Robustness scores in fattening pigs estimated from phenotypes measured routinely: definition and genetic parameters

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ABSTRACT

The objective of this study was to define robustness scores based on data collected routinely on farm to allow phenotyping of this trait in fattening pigs. A total of 7 256 pigs, from 2 Piétrain paternal lines (Pie and Pie NN), were controlled at the Axiom boar testing station (Azay-sur-Indre, France), in 2019-2021. During the fattening period (from 75 to 150 days of age), individual performance indicators were recorded (growth, backfat, loin depth, feed intake, feed conversion ratio) together with indicators such as mortality, clinical signs, antibiotic and anti-inflammatory injections. These indicators were combined to estimate a set of three categorical robustness traits: R1, R2 and R3. Genetic parameters were estimated using an animal linear model. The robustness score R2 (selectable or not selectable animal) that combines information from status at testing and mortality presented the most interesting heritability, from 0.12 (±0.03) to 0.13 (±0.02) depending of the line. The score R3 that combines information from the score R2 with antibiotic and anti-inflammatory injections presented slightly lower heritability estimates (0.08 ±0.02 to 0.11±0.03). Genetic correlations between R2 and R3 were high and favorable (0.93 ±0.04 to 0.95 ±0.03). These two robustness scores were also highly and favorably genetically correlated with initial body weight, average daily gain and 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 feed conversion ratio 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.

Key words: robustness, genetic parameters, pig

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 liveweight

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 liveweight

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 exposure of pigs to antibiotics decreased by 41% from 2012 to 2016 (Hémonic et al., 2019). In this situation, it is important to avoid degrading welfare by breeding animals that are more robust. The more general context of global warming implies an increase in the frequency of extreme events, such as heat waves or droughts (Hansen et al., 2012) having direct (breeding temperature) and indirect impacts (availability of raw materials for feed production) on animals' performance and welfare. All these challenges require having animals able to adapt to these new conditions, which can be defined as 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 viability and reducing treatment costs (Phocas et al., 2016).

Today, there is no real consensus on the definition of robustness as well as on the way to phenotype it. Several authors have proposed a definition of robustness adapted to the context of livestock farming. Knap (2005) defined the 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 to a phenotype of interest, such as growth, feed conversion ratio, etc.

Traits that may be associated with robustness are mainly related to the health status of animals or to the longevity of breeding animals (Knap, 2005; Berghof et al., 2019), but traits related to global robustness of pigs during fattening period are not currently directly integrated into genetic evaluations of breeders. Incorporating one or more specific traits to evaluate robustness in genetic selection would be a key element in developing more sustainable breeding goals, with the advantage of providing cumulative gains that favorably affect following generations (Berghof et al., 2019). At first sight, animals that have the best performance could be considered to be the most robust because they expressed the best performance in a given environment compared to their contemporaries reared in the same environment. But this approach is limited to evaluation through technical performances and does not include any assistance that the animal may have had during the period of evaluation. Studies have already approached this subject but mainly focused on health-related traits that reflect mainly resistance to disease, with the risk to focus on specific diseases, and not general robustness (Berghof et al., 2019). For example, in rabbits, non-specific diseases resistance traits based on routinely collected phenotypes show non-zero heritabilities from 0.04 to 0.11 (Gunia et al., 2018).

The objective of this study is to go further than disease resistance and to propose a panel of robustness proxies for fattening pigs, based on phenotypes commonly available on farm, and to evaluate their genetic determinism. In this context, we define robustness as the ability of an animal to express or adapt its production potential in the face of changes in the environment compared to conspecific animals that have been raised under the same conditions.

MATERIAL AND METHODS

Populations

Animals from 2 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 feed conversion ratio (FCR) during the fattening period. The selection objective is also to meet European market requirements for carcass qualities at 100 kg by reducing backfat thickness and improving loin thickness. In both lines, ADG showed moderate unfavorable genetic correlations with FCR and backfat thickness. In the Pie NN line, ADG is moderately and favorably correlated with loin thickness. In the Pie line, FCR is moderately and unfavorably with carcass qualities.

The animals considered in this study were entire males (5116 Pie and 2140 Pie NN) raised from January 2019 to April 2021 at the boar testing station of the breeding company AXIOM Genetics (Azay-sur-Indre, France), built in 2015, located in "region Centre" in France. These males were born in 6 different farms (4 farms for Pie and 2 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, Swine dysentery) and vaccinated for *Mycoplasma pneumoniae* and PCV2.

They entered the boar testing station between 25 and 35 days of age (8 ± 3 kg body weight (BW)) at the rate of one group of 336 piglets every 3 weeks. They were raised in air-filtered quarantine rooms for 5 weeks 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 case of positive animals for monitored diseases, the whole group was excluded from the farm. Then, animals were raised in post-weaning rooms for 2 weeks and transferred to fattening rooms when they were approximately 70 to 80 days of age (≃35 kg BW). They were kept in fattening rooms during 65 to 77 days until the individual candidate test at around 140-150 days of age (≃34.5 kg BW). Fattening rooms are equipped with 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 are fed *ad-libitum* with commercial diets adapted to their physiological needs. The provided diets are non-limiting in amino-acids.

The station consisted in 2 quarantine rooms, 2 post-weaning rooms and 10 fattening rooms with 12 identical pens each, housing a maximum of 14 pigs per pen, leading to a total capacity of 2638 places. Each group, from the same week of introduction in the station, was divided in two fattening rooms (24 pens with 14 pigs). Sick pigs were treated by individual medication according to veterinary requirements. The station was not equipped with an air-cooling system.

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) was 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 backfat thickness (BF = mean of 3 measurements in mm) and ultrasonic longissimus dorsi thickness (LD = 1 measurement in mm). The BF and LD measures were transformed to correspond to their values at 100kg liveweight (BF100 and LD100 respectively) to compare animals at equivalent weight. This transformation was done by applying linear coefficients that multiply by the difference between 100kg and TBW. Coefficients used are 0.04mm/kg for BF100 and 0.27 mm/kg for LD100 (Sourdioux et al., 2009). A visual observation of the animals was then carried out in order to note the morphological defects, anomalies and clinical signs of disease according to a frame of reference (Appendix 1). Part of these observations was used to construct the robustness traits. Animals weighing less than 70kg are considered non-testable, that is to say that measures of BF and LD are not realized due to insufficient body development. These animals are only weighed and noted with the observation: "Out of test". The average daily gain (ADG) was calculated for animals as the difference between TBW and IBW divided by the number of days elapsed. 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):

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

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 sanitary events recorded during the fattening period (Table 1). The objectives of these synthetic traits are to describe the ability of the animal to be in good health and to have expressed minimal performance (growth) during individual testing. The trait R1 corresponds 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 at the time of the individual test (Note= 0). The trait R2 differentiates animals that are selectable, tested and without any negative observation (Note=

1), from those that are not tested or tested with a negative observation (Note= 0). We considered as a negative observations factors such as weak development and similar that were estimated to relate to the robustness of the animal (see Appendix 1 for full description). The trait R3 is a decomposition of the trait R2 in which the category of "selectable" animals is differentiated into those pigs that received at least one antibiotic of anti-inflammatory injection during the fattening period (Note=1) and those that didn't receive any injection (Note = 2). We didn't included symptoms in the trait definition due to the subjectivity of the observations.
In addition, the resilience phenotype during fattening period (ABC) developed by Revilla et al. (2021) was also calculated using weight measured by AFS for each candidate alive at the end of the fattening period. The trait ABC, Area Between Curves, is the accumulated difference between the unperturbed growth curve and the perturbed curve. The unperturbed growth-curve of each animal was modelled using the Gompertz equation. The perturbed curve was constructed using linear interpolation of body weight measurements recorded by AFS.

Genetic parameters estimation

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

$$\mathbf{y} = \boldsymbol{\mu} + \mathbf{X}\boldsymbol{\beta} + \mathbf{V}\mathbf{b} + \mathbf{Z}\mathbf{u} + \mathbf{e}$$

where $\mathbf{y}$ is the vector of phenotypes for the considered trait (R1, R2, R3 considered as continuous phenotypes, IBW, ADG, LD100, BF100, FCR, DFI and ABC), $\boldsymbol{\mu}$ the overall mean, $\boldsymbol{\beta}$ is the vector of fixed effects. $\mathbf{b}$ is the vector of random fattening group effect, with $\mathbf{b} \sim N(0, \mathbf{I}\sigma_b^2)$, where $\mathbf{I}$ is the identity matrix of appropriate size. $\mathbf{u}$ is the vector of additive genetic random effects with $\mathbf{u} \sim N(0, \mathbf{A}\sigma_u^2)$ where $\mathbf{A}$ is the pedigree-based relationship matrix. $\mathbf{X}$, $\mathbf{Z}$ and $\mathbf{V}$ are the known incidence matrices for fixed, animal genetic and fattening group effects, respectively. $\mathbf{e}$ is the vector of residual random effects with $\mathbf{e} \sim N(0, \mathbf{I}\sigma_e^2)$. For all estimated traits, the fixed effects tested at an α-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 The pedigrees contained 11 325 animals across 22 generations for Pie and 3 944 animals across 24 generations for Pie NN.
In the second step of the analysis, to follow the assumption of the BLUP method, which should be applied to a non-selected base population, and to estimate the covariance between traits, a series of multi-traits models including the 4 traits under selection (ADG, BF100, LD100 and FCR) and 2 of the other traits were applied to the data. Firstly, variance and covariance components were estimated with a 4-trait linear animal model including ADG, FCR, BF100 and LD100 traits, to estimate heritabilities and genetic correlations of traits under selection. Secondly, to estimate heritability for each non-selected trait (R1, R2, R3, IBW, DFI, RFI, and ABC) and their genetic correlations with the traits under selection, 5-trait linear animal models including the 4 traits under selection and 1 trait to be estimated were used. Thirdly, to estimate genetic correlations between the non-selected traits (R1, R2, R3, ABC, IBW, DFI and RFI), 6-trait linear animal models including the 4 traits under selection as well as the 2 traits for which the genetic correlation is estimated were performed.

Heritability (h^2) were calculated as the ratio of animal genetic variance to the total variance estimated with the 4-trait model for the traits under selection and with the 5-trait models for the non-selected traits.

RESULTS

Phenotypic means and distributions

The phenotypic mean of each production trait and of the resilience index (ABC) with its standard deviation (SD) are presented for each line in Table 2. Means of IBW, TBW and FCR were similar between the two lines. The Pie NN animals had slightly lower non-significant average values for ADG (-17g/d), DFI (-23g/d), LD100 (-4.8mm) and higher average BF100 (+0.6mm) than Pie. The mean and SD for ABC values were higher for Pie NN animals compared to Pie (+5223, i.e., +20.5% of area between curves), indicating more important deviations between unperturbed and perturbed growth. Figure 1 shows the distribution of the different modalities for the traits R1, R2 and R3 for the two lines. For the traits R1 and R2, the distributions were very similar between Pie and Pie NN. Approximatively 95% of the animals introduced in fattening rooms were "Present" (Trait R1 – Note=1) the day of individual testing and around 80% were "Selectable" (Trait R2 – Note=1). For the trait R3, the Pie line had a higher proportion of animals "Selectable with medicine" (Trait R3 – Note=1) than the Pie NN line (32.2% vs 19.7% respectively).

Variance-Covariance components

Estimates of heritability (h^2) and proportion of phenotypic variance due to fattening group effect (b^2) are given in Table 3. For the robustness traits R1, R2 and R3, heritability estimates were low and in the same range for the 2 lines, ranging from 0.04 ±0.02 to 0.13 ±0.02 Heritability estimates for R2 and R3 tended to be higher than for R1 in each line. Heritability estimates for the resilience index (ABC) were moderate for Pie (0.23±0.04) and low for Pie NN (0.06±0.03). For the traits under selection (ADG, FCR, BF100 and LD100), IBW, DFI and RFI, heritability estimates were moderate to high in the Pie line, ranging from 0.28 ±0.04 to 0.59 ±0.04. Except for ADG, heritability estimates tended to be lower in the Pie NN line compared to Pie; they ranged from 0.15 ±0.04 to 0.46 ±0.06. The fattening group effect ranged from 0.02 ±0.01 to 0.38 ±0.07 for the studied traits.

The genetic correlations between robustness scores (R1, R2, R3), resilience index (ABC) and production traits are presented in Table 4 for Pie line and Table 5 for Pie NN. The genetic correlations between all studied traits are presented in Appendix2 for Pie and in Appendix3 for Pie NN. Several estimates of genetic correlations had large standard errors and should be interpreted with caution. Genetic correlations between R1 and the 2 other robustness traits were moderate in Pie NN line, ranging from 0.33 ±0.21 to 0.38 ±0.21 and higher in Pie line, ranging from 0.49 ±0.17 to 0.60 ±0.14. In both paternal lines, the genetic correlation between R2 and R3 was high (0.93 ±0.03 and 0.95 ±0.03, 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 -0.14 to -0.17) and negative or null in the Pie line (ranging from -0.17 to 0.09), 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 0.73), and moderately correlated

with FCR, from 0.35 ±0.21 to 0.46 ±0.20. R1 were moderately correlated with ADG from 0.21 ±0.17 in Pie line to 0.22 ±0.19 in Pie NN line. The carcass traits (BF100 and LD100) tended to be positively correlated with the three robustness traits, (estimates ranged from 0.17 ±0.16 to 0.45 ±0.16). For the non-selected traits, R2 and R3 were highly correlated with IBW and DFI (correlations higher than 0.73). In Pie line, R1 were moderately correlated with IBW and DFI, 0.47 ±0.13, correlations were lower for the Pie NN line (ranging from 0.13 to 0.15). 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 values close to 0, expect in the Pie line for IBW (-0.26±0.19).

DISCUSSION

Genetic parameters for robustness traits

The heritabilities for the traits R1, R2 and R3 are low but not null, with the exception of R1 in Pie line (related to the standard deviation of the estimate). Most references to similar traits have focused on traits related to the resistance to non-specific or specific diseases or related to the use of antibiotics (Gunia et al., 2015; Gunia et al., 2018; Putz et al., 2019; Shrestha et al., 2020; Gorssen et al., 2021). The estimated heritabilities from our study were in the same range as those presented in these different publications.

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, 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. Gunia et al. (2018) estimated a similar value in rabbits for the trait resistance to non-specific disease in the selection environment (0.04 ±0.01).

The present study was carried out in a standard breeding environment, i.e. designed to minimize exposure to environmental challenges. In some studies, the animals were reared under challenging conditions which seems to allow a better phenotyping of the robustness of the animals and probably then to obtain higher heritability estimates. Indeed, Gunia et al. (2018) estimated higher heritabilities for resistance to non-specific 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 of 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 expressed and conditions that favor expression of robustness. This is a relevant question for future selection strategies that aim to produce efficient and robust animals.

Among the robustness traits, R2 was the trait with the highest heritability value in the two lines. It was highly genetically correlated (>0.93) with R3 and, compared to R3, required less

information in order to be calculated (R3 includes antibiotic and anti-inflammatory injections). The trait R2 meets the objective of a trait to select on in order to have live and healthy animals at the end of the period. Nonetheless, even if R3 had a slightly lower heritability than R2 and required more information to be calculated, this trait could be more interesting to select for because it in addition would favor the reduction of the use of medication. This reduction corresponds to both the societal expectation and the economic expectation of modern pig production.

Fattening group treated 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, described by Van Vleck (1987).

The risks associated with treating contemporary group as a random effect is to obtain biased breeding values if there is a non-random 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 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 is expected to avoid overestimating heritabilities.

In this study, the sires from the 2 lines were used at least in two mating groups in each farm and in two different farms, this limits the risk of confounding between environmental (i.e. fattening group) and genetic effects. Each fattening group consists of animals sourced from between 1 and 3 farrowing farms in the Pie line and from 1 or 2 farrowing farms in the Pie NN line. Given this, the effect of farrowing farm was included as a fixed effect.

Binary traits: threshold vs linear models

The analysis of R1 and R2 traits was carried out using a linear model whereas they are binary traits. Theoretically, the use of linear models to analyze binary 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 results between the two methods, when the prevalence of the analyzed traits was between 25% and 75%. The trait R1 didn't meet this condition with a prevalence of 4.8% and 5.7% while R2 were close to the condition with a prevalence of 19.3% and 20.2%. To evaluate the consequences of applying a linear model for R1 and R2 instead of a threshold model, we compared the linear and threshold models for each of these two traits analyzed separately. For R1, threshold model, heritabilities estimated on the observed scale, after applying the transformation proposed by Dempster and Lerner (1950), were 0.02 ±0.01 for the Pie line and 0.03 ±0.02 for the Pie NN line. For R2, the heritabilities from the threshold

model were 0.04 ±0.01 in the Pie line and 0.05 ±0.02 in the Pie NN line. For both R1 and R2, these values estimated using a single-trait linear model are of the same amplitude as those estimated using the threshold model.

Heritability estimates for production traits

Heritability estimates for ADG and DFI were consistent with those reported in literature for Piétrain or Large-White pigs raised in similar environmental conditions, which are respectively from 0.29 to 0.50 and from 0.31 to 0.55 (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: 0.38-0.48 ; LD100: 0.25-0.34). Our estimates of heritability for FCR and RFI in Pie and Pie NN lines were lower, especially for Pie NN, than values presented by Saintilan et al. (2013) and Déru et al. (2020), which are respectively from 0.33 to 0.34 and from 0.40 to 0.47. 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 0.13 to 0.35. 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 3686 and 6667 for RFI.

Heritability estimates for resilience trait (ABC)

For the trait ABC, the heritability for the Pie NN line was consistent with that published by Revilla et al. (2021; 0.04) but we found a much higher heritability in the Pie line. This difference is the result of a lower phenotypic variance in both lines and a higher genetic variance in the Pie line compared to those reported by Revilla (2021 - phenotypic variance: $4.95_{E}{}^{+08}$ vs $10.97_{E}{}^{+08}$ in Pie and $6.20_{E}{}^{+08}$ vs $12.75_{E}{}^{+08}$ in Pie NN, genetic variance: $1.14_{E}{}^{+08}$ vs $0.42_{E}{}^{+08}$ in Pie line and 0.38^{+08} vs $0.40_{E}{}^{+08}$). In the present study, an improved outlier detection procedure was used on the raw data, which reduced the contribution of erroneous measures to the phenotypic variance.

Genetic correlations between robustness and production traits

The two growth traits (IBW and ADG) were strongly correlated with R2 and R3. Shrestha et al. (2020) identified also a strong and favorable genetic correlation between a resistance trait and growth at different periods in rabbit (from -0.60 to -0.94). Correlations with IBW showed that growth during post-weaning, i.e. pre-test period, had a strong impact on the robustness scores evaluated during the fattening period. 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 to -0.70). 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 years, 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 to growth traits and thus would, if selection

is made using these traits, allow us to improve animal's 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. 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 non-productive 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 criteria and the RFI are close to 0 in the Pie NN line or slightly unfavorable in the Pie line. For the relation between RFI and robustness, it is hypothesized that selection for low RFI may limit the animals' ability to allocate nutrients to functions to face with perturbations (Gilbert et al., 2017). In contrast, several studies have shown, through divergent selection experiments on RFI, the favorable effects of lines with low RFI on sensitivity to the PRRS virus (Dunkelberger et al., 2015) or on the risk of being reformed between 70 days of age and slaughter (Gilbert et al., 2017).

Genetic correlations of robustness traits with the ABC were difficult to interpret, due to low precision, but would tend to show a slightly favorable relation in Pie NN for all robustness traits and for R1 in Pie. The trait based on a dynamic analysis of the evolution of the weight (ABC) approach is therefore relatively independent of the criteria created from the static data (R1, R2, 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, i.e., 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 finer criteria of robustness.

CONCLUSION

This study showed through traits R2 and R3 that it was possible to set up a selection based on robustness in growing pigs from scores calculated with 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, but on the other hand R3 includes the objective of favoring animals that have less received medicine treatments. The introduction of R2 or R3 traits in the breeding goal of paternal lines is relevant but would require investigating more on the potential genetic gain achievable in a multi-trait breeding goal. 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 the whole animal's life. Indeed, is a robust fattening pig also robust throughout its life?

LITERATURE CITED

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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…), 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

Table 2. Descriptive statistics (Mean and SD: standard deviation) for ABC and production traits for each line[2]

	Pie		**Pie NN**	
Trait (unit)[1]	Mean	*SD*	Mean	*SD*
IBW (kg)	34.5	*6.1*	34.5	*6.2*
TBW (kg)	108.9	*11.4*	108.8	*11.5*
ADG (g/d)	1009	*104*	992	*108*
FCR (kg/kg)	2.25	*0.18*	2.26	*0.19*
DFI (g/d)	2263	*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	25503	*21603*	30726	*24764*

[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 100kg liveweight; LD100= longissimus dorsi thickness estimated at 100 kg liveweight; ABC= relisience index

[2] Pie= Piétrain Français; Pie NN= Piétrain NN Français free from halothane-sensitivity

Table 3. Estimates of heritability (h^2) and group effect ratio (b^2) for the traits recorded (± standard error) for each line[2]

	Pie		Pie NN	
Trait[1]	h^2	b^2	h^2	b^2
R1[4]	0.04 ± 0.02	0.02 ± 0.01	0.08± 0.03	0.04± 0.02
R2[4]	0.13 ± 0.02	0.03± 0.01	0.12± 0.03	0.02± 0.01
R3[4]	0.08 ± 0.02	0.07± 0.02	0.11± 0.03	0.03± 0.01
ABC[43]	0.23 ± 0.03	0.07± 0.02	0.06± 0.03	0.05± 0.02
IBW[4]	0.59 ± 0.04	0.16± 0.04	0.46± 0.06	0.20± 0.04
ADG[3]	0.32 ± 0.04	0.13± 0.03	0.40± 0.06	0.12± 0.03
FCR[3]	0.29± 0.04	0.15± 0.04	0.15± 0.04	0.13± 0.03
DFI[4]	0.44 ± 0.04	0.16± 0.04	0.41± 0.06	0.16± 0.04
RFI[4]	0.28± 0.04	0.15± 0.04	0.14± 0.04	0.12± 0.03
BF100[3]	0.39± 0.04	0.12± 0.03	0.35± 0.06	0.12± 0.03
LD100[3]	0.42± 0.06	0.21± 0.04	0.28± 0.05	0.38± 0.07

[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 100kg liveweight; LD100= longissimus dorsi thickness estimated at 100 kg liveweight; ABC= resilience index

[2] Pie= Piétrain Français; Pie NN= Piétrain NN Français free from halothane-sensitivity

[3]Estimates from a 4-traits multiple trait model (ADG, FCR, BF100, LD100)

[4]Estimates from a 5-traits multiple trait model (ADG, FCR, BF100, LD100 and the trait under consideration)

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

Trait[1]	**R1**	**R2**	**R3**	**ABC**
R1		0.60 ±0.14[3]	0.49 ±0.17[3]	-0.17 ±0.18[3]
R2	0.60 ±0.14[3]		0.95 ±0.03[3]	0.01 ±0.13[3]
ABC	-0.17 ±0.18[3]	0.01 ±0.13[3]	0.09 ±0.14[3]	
IBW	0.47 ±0.13[3]	0.73 ±0.06[3]	0.75 ±0.07[3]	0.09 ±0.09[3]
ADG	0.21 ±0.17[2]	0.78 ±0.06[2]	0.76 ±0.08[2]	-0.08 ±0.11[2]
FCR	0.43 ±0.17[2]	0.43 ±0.11[2]	0.38 ±0.13[2]	0.04 ±0.11[2]
DFI	0.47 ±0.13[3]	0.84 ±0.05[3]	0.79 ±0.08[3]	-0.03 ±0.10[3]
RFI	0.23 ±0.17[3]	0.12 ±0.12[3]	0.10 ±0.13[3]	-0.02 ±0.11[3]
BF100	0.17 ±0.16[2]	0.20 ±0.11[2]	0.20 ±0.13[2]	-0.04 ±0.10[2]
LD100	0.45 ±0.16[2]	0.28 ±0.11[2]	0.38 ±0.13[2]	0.02 ±0.11[2]

[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 100kg liveweight; LD100= longissimus dorsi thickness estimated at 100 kg liveweight; ABC= resilience index

[2]Estimates from a 5-traits multiple trait model (ADG, FCR, BF100, LD100 and the trait under consideration)

[3]Estimates from a 6-traits multiple trait model (ADG, FCR, BF100, LD100 and the two traits under consideration)

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

Trait[1]	R1	R2	R3	ABC
R1		0.33 ±0.21[3]	0.38 ±0.21[3]	-0.15 ±0.31[3]
R2	0.33 ±0.21[3]		0.93 ±0.04[3]	-0.17 ±0.26[3]
ABC	-0.15 ±0.31[3]	-0.17 ±0.26[3]	-0.14 ±0.27[3]	
IBW	0.13 ±0.17[3]	0.80 ±0.09[3]	0.74 ±0.11[3]	-0.26 ±0.19[3]
ADG	0.22 ±0.19[2]	0.87 ±0.08[2]	0.73 ±0.11[2]	-0.15 ±0.22[2]
FCR	0.15 ±0.20[2]	0.46 ±0.20[2]	0.35 ±0.21[2]	0.16 ±0.28[2]
DFI	0.15 ±0.20[3]	0.90 ±0.08[3]	0.73 ±0.12[3]	-0.05 ±0.23[3]
RFI	0 ±0.25[3]	0.03 ±0.22[3]	-0.03 ±0.23[3]	0.21 ±0.29[3]
BF100	0.21 ±0.20[2]	0.29 ±0.16[2]	0.29 ±0.17[2]	0.21 ±0.23[2]
LD100	0.20 ±0.19[2]	0.17 ±0.16[2]	0.23 ±0.17[2]	-0.07 ±0.23[2]

[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 100kg liveweight; LD100= longissimus dorsi thickness estimated at 100 kg liveweight; ABC= resilience index

[2]Estimates from a 5-traits multiple trait model (ADG, FCR, BF100, LD100 and the trait under consideration)

[3]Estimates from a 6-traits multiple trait model (ADG, FCR, BF100, LD100 and the two traits under consideration)

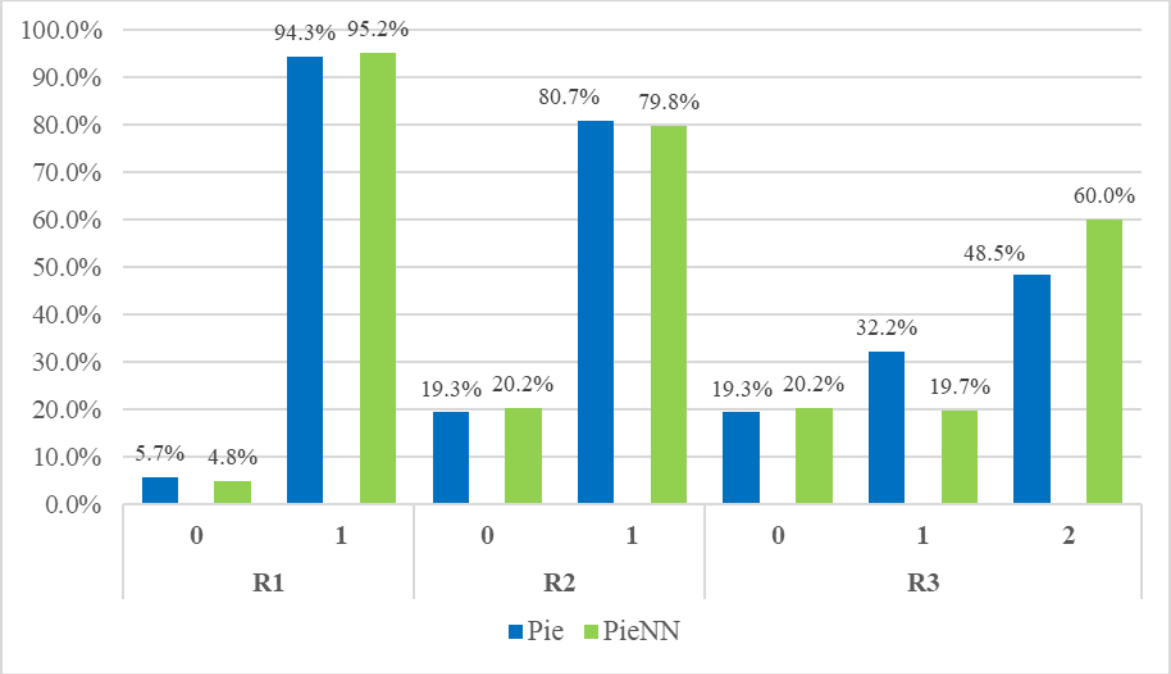


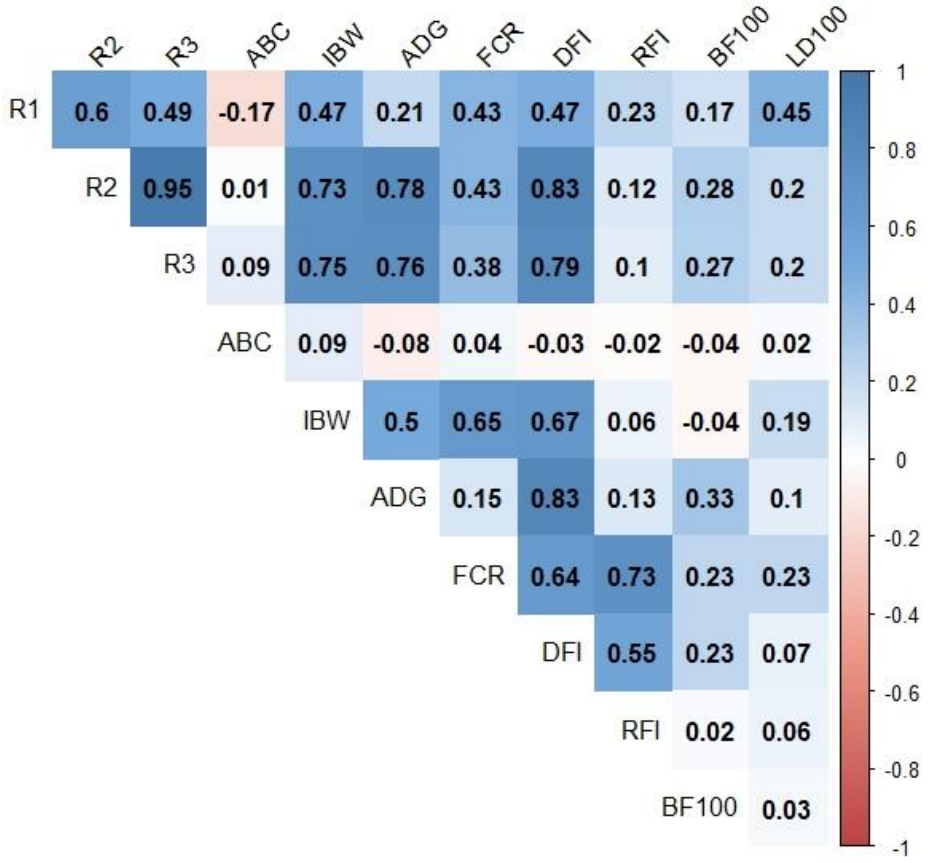
Figure 1. Distribution of modalities for the 3 robustness traits (R1, R2 and R3) for the Pie and Pie NN lines.

Pie= Piétrain Français; Pie NN= Piétrain NN Français free from halothane-sensitivity

Appendix 1. List of individuals observations performed during the individual test

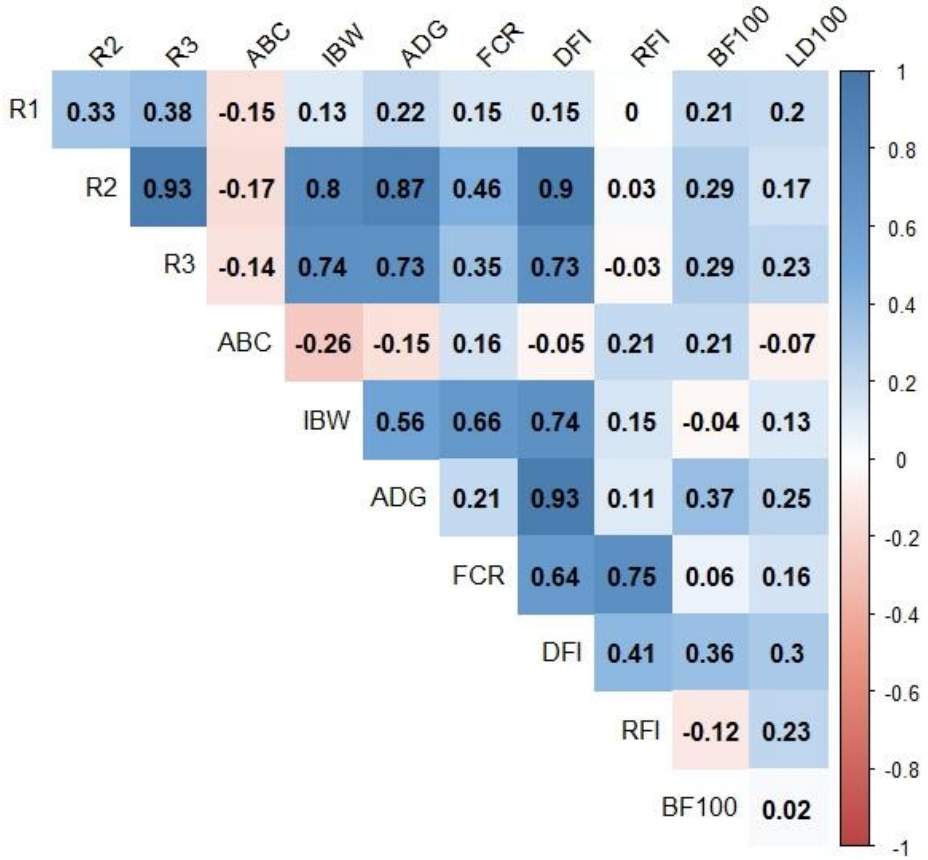
	Observation
Observations taken into account to define the robustness traits	Abcess Cannibalism Capelet Weak development / Low body condition Callus Shortness of breath Necrotic ear Out of test (testing body weight < 70kg) Shaker
Observations not taken into account to define the robustness traits	Lack of leg soundness Low and short Conformation / Body development Culard Important conformation Fat animal Asymmetric hooves Teats default Incorrect conformation Hernia

Appendix 2. Estimates of genetic correlations (r^2a) between robustness (R1, R2 and R3), ABC and production traits for Piétrain line (Pie).



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 100kg liveweight; LD100= longissimus dorsi thickness estimated at 100 kg liveweight; ABC= resilience index

Appendix 3. Estimates of genetic correlations (r^2a) between robustness (R1, R2 and R3), ABC and production traits for Piétrain NN line (Pie NN).



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 100kg liveweight; LD100= longissimus dorsi thickness estimated at 100 kg liveweight; ABC= resilience index