Optimal definition of contemporary groups for crossbred pigs in a joint purebred and crossbred genetic evaluation

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ABSTRACT

In the pig industry, purebred animals are raised in nucleus herds and selected to produce crossbred progeny to perform in commercial environments. Crossbred and purebred performances are different, correlated traits. All purebreds in a pen have their performance assessed together at the end of a performance test. However, only selected crossbreds are removed (based on visual inspection) and measured at different times, creating many small contemporary groups (CG). This may reduce EBV prediction accuracies. Considering this sequential recording of crossbreds, the objective was to investigate the impact of different CG definitions on genetic parameters and EBV prediction accuracy for crossbred traits. Growth rate ($G_p$) and ultrasound backfat ($BF_p$) records were available for purebreds. Lifetime growth ($G_X$) and backfat ($BF_X$) were recorded on crossbreds. Different CG were tested: CG_all included farm, sex, birth year and birth week, CG_week added slaughter week, and CG_day used slaughter day instead of week. Data of 124,709 crossbreds were used. The purebred phenotypes (62,274 animals) included 3 generations of purebred ancestors of these crossbreds and their CG mates. Variance components for 4-trait models with different CG definitions were estimated with average information REML. Purebred traits’ variance components remained stable across CG definitions and varied slightly for $BF_X$. Additive genetic variances (and heritabilities) for $G_X$ fluctuated more: $812 \pm 36 (0.28 \pm 0.01)$, $257 \pm 15 (0.17 \pm 0.01)$ and $204 \pm 13 (0.15 \pm 0.01)$ for CG_all, CG_week, and CG_day, respectively. Age at slaughter (AAS) and HCW adjusted for age were investigated as alternatives for $G_X$. Both have potential for selection but lower heritabilities compared to $G_X$: $0.21 \pm 0.01 (0.18 \pm 0.01)$, $0.16 \pm 0.02 (0.16 \pm 0.01)$, and $0.10 \pm 0.01 (0.14 \pm 0.01)$ for AAS (HCW) using CG_all, CG_week, and CG_day, respectively. The predictive ability, linear regression (LR) accuracy, bias, and dispersion of crossbred traits in
crossbreds favored CG_day, but correlations with unadjusted phenotypes favored CG_all. In purebreds, CG_all showed the best LR accuracy, while showing small relative differences in bias and dispersion. Different GC scenarios showed no relevant impact on BF\textsubscript{X} EBV. This study shows that different CG definitions may affect evaluation stability and animal ranking. Results suggest that ignoring slaughter dates in CG is more appropriate for estimating crossbred trait EBV for purebred animals.

**Keywords:** sequential selection, commercial pigs, grading, predictive ability, model validation
### ABBREVIATIONS

| Abbreviation | Description |
|--------------|-------------|
| AAS          | Age at slaughter |
| BF<sub>P</sub> | Backfat in purebred animals |
| BF<sub>X</sub> | Backfat in crossbred animals |
| CG           | Contemporary group |
| CG<sub>all</sub> | Contemporary group based on farm, sex, birth year and birth week |
| CG<sub>day</sub> | Contemporary group based on farm, sex, birth year, birth week and slaughter day |
| CG<sub>week</sub> | Contemporary group based on farm, sex, birth year, birth week and slaughter week |
| EBV          | Estimated breeding value |
| EW           | Weight at end of growth test period (measured in purebred animals) |
| G<sub>P</sub> | Growth in purebred animals |
| G<sub>X</sub> | Growth in crossbred animals |
| HCW          | Hot carcass weight (measured in crossbred animals) |
| IGE          | Indirect genetic effects |
| LR           | Linear regression, or Legarra-Reverter, method |
| REML         | Restricted maximum likelihood |
INTRODUCTION

Crossbreeding is a common practice in the pig industry. Similar traits measured in crossbred and purebred animals may be considered as effectively different traits (Wei and van der Werf 1994; Lutaaya et al. 2001; Christensen et al. 2014). This difference can largely be attributed to environmental factors. However, traits may also be measured or determined differently. For instance, growth in purebred animals is often calculated as live weight at the end of a growth test divided by age, whereas crossbred growth is calculated as hot carcass weight divided by age. These differences in cross- and purebred performances are important since purebred animals are selected to produce crossbred animals expected to perform optimally in a commercial environment. As these traits are different and genetic merits for them are likely influenced by different genetic factors, the animals that produce the best purebred offspring may not produce the best crossbred offspring (Lutaaya et al. 2001).

Crossbred and purebred animals perform in considerably different environments. Housing conditions are better controlled for purebred animals while conditions for crossbred animals may be harsher and more variable. The environmental effects accounted for in purebred animals, may not be as relevant in crossbred animals, and vice versa. Additionally, crossbred animals are kept in pens with large pen mate groups, which can affect growth adversely, especially for the smallest pigs. This is known as social interaction (or competition) effects, which is an indirect genetic effect (IGE) that individuals have on their peers (Bijma 2014). Because of the resulting growth rate heterogeneity, crossbred pen mates reach the market size/weight (based on visual inspection) in different time periods and are removed from the pen sequentially (i.e. fast growers are removed first). This practice helps to create more space for the smallest pigs to grow and allows the pork industry to have more uniform carcasses. However, as
a consequence, there is usually no single point at which all animals in the pen are measured together, and not all animals initially in the pen experience the same IGE until slaughter. Conversely, purebreds remain in the same group over the growth test period and are measured together at the conclusion of the test.

The fact that crossbred animals in the same pen are slaughtered, and therefore, phenotyped at different times should, at best, be accounted for by the model to avoid EBV bias and preserve its accuracy. Including selection day in the construction of contemporary groups (CG) creates multiple small groups that compare only the best animals in the pen at that time. These superior animals could be unfairly penalized by never being compared to their more inferior contemporaries, while the inferior animals can benefit. Age adjustments are questionable since animals are removed from the pen based on size, regardless of age, producing growth curves that are not truly reflective of the physiological process. Additionally, it has been shown that earlier weights are poor predictors of later growth of pigs within the same pen. Shull (2013) found that only 57.8% of pigs were in the same live weight quartile at 10- and 22-week post-wean and the rank correlation between birth weight and weaning weight was only 0.50. When CG have more animals, accuracy of evaluation may increase because of better estimation of CG effects. However, ideal contemporary groups should not only be larger, but also appropriately defined. Bias can be introduced if animals in the group are not exposed to the same conditions (Carabaño et al. 2004; Vasconcelos et al. 2008; Crump et al. 2010).

The objective of this study was to find an optimal contemporary group definition to evaluate crossbred traits for both purebred and crossbred animals when recording is incomplete, and animals are sequentially phenotyped based on prior visual inspection.
MATERIALS AND METHODS

Animal Care and Use Committee approval was not needed because information was obtained from pre-existing databases.

Data

Data from three crossbred farms recorded from January 2016 to May 2020 were used for this study, totaling 124,709 animals. Crossbred animals had phenotypes for growth ($G_X$) and backfat ($BF_X$). The purebred population included three generations of ancestors of the crossbred individuals as well as their contemporary group mates. Purebred ancestors of crossbred pigs totaled 12,533 individuals, but only 1,793 of them had measurements for both growth ($G_P$) and ultrasound backfat ($BF_P$). The total number of purebred animals with measurements was 62,274. The pedigree included 203,374 animals, of which 1,430 were sires and 22,758 were dams. The instrumentations used to measure $BF_X$ may differ between harvest sites. These instrumentation effects are accounted for through the inclusion of farm in the CG definition. To further reduce potential bias introduced by different instruments, purebred sires are represented across farms. The $G_P$ was calculated as the live weight at the end of the growth test divided by age, whereas $G_X$ was calculated as the carcass weight divided by age. Therefore, $G_P$ and $G_X$ make two major assumptions – growth has a linear behavior and birth weight is zero for all animals. The summary statistics for traits and age are presented in Table 1. Purebred animals were measured at a considerably younger age than crossbred animals, thus traits in each group may capture different phases of the growth curve. Additionally, purebred animals remained in the same pen for the duration of the weight test, whereas crossbred animals were removed for slaughter at
different time points based on visual inspection. The remaining animals were not weighed at the time when selected pen mates were removed.

Pen information was not available to be included in contemporary groups, but pen sizes were known to accommodate 30-60 pigs. Contemporary group for purebred animals was compiled of farm, line, sex, birth year, and birth week. Three different contemporary group compositions for crossbred traits were tested, including 1) CG_all, which was compiled of birth farm, sex, birth year, and birth week, 2) CG_week, which was compiled of birth farm, sex, birth year, birth week, and slaughter week, 3) CG_day, which was compiled of birth farm, sex, birth year, birth week, and slaughter day. In the CG_day scenario, there were 10,598 groups with size ranging from 1 to 231 animals, with an average of 11.8 animals. Within these groups, 1,928 (18.2%) had only one animal and 2,981 (28.1%) only included individuals sired by the same single boar. In the CG_week scenario, there were 5,850 groups with sizes ranging from 1 to 266 animals, with an average size of 21.3 animals. Within these groups, 532 (9.09%) had only one animal and 813 (13.9%) only included individuals sired by the same single boar. There was, on average, 1.5 slaughter dates within each group. CG_all had 970 groups ranging from 1 to 566 animals, with an average size of 128.6 animals. Only 2 (0.21%) groups had only one animal and 12 (1.24%) had all individuals sired by the same single boar. There was an average of 9 slaughter dates per group, with 359 groups (37.01%) having 10 or more slaughter dates, up to a maximum of 22. Only CGs with more than 4 animals were considered for variance component estimation. However, all animals were included for breeding value prediction. Primarily, a four-trait model for $G_p$, $BF_p$, $G_X$, and $BF_X$ was used:

$$y = Xb + Wc + Zu + e$$
where \( y \) is the vector of phenotypes; \( b \) is a vector of solutions for fixed effects while \( X \) is an incidence matrix relating phenotypes to these effects (all traits had CG as fixed effect, but BF\(_P\) and BF\(_X\) also included weight as covariate); \( c \) is a vector of random litter effects while \( W \) is an incidence matrix relating phenotypes to these effects; \( u \) is a vector of direct additive genetic effects while \( Z \) is an incidence matrix relating phenotypes to the additive effect; \( e \) is a vector of residuals. Vector \( c \) is distributed as MVN(0, \( \mathbf{I}_L \))

\[
\mathbf{L}_0 = \begin{bmatrix}
\sigma^2_{lp} & \sigma_{lp,lbfp} & 0 & 0 \\
\sigma_{lp,lbfp} & \sigma^2_{lbfp} & 0 & 0 \\
0 & 0 & \sigma^2_{lgx} & \sigma_{lgx,lbfx} \\
0 & 0 & \sigma_{lgx,lbfx} & \sigma^2_{lbfx}
\end{bmatrix}
\]

vector \( a \) is distributed as MVN(0, \( \mathbf{A}_0 \))

\[
\mathbf{G}_0 = \begin{bmatrix}
\sigma^2_{agp} & \sigma_{agp,abfp} & \sigma_{agp,agx} & \sigma_{agp,abfx} \\
\sigma_{agp,abfp} & \sigma^2_{abfp} & \sigma_{abfp,agx} & \sigma_{abfp,abfx} \\
\sigma_{agp,agx} & \sigma_{abfp,agx} & \sigma^2_{agx} & \sigma_{agx,abfx} \\
\sigma_{agp,abfx} & \sigma_{abfp,abfx} & \sigma_{agx,abfx} & \sigma^2_{abfx}
\end{bmatrix}
\]

vector \( e \) is distributed as MVN(0, \( \mathbf{R}_0 \))

\[
\mathbf{R}_0 = \begin{bmatrix}
\sigma^2_{egp} & \sigma_{egp,ebfp} & 0 & 0 \\
\sigma_{egp,ebfp} & \sigma^2_{ebfp} & 0 & 0 \\
0 & 0 & \sigma^2_{egx} & \sigma_{egx,ebfx} \\
0 & 0 & \sigma_{egx,ebfx} & \sigma^2_{ebfx}
\end{bmatrix}
\]

where \( \sigma^2_a \) is the additive variance, \( \sigma^2_l \) is the litter variance, and \( \sigma^2_e \) is the residual variance. Age at slaughter (AAS) and carcass weight (HCW) were also investigated as potential replacement traits for crossbred growth. Accordingly, models for these two traits included the relevant contemporary group as fixed effect, and litter and additive genetic effects as random.
Furthermore, HCW included age at slaughter as covariate. This should be a reflection of $G_X$ since $G_X$ is measured as HCW divided by age, while this approach is HCW adjusted for age. However, regression coefficients are recalculated at every genetic evaluation and is therefore dependent on data changes. We used AIREMLf90 to estimate variance components and BLUP90IOD to compute EBV. Both programs belong to the BLUPf90 software family (Misztal et al. 2014). The variance of the solutions for CG was used to measure the amount of variance absorbed by the CG effect when different CG definitions are used for $G_X$ and $BF_X$.

Cross-validation tests were used to compare models with different CG definitions. The accuracy of predicting future EBV and the ability to predict future performance were evaluated for purebreds and crossbreds. The crossbred validation data set consisted of 66,585 animals born in 2018 and 2019. The purebred validation set consisted of parents of the crossbred validation animals, totaling 7,454 animals, out of which 377 had both $G_P$ and $BF_P$ measurements. Predicted breeding values of validation animals were obtained with all data ($\hat{u}_{\text{whole}}$), and without phenotypes of crossbred validation animals ($\hat{u}_{\text{partial}}$). Different validation measures were used to evaluate the changes in accuracy, including the linear regression method (Legarra and Reverter 2018), the predictive ability, and Pearson correlations between $\hat{u}_{\text{whole}}$ and unadjusted phenotypes. Different measures to evaluate stability included the regression coefficient (dispersion), difference between $\hat{u}_{\text{whole}}$ and $\hat{u}_{\text{partial}}$ (bias), and Pearson correlations between the $\hat{u}_{\text{whole}}$ obtained using different CG definitions. The linear regression (LR) method (Legarra and Reverter 2018) calculates validation accuracy as

$$acc_{LR} = \sqrt{\frac{\text{cov}(\hat{u}_{\text{whole}}, \hat{u}_{\text{partial}})}{(1-F)\sigma_a^2}},$$
where $acc_{LR}$ stands for accuracy from the LR method, $\bar{F}$ is the average inbreeding coefficient of the validation population and $\sigma_a^2$ is the additive genetic variance. The dispersion was measured as the regression coefficient ($b_1$) of the regression of $\hat{u}_{whole}$ on $\hat{u}_{partial}$:

$$b_1 = \frac{cov(\hat{u}_{whole}, \hat{u}_{partial})}{var(\hat{u}_{partial})},$$

and bias as $\bar{u}_{partial} - \bar{u}_{whole}$. The Pearson correlation between $\hat{u}_{whole}$ and $\hat{u}_{partial}$ was to measure the stability of model-based predictions when phenotypes are added to the data.

The ability to predict future performance (i.e., predictive ability) was calculated on the basis of $cor(y_{adj}, \hat{u}_{partial})$. However, this correlation was transformed for each trait to the accuracy scale as:

$$acc_{PRED} = cor(y_{adj}, \hat{u}_{partial})/h,$$

where $acc_{PRED}$ stands for accuracy transformed from predictive ability, $y_{adj}$ is the vector of phenotypes adjusted for all other effects in the model and $h$ is the square root of trait heritability (Legarra et al. 2008). Since only crossbred animals have phenotypes for $G_X$ and $BFX$, this could only be estimated for crossbred animals.

Because fixed effects for crossbred phenotypes changed across scenarios, the benchmark for each model was different. Therefore, we calculated Pearson correlations between unadjusted phenotypes for crossbred animals and $\hat{u}_{partial}$ or $\hat{u}_{whole}$. The $\hat{u}_{whole}$ estimated under different CG definitions were also compared to each other with Pearson correlations.
RESULTS

Estimated values for variances of crossbred traits (Table 2) decreased in general as contemporary group composition became more specific (from CG_all to CG_day). The additive genetic variance for G_X using CG_all was exceptionally large (812 vs 257 for CG_week and 204 for CG_day). The variances of the solutions for CG effect on G_X (and BF_X) were 23 451 (25.68), 35 313 (34.60), and 67 842 (60.09) for CG_day, CG_week and CG_all, respectively.

Variance estimates for purebred traits are not included in the table. Estimates for litter, additive, and residual variances remained stable for purebred traits, which is expected since no changes were made to contemporary groups of purebred animals themselves. The estimated values for variance components for G_P and BF_P were 809 ± 25 and 0.20 ± 0.01 for litter effects, 1 404 ± 77 and 1.41 ± 0.05 for additive genetic effects, and 3 022 ± 43 and 1.84 ± 0.03 for residuals, respectively.

Heritability and genetic correlation estimates for G_P, BF_P, G_X, and BF_X are presented in Table 3. The heritability estimates remained stable for G_P, BF_P and BF_X, whereas the heritability for G_X increased as the CG became more inclusive. Genetic correlations between BF_X and purebred traits remained relatively stable under all contemporary groups definitions. The correlations between G_X and BF_P were more sensitive to change and became stronger as contemporary group size increased. Correlations between G_X and G_P showed the greatest discrepancy. The standard errors of genetic parameters remained stable across different contemporary group definitions.

Heritability and genetic correlation estimates with AAS replacing G_X in the 4-trait model are presented in Table 4. Heritability estimates for AAS halved as contemporary group size decreased from CG_all to CG_day and are lower than G_X heritability under the analogous 4-trait
model. The correlation between $G_P$ and AAS was also favorable (i.e., negative) but weaker relatively to the $G_P$-$G_X$ association ($-0.46 \pm 0.07$ vs. $0.56 \pm 0.06$, respectively).

Heritability and genetic correlation estimates when HCW replaces $G_X$ in the 4-trait model are presented in Table 5. The heritability estimates for HCW using CG_all were substantially lower than that of $G_X$ in an analogous 4-trait model (0.18 vs 0.28), but similar for CG_week (0.16 vs 0.17) and CG_day (0.14 vs 0.15). Correlations of purebred traits with HCW were stronger than those with $G_X$ using CG_week and CG_day, but weaker when using CG_all.

Model comparison results based on the LR method for purebred animals and crossbred animals are presented in Tables 6 and 7, respectively. The breeding values obtained using different variance components and CG did not lead to marked changes for BF_X. Accuracies, dispersion, bias, and correlations remain similar across scenarios for BF_X in purebred validation animals and barely changed for crossbred validation animals. Conversely, more performance variability was observed for $G_X$ for both purebred and crossbred validation sets. The LR accuracy was highest for purebred animals for CG_all at 0.36 versus 0.33 for CG_day and 0.31 for CG_week. Bias was least for CG_day (0.02) and most for CG_all (0.06). For $G_X$ in crossbred animals, predictive ability was highest for CG_day (0.30) and lowest for CG_all (0.27). LR accuracy was also highest for CG_day (0.28) but lowest for CG_week (0.26). Relatively greater performance discrepancies are observed for correlations (0.53, 0.49 and 0.43 for CG_day, CG_week and CG_all), dispersion (1.00, 0.97 and 0.86 for CG_day, CG_week and CG_all) and bias (0.03, 0.38 and 0.88 for CG_day, CG_week and CG_all). The covariances between $\hat{u}_{whole}$ and $\hat{u}_{partial}$ for crossbred traits in purebred validation animals were generally higher than those for crossbred validation animals, which may explain the higher LR accuracies of crossbred traits in purebred animals compared to crossbred animals. As an illustration, the covariances for $G_X$ in
purebred (and crossbred) validation animals were 22.53 (16.82), 24.05 (17.93) and 105.42 (58.20) for CG_day, CG_week and CG_all, respectively.

The Pearson correlation between $\hat{u}_{\text{partial}}$ of crossbred validation animals and their unadjusted phenotype for $G_X$ was highest for CG_all (0.08), followed by 0.06 for both CG_week and CG_day. These differences are small enough to be negligible. Correlations with unadjusted $BFX$ barely varied between scenarios (0.26, 0.26 and 0.27 for CG_all, CG_week and CG_day). Correlations between unadjusted phenotype and $\hat{u}_{\text{whole}}$ of crossbred validation animals for $G_X$ ($BFX$) were 0.70 (0.72), 0.47 (0.69) and 0.43 (0.67) using CG_all, CG_week and CG_day, respectively. Correlations between $\hat{u}_{\text{whole}}$ of $G_X$ (and $BFX$) for crossbred validation animals were 0.95 (0.98) between CG_day and CG_week, 0.73 (0.95) between CG_day and CG_all, and 0.76 (0.97) between CG_all and CG_week, while correlations of $G_X$ (and $BFX$) for purebred validation animals were 0.94 (0.97) between CG_day and CG_week, 0.76 (0.94) between CG_day and CG_all, and 0.79 (0.97) between CG_week and CG_all.

DISCUSSION

The genetic parameters obtained with CG_all are the most favorable, with the highest heritability estimate for $G_X$, similar heritability estimates for other traits, and stronger correlations with crossbred traits. Such values would indicate a possibility of faster response to selection provided that they best represent the “true” population parameters. Parameters estimated under CG_all were also most favorable when replacing $G_X$ with AAS or HCW. The additive genetic variance estimated for $G_X$ was more than 3 times higher for CG_all than for the other scenarios. Using simulated data, Gao et al. (2019) found decreased additive genetic variance estimates when ignoring dropout animals (reflecting our CG_day and CG_week
More specifically, additive genetic variance was only 69% of estimates obtained when animals never dropped out. Their group size was 12 animals and a total of 15% of the worst performing animals were dropped over 6 different time periods. Weights for all animals were available for each time period and used in a regression model. The number of animals per pen in our study was large (30-60 animals) and the average contemporary group size ranged from 11.77 for CG_day and 128.57 for CG_all. The variance captured by CG (as measured by the variance of the solutions for CG effect) also increased as our CG definition became less specific.

Additive genetic variance for CG_all in our study could be overestimated, the degree of which will depend on suitability of contemporary group compilation and accounting for either the relative time spent in the pen or relative space allowance (Ask et al. 2020). Total genetic variance in pigs for traits measured in group housing conditions is composed of direct genetic effect of the individual, and the indirect genetic effect (IGE) of the group mates (Bijma et al. 2007). The IGE in a group also depends on a dilution parameter, since the effect of one animal on another in the group will be smaller when the group is large (Arango et al. 2005; Bijma 2010; Heidaratbar et al. 2019). The reason for this expectation is that pairwise interactions are less frequent in large groups, leading to larger dilution parameter values (Canario and Bijma, 2010).

In the current study, IGE is less of a concern since food was available ad libitum in large troughs, which decreases, although does not eliminate, the social effect on growth (Bergsma et al. 2008). Neither the indirect genetic effect nor the dilution parameter could be inferred in our study due to the lack of pen information. Additionally, animals that were removed first, were always sharing a pen with a large number of animals. Conversely, animals remaining until the latest dates (after other animals were removed several times before), were housed with fewer pen-mates for part of
their growing period. This means that although some scenarios have small CG, this should not be understood as if they would have more pairwise social interactions, because CG sizes are not reflecting the number of pen mates. Pen information is often not recorded in pig breeding, but the inclusion thereof may be essential to avoid biased genetic parameters, even when pen size is the same (Bergsma et al. 2008).

The definition of growth in this study considers that $G_X$ and $G_P$ are essentially indices of both weight and growth, instead of weight change over time. Also accommodating an initial weight, such as birth weight or weaning weight, would be useful to capture growth alone, but these weights may not be available, especially for crossbreds. The birth weight of piglets has an influence on future growth, with piglets that are heavier at birth growing faster (Shull, 2013). Age at slaughter is an attractive alternative trait, especially because it is easy to measure and less susceptible to human error, unlike carcass weight. This latter trait is particularly prone to be affected by various factors that day. The heritability of 0.21 for AAS with CG_all suggests it would respond to selection, albeit less than $G_X$ (0.28). The heritability estimates are even lower for CG_week and CG_day. Although age at slaughter is not commonly researched as a trait, Torres Filho et al. (2004) found heritability estimates ranging from 0.13 to 0.20 for age at 100kg body weight, which is similar to the range of heritability estimates in this study (0.10 to 0.21). Santos et al. (2015) used a few hundred genomic markers and found heritability estimates ranging from 0.02 to 0.23 for AAS depending on model used and the number of markers selected. In Irish beef cattle, the heritability of deviation of age at slaughter ranged from 0.23 to 0.26 (Berry et al. 2017).

The AAS also shows weaker correlations with other traits. The negative correlation between GP and AAS for CG_all suggests that selection for faster growth in purebred animals
may lead to earlier slaughter age for crossbred offspring, which is desirable. However, this correlation is not only weaker, but also positive when using CG_week and CG_day. The genetic parameters in this study suggest that, although it is possible to use AAS as a replacement for G_X, genetic change is expected to be faster when using G_X. Furthermore, the inconsistency of correlation between AAS and G_P when using different contemporary groups makes G_X a safer choice. The results suggest that HCW could be a more appropriate alternative trait to use if contemporary groups are based on week or day, but not when excluding slaughter information.

Although CG_all has the most favorable variance component estimates, GC_day delivered the highest predictive ability, highest validation accuracy, least dispersion, and least bias. Validation accuracy measured as predictive ability is a measure of how well the model is correcting for effects, but not an indication whether the effects themselves are appropriate. Over-parametrized models will also overestimate the predictive ability (Bermann et al, 2020, in review process). Additionally, Legarra and Reverter (2018) showed that using adjusted phenotypes as a benchmark is questionable when variance components are wrong or when fixed effects have a large number of levels. In the latter, the error associated with the estimation of effects of all levels is high if the number of observations per level is small, causing an upward bias. The bias is then inversely proportional to the number of levels of a fixed effect. The higher predictive ability achieved with CG_day can be partially explained by the far greater number of contemporary groups in the model (10 589 groups for CG_day, 5 850 for CG_week and only 970 for CG_all). Correlations with adjusted phenotypes will also be influenced by the overall population accuracy, heritability, and errors in estimating the fixed effects corrected for (Legarra and Reverter 2018).
The accuracy measured by the LR method remained essentially unchanged for BF\textsubscript{X} across GC scenarios, at around 0.41 for purebred animals and 0.37 for crossbred animals. The higher values for purebred validation animals were driven by the higher covariances between breeding values with all the data and breeding values computed without measurements of the crossbred validation animals. The LR accuracies for G\textsubscript{X} in crossbred animals essentially remained unchanged (between 0.26 and 0.28), while differences in predictive ability are slightly bigger (0.27 to 0.30). These small differences make it difficult to draw a definitive conclusion regarding crossbred animals. However, the differences in accuracy for G\textsubscript{X} in purebred animals varied more – 0.36, 0.31 and 0.33 for CG\_all, CG\_week and CG\_day. In the pig industry, purebred animals are selected for crossbred performance and therefore the breeding value accuracies for G\textsubscript{X} and BF\textsubscript{X} are crucial. CG\_all gave the highest accuracy for G\textsubscript{X} in purebred animals, but second highest for crossbred animals. Based on these results, CG\_all is the most appropriate for G\textsubscript{X} selection in purebred animals, but CG\_day may be most appropriate in crossbred animals. Although the LR method for calculating accuracy is designed to overcome some flaws of predictive ability tests, it relies on the estimated additive variances. As discussed above, estimating the true additive variance with dropout animals is difficult.

The correlations between EBV obtained under different CG definitions indicate how these definitions affect the animals. Smaller CG comparing similar animals could be a disadvantage for the superior animals and an advantage for inferior animals. This would be reflected in a negative correlation. Results in this study show high correlations (>0.94) for BF\textsubscript{X} for all comparisons and both purebred and crossbred animals, while correlations for G\textsubscript{X} are lower, but still positive, for all comparisons. Comparisons of G\textsubscript{X} between CG\_day and CG\_week show strong correlations, suggesting little difference in ranking. Greater differences are observed
when comparing results to CG_all, where correlations are between 0.71 and 0.76. This indicates significant changes in ranking, although the overall trend will be similar. Adjusting measurements for age is an attractive option but it may not be a suitable reflection of the true growth curve. Although animals are weighed at different ages, they are chosen for slaughter based on size and only weighed once in their lifetime. Thus, weights are more or less similar regardless of age. Multiple records over time would allow better adjustments for age. Additionally, age is used in the calculation of growth. Adjusting for a factor that is part of the trait may remove some of the genetic component of the trait.

A higher Pearson correlation between EBV and less bias are not necessarily indications of improvement since it shows the magnitude of changes from parent average to a breeding value based also on phenotypic records, not whether the change is moving towards the true breeding value (which is unknown). A model that gives a higher correlation will be more stable between evaluations, indicating less changes when phenotypes are recorded, but it might not be the most correct.

Correlations between EBV of crossbred validation animals and their unadjusted phenotypes favored CG_all, especially when phenotypes were included in the evaluation ($\hat{u}_{whole}$). This reflects the higher heritability estimate calculated using this CG definition. It may be that, under CG_all, less statistical signals are captured by CG and more remain for the breeding value. Caution should be used when interpreting correlations with unadjusted phenotype, but these higher values may suggest that the exclusion of slaughter date from CG was able to better capture the genetic merit of animals. However, some traits may be more sensitive to CG changes than others, as was the case of growth but not backfat in our study.
CONCLUSIONS

This study reflects the complexity of evaluating the appropriateness of contemporary group compilation and accuracy of breeding values. Accuracy measures assume that the model was able to adequately correct for all effects and that the estimated variance components are correct, which may not be true. Selecting purebred animals for crossbred growth is essential in the pig industry. Results suggest that, for the estimation of crossbred traits in purebred animals, it is best to include all crossbred animals finished together in a single contemporary group, as opposed to multiple groups based on slaughter date. Routine pen information recording would allow finer tuning of contemporary groups and the estimation of indirect genetic effects. Age at slaughter shows potential as an alternative growth trait for crossbreds. However, heritability estimates are lower and correlations with other traits are weaker.

DISCLOSURES

The authors declare that there are no conflicts of interest

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Table 1. Summary statistics for traits and effects on purebred, and crossbred animals. Traits are hot carcass weight of crossbreds (HCW), end weight of purebreds (EW), purebred and crossbred growth (G_P and G_X), purebred and crossbred backfat (BF_P and BF_X) and purebred and crossbred age

| Trait              | N   | Min | Max  | Mean | SD  |
|--------------------|-----|-----|------|------|-----|
| HCW (kg)           | 124,709 | 60  | 144.24 | 98.16 | 8.89 |
| EW (kg)            | 62,274 | 62.6 | 182.5 | 121.5 | 14.61 |
| G_P (g/day)        | 62,274 | 450.3 | 1,106.1 | 766.6 | 90.72 |
| G_X (g/day)        | 124,709 | 301  | 758  | 528.4 | 60.63 |
| BF_P (mm)          | 62,274 | 5    | 32.7  | 8.56  | 2.13 |
| BF_X (mm)          | 124,709 | 5    | 38.7  | 14.82 | 4.05 |
| Age_{purebred} (days) | 62,274 | 127  | 200  | 158.6 | 7.02 |
| Age_{crossbred} (days) | 124,709 | 143  | 250  | 186.2 | 13.20 |
Table 2. Variance components and standard errors estimated with AIREML when using different contemporary groups. CG_all includes birth farm, sex, birth year and birth week. CG_week includes birth farm, sex, birth year, birth week and slaughter week. CG_day includes birth farm, sex, birth year, birth week and slaughter day

|               | Additive variance |             | Litter variance |             | Residual variance |             |
|---------------|-------------------|-------------|-----------------|-------------|-------------------|-------------|
|               | $G_X$             | $BF_X$      | $G_X$           | $BF_X$      | $G_X$             | $BF_X$      |
| CG_all        | 812 ± 36          | 4.28 ± 0.13 | 322 ± 11        | 0.50 ± 0.03 | 1790 ± 20         | 5.69 ± 0.07 |
| CG_week       | 257 ± 15          | 4.03 ± 0.12 | 116 ± 5         | 1.72 ± 0.03 | 1130 ± 9          | 5.16 ± 0.07 |
| CG_day        | 204 ± 13          | 4.00 ± 0.12 | 78 ± 4          | 0.36 ± 0.03 | 1084 ± 8          | 5.04 ± 0.07 |
Table 3: Heritability estimates (diagonal) and genetic correlations (off-diagonal) for purebred growth ($G_P$), purebred backfat ($BF_P$), crossbred growth ($G_X$) and crossbred backfat ($BF_X$). CG_all includes birth farm, sex, birth year and birth week. CG_week includes birth farm, sex, birth year, birth week and slaughter week. CG_day includes birth farm, sex, birth year, birth week and slaughter day.

|       | $G_P$       | $BF_P$       | $G_X$       | $BF_X$       |
|-------|-------------|--------------|-------------|--------------|
| **CG_all** |             |              |             |              |
| $G_P$ | $0.27 \pm 0.01$ | $0.45 \pm 0.02$ | $0.56 \pm 0.06$ | $0.23 \pm 0.05$ |
| $BF_P$ |             | $0.41 \pm 0.01$ | $0.17 \pm 0.06$ | $0.78 \pm 0.03$ |
| $G_X$  |             |              | $0.28 \pm 0.01$ | $0.27 \pm 0.02$ |
| $BF_X$ |             |              |              | $0.41 \pm 0.01$ |
| **CG_week** |             |              |             |              |
| $G_P$ | $0.27 \pm 0.01$ | $0.46 \pm 0.03$ | $0.44 \pm 0.07$ | $0.21 \pm 0.06$ |
| $BF_P$ |             | $0.41 \pm 0.01$ | $0.11 \pm 0.06$ | $0.78 \pm 0.03$ |
| $G_X$  |             |              | $0.17 \pm 0.01$ | $0.24 \pm 0.03$ |
| $BF_X$ |             |              |              | $0.42 \pm 0.01$ |
| **CG_day** |             |              |             |              |
| $G_P$ | $0.27 \pm 0.01$ | $0.46 \pm 0.02$ | $0.49 \pm 0.07$ | $0.22 \pm 0.05$ |
| $BF_P$ |             | $0.41 \pm 0.01$ | $0.10 \pm 0.06$ | $0.78 \pm 0.03$ |
| $G_X$  |             |              | $0.15 \pm 0.01$ | $0.19 \pm 0.03$ |
| $BF_X$ |             |              |              | $0.42 \pm 0.01$ |
Table 4: Heritability estimates (diagonal) and genetic correlations (off-diagonal) for purebred growth (G<sub>P</sub>), purebred backfat (BF<sub>P</sub>), age at slaughter (AAS) and crossbred backfat (BF<sub>X</sub>). CG_all includes birth farm, sex, birth year and birth week. CG_week includes birth farm, sex, birth year, birth week and slaughter week. CG_day includes birth farm, sex, birth year, birth week and slaughter day.

|       | G<sub>P</sub> | BF<sub>P</sub> | AAS   | BF<sub>X</sub> |
|-------|-------------|---------------|-------|---------------|
| **CG_all** |             |               |       |               |
| G<sub>P</sub> | 0.27 ± 0.01 | 0.46 ± 0.03   | -0.46 ± 0.07 | 0.23 ± 0.05   |
| BF<sub>P</sub> | 0.41 ± 0.01 | -0.14 ± 0.06  | 0.78 ± 0.03  |               |
| AAS   | 0.21 ± 0.01 | -0.12 ± 0.03  |       |               |
| BF<sub>X</sub> |            | 0.41 ± 0.01   |       |               |
| **CG_week** |             |               |       |               |
| G<sub>P</sub> | 0.27 ± 0.01 | 0.46 ± 0.02   | 0.20 ± 0.09 | 0.21 ± 0.06   |
| BF<sub>P</sub> | 0.41 ± 0.01 | 0.11 ± 0.07   | 0.77 ± 0.03 |               |
| AAS   | 0.16 ± 0.02 | -0.06 ± 0.04  |       |               |
| BF<sub>X</sub> |            | 0.42 ± 0.01   |       |               |
| **CG_day** |             |               |       |               |
| G<sub>P</sub> | 0.27 ± 0.01 | 0.46 ± 0.02   | 0.19 ± 0.10 | 0.22 ± 0.06   |
| BF<sub>P</sub> | 0.41 ± 0.01 | 0.13 ± 0.08   | 0.77 ± 0.03 |               |
| AAS   | 0.10 ± 0.01 | -0.02 ± 0.05  |       |               |
| BF<sub>X</sub> |            | 0.42 ± 0.01   |       |               |
Table 5: Heritability estimates (diagonal) and genetic correlations (off-diagonal) for purebred growth (G_P), purebred backfat (BF_P), hot carcass weight (HCW) and crossbred backfat (BF_X). CG_all includes birth farm, sex, birth year and birth week. CG_week includes birth farm, sex, birth year, birth week and slaughter week. CG_day includes birth farm, sex, birth year, birth week and slaughter day.

|         | G_P    | BF_P   | HCW    | BF_X   |
|---------|--------|--------|--------|--------|
| **CG_all** |        |        |        |        |
| G_P     | 0.27 ± 0.01 | 0.46 ± 0.02 | 0.47 ± 0.07 | 0.24 ± 0.05 |
| BF_P    | 0.41 ± 0.01 | 0.16 ± 0.06 | 0.78 ± 0.03 |        |
| HCW     | 0.18 ± 0.01 | 0.32 ± 0.03 |        |        |
| BF_X    | 0.41 ± 0.01 |        |        |        |
| **CG_week** |        |        |        |        |
| G_P     | 0.27 ± 0.01 | 0.46 ± 0.03 | 0.48 ± 0.07 | 0.21 ± 0.05 |
| BF_P    | 0.41 ± 0.01 | 0.13 ± 0.06 | 0.78 ± 0.03 |        |
| HCW     | 0.16 ± 0.01 | 0.23 ± 0.03 |        |        |
| BF_X    | 0.42 ± 0.01 |        |        |        |
| **CG_day** |        |        |        |        |
| G_P     | 0.27 ± 0.01 | 0.46 ± 0.02 | 0.50 ± 0.07 | 0.21 ± 0.05 |
| BF_P    | 0.41 ± 0.01 | 0.12 ± 0.06 | 0.78 ± 0.03 |        |
| HCW     | 0.14 ± 0.01 | 0.19 ± 0.03 |        |        |
| BF_X    | 0.42 ± 0.01 |        |        |        |
### Table 6. Validation statistics for crossbred growth ($G_X$) and crossbred backfat ($BF_X$) in purebred animals. CG_all includes birth farm, sex, birth year and birth week. CG_week includes birth farm, sex, birth year, birth week and slaughter week. CG_day includes birth farm, sex, birth year, birth week and slaughter day.

| Trait          | Scenario | $\text{cor}(\Hat{u}_{\text{whole}},\Hat{u}_{\text{partial}})^a$ | $b_1^b$ | Bias$^c$ | $\text{acc}_{LR}^d$ |
|----------------|----------|---------------------------------------------------------------|--------|---------|-------------------|
| Growth ($G_X$) | CG_all   | 0.59                                                          | 1.01   | 0.06    | 0.36              |
|                | CG_week  | 0.58                                                          | 1.00   | 0.05    | 0.31              |
|                | CG_day   | 0.61                                                          | 1.01   | 0.02    | 0.33              |
|                | CG_all   | 0.60                                                          | 1.01   | -0.01   | 0.41              |
| Backfat ($BF_X$) | CG_week | 0.60                                                          | 1.03   | -0.01   | 0.42              |
|                | CG_day   | 0.60                                                          | 1.03   | -0.02   | 0.41              |

$^a$Correlation between EBV with whole and partial data;
$^b$Coefficient of the regression of EBV with partial data on EBV with whole data;
$^c$Defined as the difference between average EBV with partial and whole data;
$^d$Accuracy based on linear regression metrics.
Table 7. Validation statistics for crossbred growth ($G_X$) and crossbred backfat ($BF_X$) in crossbred animals. CG_all includes birth farm, sex, birth year and birth week. CG_week includes birth farm, sex, birth year, birth week and slaughter week. CG_day includes birth farm, sex, birth year, birth week and slaughter day

| Trait       | Scenario  | $\text{cor}(\hat{u}_{\text{whole}}, \hat{u}_{\text{partial}})^a$ | $b_1^b$  | Bias$^c$ | $\text{acc}_{LR}^d$ | $\text{acc}_{\text{PRED}}^e$ |
|-------------|-----------|---------------------------------------------------------------|-----------|-----------|---------------------|---------------------|
| Growth      | CG_all    | 0.43                                                          | 0.86      | 0.88      | 0.27                | 0.27                |
|             | CG_week   | 0.49                                                          | 0.97      | 0.38      | 0.26                | 0.28                |
|             | CG_day    | 0.53                                                          | 1.00      | 0.03      | 0.28                | 0.30                |
| Backfat     | CG_all    | 0.54                                                          | 1.03      | 0.01      | 0.37                | 0.41                |
|             | CG_week   | 0.54                                                          | 1.03      | 0.00      | 0.37                | 0.42                |
|             | CG_day    | 0.55                                                          | 1.03      | -0.02     | 0.38                | 0.43                |

$^a$ Correlation between EBV with whole and partial data;  
$^b$ Coefficient of the regression of EBV with partial data on EBV with whole data;  
$^c$ Defined as the difference between average EBV with partial and whole data;  
$^d$ Accuracy based on linear regression metrics;  
$^e$ Accuracy based on predictive ability;