait R1 had low correlations with ADG, which were 0.22 ± 0.25 in Pie line and 0.31 ± 0.25 in Pie NN line. The carcass traits (BF100 and LD100) tended to be positively correlated with the three robustness traits (estimates ranged from 0.11 ± 0.21 to 0.44 ± 0.25). For the nonselected traits, R2 and R3 were moderate to highly correlated with IBW and DFI (correlations higher than 0.45 ± 0.18). Correlations of R1 with IBW and DFI were null or moderate, ranging from −0.02 ± 0.23 to 0.33 ± 0.27, in both lines. Estimates of genetic correlations of RFI with robustness traits were not significantly different than 0 in both lines. Estimates of genetic correlations of ABC with other traits had large standard errors and showed estimates close to 0, except for IBW in both lines and for LD100 in Pie line with negative correlations. In addition, the

**Table 2.** Descriptive statistics (mean and SD) for area between curves and production traits for each line[1] and significance level of difference (*P*)

| Trait, unit[2] | Pie (*n* = 5,116) | | Pie NN (*n* = 2,140) | | *P*[3] |
|---|---|---|---|---|---|
| | Mean | SD | Mean | SD | |
| IBW, kg | 34.5 | 6.1 | 34.1 | 5.7 | * |
| TBW, kg | 108.9 | 11.4 | 108.8 | 11.5 | |
| ADG, g/d | 1,009 | 104 | 992 | 108 | * |
| FCR, kg/kg | 2.25 | 0.18 | 2.26 | 0.19 | * |
| DFI, g/d | 2,263 | 268 | 2240 | 287 | * |
| RFI, g/d | 0 | 150 | 0 | 159 | |
| BF100, mm | 6.0 | 0.8 | 6.6 | 0.8 | * |
| LD100, mm | 72.8 | 5.1 | 68.0 | 5.3 | * |
| ABC | 25,503 | 21,603 | 30,726 | 24,764 | * |

[1]Pie, Piétrain Français; Pie NN, Piétrain NN Français free from halothane-sensitivity.
[2]IBW, initial body weight; TBW, testing body weight; ADG, average daily gain; FCR, feed conversion ratio; DFI, average daily feed intake; RFI, residual feed intake; BF100, backfat thickness estimated at 100 kg live weight; LD100, longissimus dorsi thickness estimated at 100 kg live weight; ABC, resilience index.
[3]*P* value for the difference between least squares means of Pie and Pie NN lines.
*$P < 0.05$.

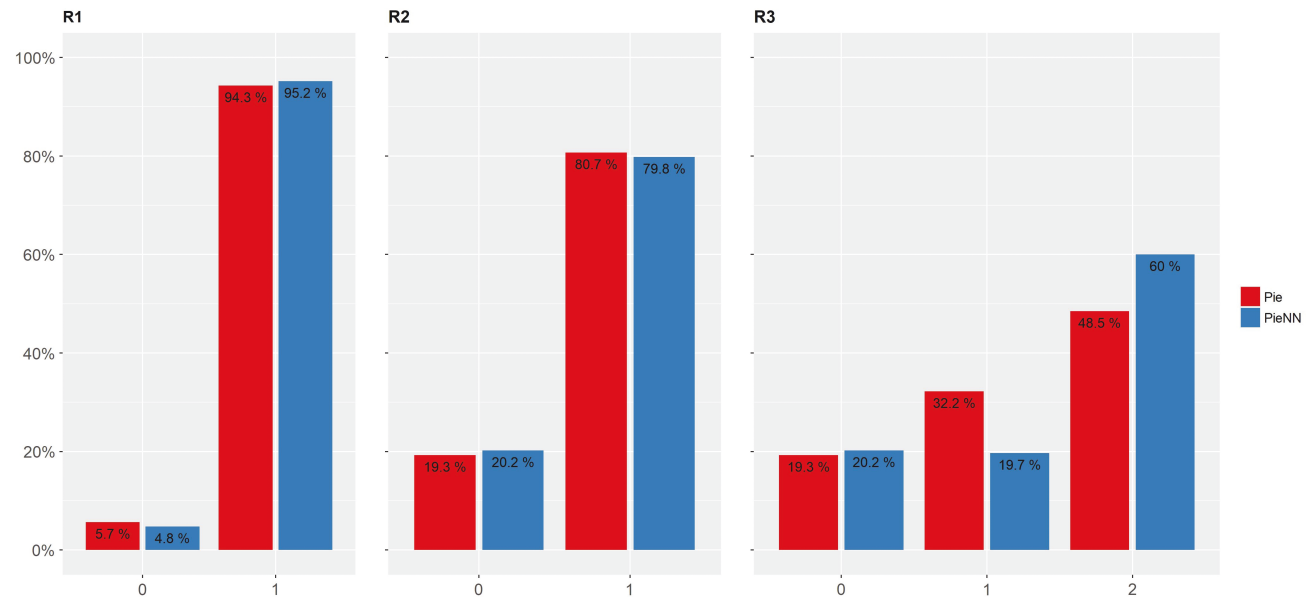


**Figure 1.** Distribution of modalities for the three robustness traits (R1, R2, and R3) for the Pie and Pie NN lines. Pie, Piétrain Français; Pie NN, Piétrain NN Français free from halothane-sensitivity.

**Table 3.** Estimates of heritability ($h^2$), fattening group effect ratio ($b^2$), common litter effect ($c^2$), and phenotypic variance (Vp) for the traits recorded (± standard error) for each line[1]

| Trait[2] | Pie | | | | Pie NN | | | |
|---|---|---|---|---|---|---|---|---|
| | $h^2$ | $b^2$ | $c^2$ | Vp | $h^2$ | $b^2$ | $c^2$ | Vp |
| R1[3] | 0.03 ± 0.01 | 0.02 ± 0.01 | 0.03 ± 0.01 | 0.054 ± 0.001 | 0.06 ± 0.03 | 0.04 ± 0.01 | 0.06 ± 0.02 | 0.045 ± 0.002 |
| R2[3] | 0.09 ± 0.02 | 0.03 ± 0.01 | 0.03 ± 0.01 | 0.157 ± 0.004 | 0.08 ± 0.03 | 0.02 ± 0.01 | 0.06 ± 0.02 | 0.162 ± 0.005 |
| R3[3] | 0.05 ± 0.02 | 0.07 ± 0.02 | 0.07 ± 0.01 | 0.590 ± 0.016 | 0.07 ± 0.03 | 0.03 ± 0.01 | 0.07 ± 0.02 | 0.648 ± 0.021 |
| ABC[3,4] | 0.09 ± 0.03 | 0.06 ± 0.02 | 0.16 ± 0.02 | $4.95 \times 10^8 \pm 1.59 \times 10^7$ | 0.06 ± 0.02 | 0.05 ± 0.02 | | $6.20 \times 10^8 \pm 2.36 \times 10^7$ |
| IBW[3] | 0.34 ± 0.05 | 0.18 ± 0.04 | 0.13 ± 0.02 | 36.38 ± 1.88 | 0.33 ± 0.06 | 0.20 ± 0.04 | 0.16 ± 0.03 | 34.88 ± 2.17 |
| ADG[4] | 0.21 ± 0.04 | 0.13 ± 0.03 | 0.07 ± 0.02 | 10,694 ± 462 | 0.32 ± 0.06 | 0.11 ± 0.03 | 0.08 ± 0.03 | 12,274 ± 623 |
| FCR[4] | 0.23 ± 0.04 | 0.15 ± 0.03 | 0.04 ± 0.01 | 0.034 ± 0.002 | 0.15 ± 0.04 | 0.13 ± 0.03 | | 0.037 ± 0.002 |
| DFI[3] | 0.29 ± 0.05 | 0.16 ± 0.04 | 0.08 ± 0.02 | 73,364 ± 3,661 | 0.31 ± 0.07 | 0.16 ± 0.04 | 0.08 ± 0.03 | 87,972 ± 5,299 |
| RFI[3] | 0.19 ± 0.04 | 0.16 ± 0.04 | 0.06 ± 0.02 | 23,575 ± 1,159 | 0.13 ± 0.04 | 0.12 ± 0.03 | | 26,363 ± 1301 |
| BF100[4] | 0.31 ± 0.04 | 0.12 ± 0.03 | 0.05 ± 0.02 | 0.624 ± 0.027 | 0.29 ± 0.06 | 0.12 ± 0.03 | 0.07 ± 0.03 | 0.717 ± 0.037 |
| LD100[4] | 0.17 ± 0.03 | 0.43 ± 0.06 | 0.03 ± 0.01 | 31.47 ± 3.54 | 0.25 ± 0.05 | 0.38 ± 0.07 | 0.03 ± 0.02 | 28.45 ± 3.08 |

[1]Pie, Piétrain Français; Pie NN, Piétrain NN Français free from halothane-sensitivity.
[2]IBW, initial body weight; TBW, testing body weight; ADG, average daily gain; FCR, feed conversion ratio; DFI, average daily feed intake; RFI, residual feed intake; BF100, backfat thickness estimated at 100 kg live weight; LD100, longissimus dorsi thickness estimated at 100 kg live weight; ABC, resilience index.
[3]Estimates from a five-trait multiple trait model (ADG, FCR, BF100, LD100, and the trait under consideration).
[4]Estimates from a four-trait multiple trait model (ADG, FCR, BF100, and LD100).

**Table 4.** Estimates of genetic correlations ($r^2a$ ± standard error) between robustness traits (R1, R2, and R3), area between curves, and production traits for Piétrain line (Pie)

| Trait[1] | R1 | R2 | R3 | ABC |
|---|---|---|---|---|
| R1 | | 0.57 ± 0.28[2] | 0.42 ± 0.36[2] | −0.17 ± 0.18[2] |
| R2 | 0.57 ± 0.28[2] | | 0.92 ± 0.06[2] | −0.22 ± 0.26[2] |
| ABC | −0.17 ± 0.18[2] | −0.22 ± 0.26[2] | −0.08 ± 0.29[2] | |
| IBW | 0.18 ± 0.22[2] | 0.50 ± 0.15[2] | 0.45 ± 0.18[2] | −0.19 ± 0.18[2] |
| ADG | 0.22 ± 0.25[3] | 0.79 ± 0.08[3] | 0.78 ± 0.12[3] | 0.00 ± 0.19[3] |
| FCR | 0.21 ± 0.31[3] | 0.39 ± 0.15[3] | 0.32 ± 0.18[3] | −0.10 ± 0.18[3] |
| DFI | 0.33 ± 0.27[2] | 0.73 ± 0.11[2] | 0.72 ± 0.12[2] | −0.02 ± 0.16[2] |
| RFI | 0.23 ± 0.17[2] | 0.10 ± 0.20[2] | 0.07 ± 0.22[2] | −0.05 ± 0.10[2] |
| BF100 | 0.21 ± 0.23[3] | 0.29 ± 0.14[3] | 0.29 ± 0.17[3] | 0.01 ± 0.17[3] |
| LD100 | 0.42 ± 0.23[3] | 0.15 ± 0.15[3] | 0.14 ± 0.18[3] | −0.30 ± 0.18[3] |

[1]IBW, initial body weight; TBW, testing body weight; ADG, average daily gain; FCR, feed conversion ratio; DFI, average daily feed intake; RFI, residual feed intake; BF100, backfat thickness estimated at 100 kg live weight; LD100, longissimus dorsi thickness estimated at 100 kg live weight; ABC, resilience index.
[2]Estimates from a six-trait multiple trait model (ADG, FCR, BF100, LD100, and the two traits under consideration).
[3]Estimates from a five-traits multiple trait model (ADG, FCR, BF100, LD100, and the trait under consideration).

genetic correlations between all studied traits are presented in Supplementary Appendix 2 for Pie and in Supplementary Appendix 3for Pie NN.

## Discussion

### Genetic parameters for robustness traits

The heritabilities for the traits R1, R2, and R3 in the present study were low but not null, with the exception of R1 in Pie line (related to the standard error of the estimate). The heritability estimates from our study were in the same range as those presented in different publications estimated at an individual level (Gunia et al., 2015, 2018; Putz et al., 2019; Shrestha et al., 2020) or at the full-sibs level (Gorssen et al., 2021). However, it should be noted that most literature references to similar traits have focused on traits related to the resistance to nonspecific or specific diseases, or related to the use of antibiotics. The heritability estimates for R1 in the two breeds were of the same order of magnitude as the values reported by Perez et al. (2021) on two survival traits (juvenile and late) in turkeys raised under classical production conditions, 0.06 ± 0.01 and 0.04 ± 0.03, respectively. In growing rabbits, the heritability for infectious mortality estimated by Gunia et al. (2015) was 0.043 (±0.004). Heritabilities of R2 and R3 traits tended to be higher than those of the R1 trait, maybe related to low occurrence of phenotype "Absent" for trait R1. Gunia et al. (2018) estimated a similar heritability in rabbits for the trait resistance to nonspecific disease in the selection environment (0.04 ± 0.01).

The present study was carried out in a standard breeding environment, that is, designed to minimize exposure to environmental challenges. In some studies, the animals were reared under challenging conditions, which seems to allow better phenotyping of the robustness of the animals. This may result in the estimation of higher heritabilities. Indeed, Gunia et al. (2018) estimated higher heritabilities for resistance to nonspecific disease in a challenging environment (0.08 ± 0.02) than in the standard selection environment. Under challenging conditions in rabbits, Shrestha et al. (2020) showed a heritability of the resistance to pasteurellosis of 0.16 ± 0.06. Putz et al. (2019) estimated the heritability for mortality traits for fattening pigs raised under disease challenging conditions to be 0.13 ± 0.03. The definition of this trait was close to that for R1, which had a slightly higher heritability. It is expected that challenging conditions better reveal variation in robustness (Theilgaard et al., 2007; Gunia et al., 2018). However, when choosing the selection environment, there is a need to balance between conditions that allow growth potential to be

**Table 5.** Estimates of genetic correlations ($r^2a$ ± standard error) between robustness traits (R1, R2, and R3), area between curves, and production traits for Piétrain NN line (Pie NN)

| Trait[1] | R1 | R2 | R3 | ABC |
|---|---|---|---|---|
| R1 | | 0.41 ± 0.30[2] | 0.25 ± 0.32[2] | −0.21 ± 0.38[2] |
| R2 | 0.41 ± 0.30[2] | | 0.95 ± 0.04[2] | −0.03 ± 0.33[2] |
| ABC | −0.21 ± 0.38[2] | −0.03 ± 0.33[2] | −0.10 ± 0.31[2] | |
| IBW | −0.02 ± 0.23[2] | 0.89 ± 0.14[2] | 0.78 ± 0.15[2] | −0.23 ± 0.19[2] |
| ADG | 0.31 ± 0.25[3] | 0.86 ± 0.11[3] | 0.76 ± 0.14[3] | 0.01 ± 0.26[3] |
| FCR | 0.21 ± 0.31[3] | 0.51 ± 0.25[3] | 0.42 ± 0.26[3] | 0.08 ± 0.31[3] |
| DFI | 0.32 ± 0.25[2] | 0.91 ± 0.07[2] | 0.81 ± 0.15[2] | −0.02 ± 0.16[2] |
| RFI | 0.15 ± 0.35[2] | 0.09 ± 0.25[2] | −0.05 ± 0.31[2] | 0.19 ± 0.33[2] |
| BF100 | 0.35 ± 0.20[3] | 0.44 ± 0.25[3] | 0.23 ± 0.21[3] | −0.05 ± 0.25[3] |
| LD100 | 0.14 ± 0.24[3] | 0.11 ± 0.21[3] | 0.42 ± 0.26[3] | 0.08 ± 0.31[3] |

[1]IBW, initial body weight; TBW, testing body weight; ADG, average daily gain; FCR, feed conversion ratio; DFI, average daily feed intake; RFI, residual feed intake; BF100, backfat thickness estimated at 100 kg live weight; LD100, longissimus dorsi thickness estimated at 100 kg live weight; ABC, resilience index.
[2]Estimates from a six-trait multiple trait model (ADG, FCR, BF100, LD100, and the two traits under consideration).
[3]Estimates from a five-trait multiple trait model (ADG, FCR, BF100, LD100, and the trait under consideration).

expressed and conditions that favor the expression of robustness. This is a relevant question for future selection strategies that aim to produce efficient and robust animals.

## Advantages and limits of robustness traits

Our objective was to build proxies of robustness based on information readily available in the context of commercial pig breeding. These proxies have to meet the expectations of pig farmers, that is to say, they identify animals that were present for testing in good health, with reasonable growth rates, and with the least amount of medical injections. In this context, we decided to combine the underlying traits into scores to build the three robustness traits, rather than focusing on specific traits such as mortality or disease resilience. This choice was pragmatic because working on specific traits will multiply the number of traits to be included in the breeding goal. The advantage of using such pragmatic measures is that they can be deployed on large scale, if shown to be useful. Among the robustness traits, R2 was the trait with the highest heritability estimate in the two lines. It was highly genetically correlated (≥0.92 ± 0.06) with R3 but required less information in order to be calculated. Thus, R2 meets the objective of finding an operational trait to select in order to have live and healthy animals at the end of the period. A limit of this robustness trait is the difficulty of estimating the impact of the genetic evolution of the synthetic trait on each of its underlying traits. As such further investigation on the impact of the improvement of this robustness trait on mortality or on disease occurrence could be useful. The use of these types of additional information, not currently available in the databases, would require improved data management systems. Furthermore, estimation of the economic value in the breeding goal of such synthetic traits is an important issue. It would be interesting to estimate the economic value of genetic evolution of the tested robustness traits in order to define a weighting in the breeding goal. Berghof et al. (2019) have published an interesting approach for estimating the economic value of resilience traits based on cost reductions of labor and treatments. Improving robustness traits also meets societal expectations, in particular animal welfare, the economic value of which is difficult to quantify.

## Fattening group fitted as a random effect

The fattening group included as a random effect in the models describes the common environmental conditions encountered by all the animals of a group entering into the station at the same date and having been raised under the same environmental conditions, including disturbances. What we call the fattening group in this article can also be more classically called the contemporary group, as described by Van Vleck (1987).

The risk associated with treating the contemporary group as a random effect is to obtain biased breeding values if there is a nonrandom association between contemporary groups and sires (Visscher and Goddard, 1993). Babot et al. (2003) showed that the estimate of genetic progress could be biased when there was an environmental trend. However, considering the contemporary group as a random effect avoids a too important loss of information encountered when it is treated as a fixed effect (Visscher and Goddard, 1993). Inclusion of fattening group as a random effect with additive genetic effects was chosen as it was expected to avoid overestimating heritabilities.

## Binary traits: threshold vs. linear models

The analysis of R1, R2, and R3 traits was carried out using a linear model, whereas they are categorical traits. Theoretically, the use of linear models to analyze categorical data is not optimal, the appropriate method being the threshold model (Gianola, 1982). However, to integrate these traits in multi-traits analysis to estimate genetic correlations and to perform a genetic evaluation, it is necessary to analyze them with a linear model to overcome convergence issues and long computing times (Kadarmideen et al., 2000). It has been shown that the linear model can be a good approximation of the threshold model under certain conditions. Meijering and Gianola (1985) showed similar heritability estimates between the two methods for binary traits, when the prevalence of the analyzed traits was between 25% and 75%. The trait R1 did not meet this condition with a prevalence of 4.8% and 5.7%, while R2 was close to the condition with a prevalence of 19.3% and 20.2%. To evaluate the consequences of applying a linear model for R1, R2, and R3 instead of a threshold model, we compared the linear and threshold models for each of these three traits analyzed separately. With the threshold model, heritabilities were estimated on the observed scale and after applying the transformation proposed by Gianola (1982). For R1, the estimates with threshold model and single-trait linear model were, respectively, 0.02 ± 0.01 and 0.02 ± 0.01 for the Pie line and 0.03 ± 0.02 and 0.06 ± 0.03 for the Pie NN line. For R2, the heritabilities from the threshold model and single-trait linear model were 0.04 ± 0.01 and 0.05 ± 0.02 in the Pie line and 0.05 ± 0.02 and 0.08 ± 0.02 in the Pie NN line. For R3, heritabilities with the threshold model and single-trait linear model were 0.04 ± 0.02 and 0.03 ± 0.02, respectively, in the Pie line, and 0.08 ± 0.04 and 0.07 ± 0.03 in the Pie NN line. For the trait R3, the correlations between estimated breeding values (**EBVs**) estimated from the linear model and EBVs

estimated from the threshold model were 0.99 for Pie and 0.98 for Pie NN. This validates the use of equidistant levels for the three categories in R3. Thus, we found no evidence that the use of the linear model was inappropriate for analyzing R1, R2, and R3.

### Heritability estimates for production traits

Heritability estimates for ADG and DFI were consistent with those reported in the literature for Piétrain or Large-White pigs raised in similar environmental conditions, which varied from 0.29 ± 0.02 to 0.48 ± 0.06 and from 0.31 ± 0.05 to 0.53 ± 0.06 (Saintilan et al., 2013; Gilbert et al., 2017; Déru et al., 2020; Gorssen et al., 2021). For carcass traits (BF100 and LD100), heritabilities were also consistent with the values estimated by Sourdioux et al. (2009) and Saintilan et al. (2013) in the Pietrain breed (BF100: 0.38 to 0.48; LD100: 0.25 to 0.34). Our estimates of heritability for FCR and RFI in Pie and Pie NN lines were lower, especially for Pie NN, than the heritabilities presented by Saintilan et al. (2013) and Déru et al. (2020), which varied from 0.33 ± 0.06 to 0.34 ± 0.05, and from 0.40 ± 0.06 to 0.47 ± 0.08, respectively. However, the heritability estimate for FCR in the Pie line was close to the values estimated by Gilbert et al. (2017), Putz et al. (2019), and Gorssen et al. (2021); from 0.24 ± 0.04 to 0.35 ± 0.07. For FCR and RFI traits, the lower heritabilities for the Pie NN line were related to a lower genetic variance than for Pie, respectively, 0.0054 and 0.0104 for FCR, and 3,686 and 6,667 for RFI.

### Heritability estimates for ABC index

For the trait ABC, the heritability for the Pie NN line was consistent with that published by Revilla et al. (2022; 0.03 ± 0.016), but we found a slightly higher heritability in the Pie line (0.09 ± 0.03 vs. 0.04 ± 0.01). This difference is the result of a lower phenotypic variance in both lines compared with those reported by Revilla et al. (2022). In the present study, the data were recorded during a different time period and an improved outlier detection procedure was used on the observations collected by AFS, which reduced the contribution of erroneous measures to the phenotypic variance, and consequently reduced the residual variance when estimating variance parameters.

### Genetic correlations between robustness and production traits

The two growth traits (IBW and ADG) were moderate to strongly correlated with R2 and R3. The correlations with IBW showed that growth during postweaning, that is, pretest period, had an impact on the robustness scores evaluated during the fattening period. In this context, Putz et al. (2019) showed that the genetic correlation of ADG with mortality was close to 0 while the genetic correlation with the number of antibiotic treatments was favorable and strong (from −0.68 ± 0.42 to −0.70 ± 0.13). It seems that the growth of less robust animals is more impacted by environmental perturbations. It is also important to take into account that growth has been a major selection trait in both breeds for over 20 yr, and lack of growth or weak body development were major causes of culling at testing. In this situation, an animal's ability to be robust is strongly linked to its ability to express optimal growth regardless of the environment. Nonetheless, even if the correlation is strong, it is different from 1, which implies that the traits R2 and R3 add an additional information regarding the robustness of the animal compared with growth traits. Thus, if the selection is made using these traits, they would allow us to improve animals' robustness more than if the selection is made only on growth traits.

There was a moderate and unfavorable relationship between the robustness traits and the FCR, although the precision of the estimates remains low. This could be related to the positive correlation between ADG and FCR, which was affected by the way these two traits were estimated. They were measured over an identical time period for all individuals but were not standardized between starting and finishing weights (ADG 30 to 110 kg). Accordingly, some of the animals tested reached their mature weight before the end of the testing period, which led to a drop in feed conversion even if they had a previously strong growth. Within these two pig populations, there were two different types of animals with low FCR: those which had a strong growth but did not approach their mature weight during the testing period, and those with a low DFI associated with low growth. In parallel, the genetic correlations of R2 and R3 with DFI were strong. This could indicate that the most robust animals during the fattening period are not the most efficient because they allocate a part of nutrients to nonproductive functions. This antagonism between short-term efficiency and robustness had been put forward by Friggens et al. (2017). Genetic correlations between robustness and BF100 were slightly unfavorable, with low precision, particularly in the Pie line. We can suppose that the capacity to be robust could be associated with more important body reserves allowing the animal to face perturbations. The genetic correlations between the robustness traits and the RFI were close to 0 or slightly unfavorable in the Pie and Pie NN lines. For the relation between RFI and robustness, it is hypothesized that selection for low RFI may limit the animals' ability to allocate nutrients to resilience functions for dealing with perturbations (Gilbert et al., 2017). In contrast, several studies have shown, through divergent selection experiments on RFI, that there can be favorable effects of lines with low RFI on sensitivity to the PRRS virus (Dunkelberger et al., 2015) or on the risk of being culled between 70 d of age and slaughter (Gilbert et al., 2017).

Genetic correlations of robustness traits with the ABC were close to zero and difficult to interpret, due to low precision. The trait based on a dynamic analysis of the evolution of the weight (ABC) approach was relatively independent of the criteria created from the static data (R1, R2, and R3). In view of the strong or moderate link between the robustness criteria, the DFI and the FCR, it would be interesting to investigate the link between the dynamics of ingestion or allocation of animals and their ability to cope with disturbances, that is, their robustness.

The robustness traits that we proposed are built on single measurements represented the effects of the accumulations of good or bad events during the measured period (Friggens et al., 2017).

A dynamic analysis of the data collected by the automatic feeders would make it possible to have an analysis of this accumulation that is dynamic and probably better able to identify the finer criteria of robustness.

## Conclusion

This study showed that it is possible to set up a selection based on robustness in growing pigs from robustness scores

(R2 and R3) calculated from data available routinely on farms. However, the low heritabilities offer limited hope for rapid genetic improvement. The trait R2 would seem the most interesting because it is more heritable and requires less information to be calculated. The introduction of the R2 trait in the breeding goal of paternal lines is relevant but would require further investigation with respect to the potential genetic gain achievable in a multi-trait breeding goal. At this stage, the trait R3 is less relevant, but its determination could be upgraded by adding additional information on the various other assistance provided by the breeder, to identify animals that have the ability to express or adapt their production potential without help. In this study, we focused on the evaluation of robustness over a short period of the animal's life but it is necessary to investigate such traits over the whole lifespan.

## Supplementary Data

Supplementary data are available at *Journal of Animal Science* online.

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## Conflict of interest statement

G.L. and L.F.-G. were employed by the company AXIOM. There is no conflict of interest to be declared.

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