Revision of adjustment methods for on farm performance traits in the Canadian Swine Improvement Program

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For several years, the weight of hog carcasses has been steadily increasing in North America. In this context, genetic evaluation programs must adapt by moving away from the traditional approach of adjusting performance to a single target weight and instead adopt more flexible approaches that consider growth and tissue deposition patterns. The aim of the study was to compare different approaches to model several time-dependent performance variables during the growth phase at the individual level. A total of 1,998 purebred animals (Duroc, Yorkshire and Landrace), were weighed at least 7 times from 30-160 kg live weight during 13 on-farm trials. Ultrasound measurements for backfat thickness and muscle depth and loin intramuscular fat were also collected. Linear models, linear models with breakpoints and the Gompertz equation were compared. The Gompertz function was selected to simulate the sigmoidal behaviour of some variables (weight and muscle depth), while a linear function was used for others (backfat thickness and intramuscular fat). For individual adjustments, a classification algorithm was applied and compared to approaches currently used in the Canadian Swine Improvement Program. The application of this new approach in the evaluation program will use machine learning, which will allow the algorithm to improve as the size of the reference database increases. This approach also makes it possible to provide precision criteria for the predictions provided.

Actualisation des méthodes d'ajustement des caractères du contrôle de performances à la ferme dans le Programme canadien pour l'amélioration génétique des porcs

Depuis plusieurs années, le poids des carcasses de porcs est en constante augmentation en Amérique du Nord. Dans ce contexte, les programmes d'évaluation génétique doivent s'adapter en s'éloignant de l'approche traditionnelle d'ajustement des performances à un poids unique pour adopter des approches plus flexibles et prenant en compte les profils de croissance et de dépôt des différents tissus. L'objectif de l'étude était de comparer différentes approches permettant de modéliser plusieurs variables de performances en phase de croissance à l'échelle individuelle. Un total de 1 998 animaux de race pure (Duroc, Yorkshire et Landrace) ont été pesés à au moins 7 reprises entre 30 et 160 kg de poids vif au cours de 13 essais en ferme. Des mesures par ultrasons pour l'épaisseur de lard et de muscle dorsal et le gras intramusculaire ont également été récoltées. Des modèles linéaires, ou linéaires avec point de rupture ou encore établis selon l'équation de Gompertz ont été comparés : la fonction de Gompertz a été retenue pour simuler le comportement sigmoïdal de certaines variables (poids et épaisseur de muscle) alors que pour d'autres, une fonction linéaire a été retenue (épaisseur de lard et gras intramusculaire). Pour l'ajustement individuel, un algorithme de classification a été appliqué et comparé aux approches actuellement utilisées dans le Programme canadien pour l'amélioration des porcs. La mise en application de cette nouvelle approche dans le programme d'évaluation fera appel à l'apprentissage automatique (machine learning) ce qui permettra à l'algorithme de s'améliorer lorsque la taille de la base de données de référence augmentera. Cette approche permet également de fournir des indicateurs de la précision des prédictions fournies.

INTRODUCTION

For several years, the weight of carcass hogs has been steadily increasing in North America. In Canada, the average carcass weight increased from 86.4 kg in 1999 to 103.3 kg in 2019 (Agriculture and Agri-Food Canada, 2020). Breeding programs had to adapt rapidly to meet this change in the target market weight. For example, selection criteria for purebred animals (age, backfat, lean depth), previously adjusted to 100 kg live weight, are now adjusted to 120 kg and, with the constant increases in market weights, this adjustment must be continuously updated. Another consequence of this development is the increase in the weight range of animals tested on farms because, as the average scan weight increases, there is still a need to test lighter animals, particularly intact males. The Canadian Swine Improvement Program (CSIP) currently centralizes on-farm performance data for animals ranging from 75 to 160 kg live weight. The current weight adjustment factors are regularly reviewed and occasionally updated to take into account the effects of selection (for example, improving growth and reducing fat have an impact on the adjustment factors for these traits). Historically, purebred animals were monitored on farm within a very narrow weight range and the performance was standardized using linear adjustments. In the current context, it appears necessary to update not only the parameters but also the adjustment methods given the wide range of weights and the fact that the kinetics of weight, fat and muscle deposition are far from linear, particularly at the end of the growth stage.

The ability to predict the weight of animals at a given age presents several advantages for making performance adjustments for the purposes of standardized economic comparisons, but also, in the context of selection, for the reliable comparison of animals tested at what can be very different weights and ages. A number of empirical models have been proposed to describe the relationship between weight and age (Schull, 2013; Lonergan *et al.*, 2019). The evolution of weight as a function of age, from birth to adulthood, follows a sigmoidal type curve, with growth rate increasing until it reaches an inflection point then decreasing until the point where the mature weight is achieved. Wellock *et al.* (2004) compared several types of equations in non-limited environments and concluded that the most adaptable equations were those using a limited number of parameters with biological significance, describing continuous growth with a singular point of inflection and one asymptote (no growth) at time of maturity. Based on these criteria, the Gompertz equation is commonly used. Many other equations have been compared in different studies (logistics, Bridges, generalised Michealis-Menten, Richards, von Bertalanffy, etc.) and their results varied depending on the populations, experimental conditions and number of available measurements. Once the best equation has been found and adapted to the data, the growth rate at a given age can be calculated using the 1st degree derivative of that equation.

Several studies have been devoted to breaking down weight gain into its principal components (fat and muscle) in order to model body composition as a function of live weight (Schinckel & de Lange, 1996; Schinckel *et al.*, 2008). Others analyse feed intake data as variables to explain the kinetics of weight, fat and muscle gain. Few studies have investigated the kinetics of intramuscular fat (IMF) deposition in pigs. Regarding individual adjustments to constant weights, growth curves provide a real advantage over linear or quadratic approaches. However, it is necessary to regularly revise the parameters of these curves, particularly in the context of continuous selection. To remedy this, machine learning methods have been proposed in cattle and pork, in order to build adaptable algorithms (Alonso *et al.*, 2015; Alsahaf *et al.*, 2018).

This study aims to define the most suitable models for evaluation of weight, backfat thickness, lean depth and intramuscular fat and to propose a flexible approach to use them in the CSIP in order to standardize measurements collected on Canadian pigs. For this, a promising approach inspired by machine learning will be proposed.

1. MATERIAL AND METHODS

1.1. Available Data

The research project involved the collection of repeated measurements on 1,998 purebred animals (Duroc, Landrace and Yorkshire) in 13 trials and raised in seven selection herds participating in the CSIP located in the provinces of Quebec and Ontario (**Table 1**). The animals were weighed around 30 kg, around 50 kg, then weighed with ultrasound measurements collected at 80 kg and every two weeks until a final weight of up to 160 kg (average final weight of 140 kg). Ultrasound measurements for backfat thickness (BF), lean depth (LD) and percentage of loin intramuscular fat (IMF) were collected, by a technician accredited on the CSIP, between the 3rd and 4th last ribs.

Table 1 – Number of animals measured by breed and sex (with at least 5 measurements)

Breed	Sex[1]	Weight	BF/LD	IMF
Duroc	B	75	54	0
	F	277	245	93
	M	316	268	86
Landrace	B	115	84	0
	F	276	252	56
	M	171	163	16
Yorkshire	B	115	89	0
	F	332	313	89
	M	163	159	17

[1] B: barrows; F: females; M: intact males.

1.2. Methodology

The proposed general approach assumes that a given trait is defined by a reference equation whose parameters vary from one individual to another. Mathematically, the value of trait *Y* at a weight *w* is expressed as follows:

$$Y(w) = f_{\vec{X},\vec{\beta}}(w) \qquad \text{[Equation 1]}$$

where *f* is the reference equation, $\vec{X}$ is a vector of the animal's identification and its group (breed, sex, owner, farm, year of birth, etc.), and $\vec{\beta}$ is a vector of the parameters of the equation. It is assumed that the general form of *f* is common to all animals and that differences among animals are at the level of the parameter vector, $\vec{\beta}$.

1.2.1. *Reference Equation*

For a given trait, the reference equation was selected from various candidate functions which possessed at least one of the following two characteristics: (i) conceptually represents the evolution of the trait and/or (ii) is based on functions already used in the CSIP (**Table 2**). The number of observations per animal did not allow the selection of functions with too many parameters. This is why, for example, the Richards equation, a growth curve with 4 parameters (France *et al.*, 1996), was not considered. And so, the Gompertz function, a 3-parameter sigmoidal growth curve, and its simplified 2-parameter version were tested (Teleken *et al.*, 2017). For all traits, with the exception of age, a linear equation, currently used as an adjustment, was tested as well as a linear equation with a break point at 120 kg. The use of this last equation was justified by the fact that the selection program currently adjusts traits to a live weight of 120 kg and it allows the non-linearity to be indirectly modeled while maintaining an approach based on the current adjustment method.

1.2.2. *Individual Adjustment*

The choice of individual adjustments goes back to the estimation strategy for the $\vec{\beta}$ vector parameters. Deterministic and Bayesian approaches were used. Note that in the examples presented in this study, it is assumed that for the tested animal, the prediction of a trait at a target weight w_1 is made from a single observation at weight w_0. Both approaches can also be applied in cases where multiple observations are available.

The deterministic approach implies that $\vec{\beta}|\vec{X}, Y(w_0)$, which follows the vector for the parameters of an individual in the group defined in $\vec{X}$ and with observation $Y(w_0)$, gives a unique result. The approach is applied in two steps. Firstly, a vector of parameters, denoted $\vec{\beta}|\vec{X}$, is defined as a function of the group (sex or breed-sex in this study). Then, a correction factor is applied to the parameters so that the function *f* passes through the measurement point $Y(w_0)$. The modified function can then predict the trait *Y* at any given weight *w*. This approach has been applied only to the linear functions and/or those already used in the Canadian program.

With the Bayesian approach, $\vec{\beta}|\vec{X}, Y(w_0)$ follows a probability distribution which is dependent on the animal's test group and is adjusted based on observation $Y(w_0)$. In this study, the empirical distribution of $\vec{\beta}|\vec{X}, Y(w_0)$ is estimated using a method inspired by *k*-nearest neighbours (*k*NN):

1- For each animal in the reference population (with repeated measurements), estimate $\vec{\beta}$. In this study, the reference population is the dataset collected in the 13 trials, excluding animals from the same trial;

2- Calculate an objective function *L* which describes the distance between observation $Y(w_0)$ for the tested animals and the value given by $f_{\vec{X},\vec{\beta}}(w_0)$ resulting from each animal in the reference population. The function *L* can also penalise or exclude animals from the reference population who are not in the same group as the tested animal;

3- Set a threshold *s* and a minimum number of animals k_0. Retain all values where $L < s$. If the number of retained values is less than k_0, then retain the k_0 values smaller than *L*. The number of retained animals is denoted by *k*. In this study, k_0 was fixed at 10 and the value of *s* depended on the trait;

4- These retained *k* values lead to *k* vectors of parameters $\vec{\beta}$ which are considered to be equally probable for the tested animal;

5- The resulting *k* functions $f_{\vec{X},\vec{\beta}}(w)$ can be used to estimate the variable of interest for the tested animal at any weight *w*.

In the presented examples, the value predicted at weight w_1 is the median of the *k* values $f_{\vec{X},\vec{\beta}}(w_1)$. The Bayesian approach is even more interesting as it gives a measure of the variability of the prediction. When applied to an evolving reference population, this approach is considered as supervised machine learning.

1.3. Comparison of prediction models

The analysed prediction models are presented in **Table 2**. Other models were tested during this study, but only the most relevant are presented in this paper. Models A0, G0 and M0 were the models used in the CSIP prior to the start of this study. Only the model for age (A1) has been updated so far using data from this project. The other models are under evaluation and are candidates for integration in the CSIP. It should be noted that the Canadian program does not currently use any adjustment for IMF.

For each trait, the models were evaluated for their capacity to predict a value at a given weight w_1 from an observation at a known weight w_0, where both weights fall in the range of 75-160 kg.

The evaluation of reference equations was based on the distribution of the residuals, which should be centred around zero and not very dispersed. The mean, standard deviation and root-mean-square error (RMSE) of the residuals were calculated for each weight class (75-90, 90-105, 105-120, 120-140 and 140-160 kg). The number of parameters in each equation was also considered.

The performance of the adjustment method can also be evaluated based on to the distribution of the residuals by comparing models with the same reference equation. In addition, for adjustments using the Bayesian approach, Talagrand diagrams were produced to evaluate whether the distribution of the *k* predictions adequately covers the values to be predicted. The variability of the distribution was linked to the residual to evaluate if it is possible to predict the quality of the prediction.

Table 2 – Prediction Models tested for all traits in this study

Variable	Model	f^1	Group	Adjustment	Data Source[2]
Age, days	A0	$Y(w_1) = Y(w_0) - \frac{w_0 - w_1}{\beta_0^{w_0/Y(w_0)}}$	Sex (F, B/M)	Deterministic	Historical
	A1	Like A0, with a break point at 120 kg	Sex (F, B/M)	Deterministic	Project
	A2	$w = \beta_1 \exp\left\{\log\left(\frac{1.5}{\beta_1}\right)\exp\left(-\beta_2 Y(w)\right)\right\}$	Sex (F, B/M)	Bayesian	Project
	A3	Like A2	Sex (F, B, M)	Bayesian	Project
	A4	Like A2	Breed and sex	Bayesian	Project
BF, mm	G0	$Y(w_1) = Y(w_0)\frac{\beta_1 + \beta_2 w_1}{\beta_1 + \beta_2 w_0}$	Breed and sex	Deterministic	Historical
	G1	Like G0	Breed and sex	Deterministic	Project
	G2	Like G0, with a break point at 120 kg	Breed and sex	Deterministic	Project
	G3	$Y(w) = \beta_1 + \beta_2 w$	Breed and sex	Bayesian	Project
LD, mm	M0	$Y(w_1) = Y(w_0)\frac{\beta_1 + \beta_2 w_1}{\beta_1 + \beta_2 w_0}$	Breed and sex	Deterministic	Historical
	M1	Like M0	Breed and sex	Deterministic	Project
	M2	Like M0, with a break point at 120 kg	Breed and sex	Deterministic	Project
	M3	$Y(w) = \beta_1 \exp\left\{\log\left(\frac{25}{\beta_1}\right)\exp(-\beta_2 w)\right\}$	Breed and sex	Bayesian	Project
IMF, %	P1	$Y(w_1) = Y(w_0)\frac{\beta_1 + \beta_2 w_1}{\beta_1 + \beta_2 w_0}$	Sex (F, M)	Deterministic	Project
	P2	$Y(g_1) = Y(g_0)\frac{\beta_1 + \beta_2 g_1}{\beta_1 + \beta_2 g_0}$	Sex (F, M)	Deterministic	Project
	P3	$Y(w) = \beta_1 + \beta_2 w$	Sex (F, M)	Bayesian	Project
	P4	$Y(g) = \beta_1 + \beta_2 g$	Sex (F, M)	Bayesian	Project

[1] *The correction factor is included in the function f for models with the deterministic approach. For models P2 and P4, the variable g is BF.*

[2] *Data source for parameter estimation. The value 'Historical' indicates that the equation and its parameters are not modified. The value 'Project' indicates that the parameters are estimated based on animals from the 13 trials, with the exception of the test animal trial.*

2. RESULTS

2.1. Analysis of Residuals

The bias, standard deviation and RMSE for each model are presented in **table 3**.

For age, the results clearly indicate that the old CSIP model (A0) is more biased than the others; it underestimates (respectively overestimates) age when the target weight is smaller (respectively greater) than the observed weight. This model was originally developed to cover a range of 75-115 kg (Kennedy and Uribe, 1994) and not for weights up to 160 kg. Model A1, developed based on model A0 but with a break point at 120 kg to better cover heavier weights, performs better than A0 but generally poorer than the models based on the 2-parameter Gompertz equations using the Bayesian adjustment method. For these models, the bias is generally very low and the models treating the sexes separately (A2 and A3) perform slightly better than the model by sex and breed (A4). By imposing more precise criteria for the definition of the group, the number of animals per group from the reference population decreases. This is a potential cause of the deterioration of results for model A4 compared to models A2 and A3.

For BF, performance is similar between models, indicating that the break point linear equation does not substantially improve the results over the linear equation. The selection of equation parameters had a limited impact on the distribution of residuals.

Table 3 – Absolute bias, standard deviation and average RMSE for each analysed model. In brackets, the highest value among the 20 combinations of target and observed weight classes.

Variable	Model[1]	|Bias|	SD	RMSE
Age, days	A0	5.2 (11.9)	5.3 (7.4)	7.6 (12.9)
	A1	2.1 (7.1)	5.3 (7.7)	5.9 (9.2)
	A2	0.7 (2.0)	5.5 (7.6)	5.6 (7.7)
	A3	0.7 (2.2)	5.4 (7.6)	5.5 (7.6)
	A4	0.8 (2.2)	5.7 (9.7)	5.8 (10.0)
BF, mm	G0	0.2 (0.6)	1.9 (3.3)	1.9 (3.3)
	G1	0.2 (0.4)	1.9 (3.3)	1.9 (3.3)
	G2	0.1 (0.2)	1.9 (3.3)	1.9 (3.3)
	G3	0.2 (0.4)	1.9 (3.1)	1.9 (3.1)
LD, mm	M0	1.1 (2.4)	4.8 (6.5)	4.9 (6.7)
	M1	0.6 (1.1)	4.8 (6.5)	4.8 (6.6)
	M2	0.2 (0.7)	4.8 (6.5)	4.8 (6.6)
	M3	0.2 (0.8)	4.7 (6.0)	4.7 (6.0)
IMF, %	P1	0.23 (0.61)	0.85 (1.5)	0.90 (1.6)
	P2	0.25 (0.62)	0.80 (1.4)	0.85 (1.5)
	P3	0.25 (0.83)	0.98 (2.5)	1.02 (2.7)
	P4	0.20 (0.48)	0.80 (1.2)	0.84 (1.3)

[1] *Models are defined in **Table 2**.*

For LD, updating the parameters (M1) of the linear equation used in the CSIP (M0) allowed for a reduced bias. Taking into account the non-linearity reduced the bias further, either by having a break point at 120 kg in the linear equation (M2) or by using the Gompertz equation (M3).

For IMF, linear models as a function of backfat (P2 and P4) have a slightly lower RMSE than linear models as a function of weight (P1 and P3).

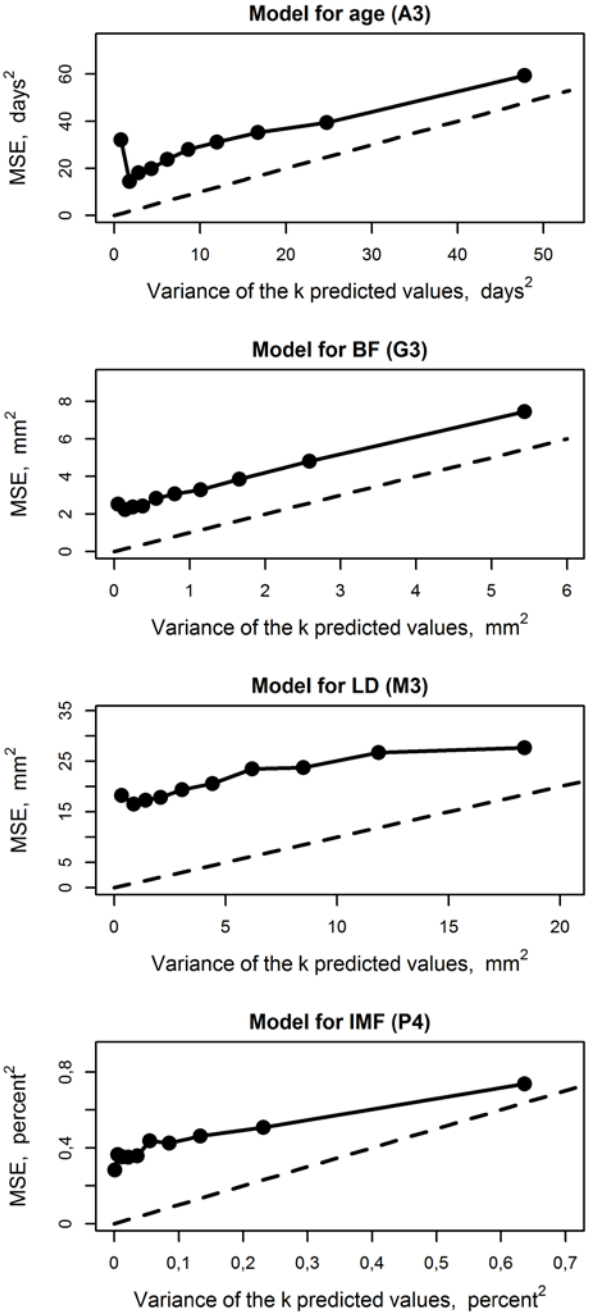

Figure 1 – MSE of the prediction as a function of the variance of the group of values generated by the Bayesian approach.

2.2. Analysis of Variability

Each prediction has an uncertainty that the deterministic adjustment methods, currently used for all traits in the CSIP, do not take into account. It could prove useful for the selection program to accompany each prediction with a degree of accuracy, either by a standard deviation or by an index of reliability that would be provided to the breeder. From this perspective, it is pertinent to verify that the variability of *k* values predicted with the Bayesian adjustment method make it possible to determine *a priori* the accuracy of a prediction.

For a given trait, all of the predictions resulting from a model with the Bayesian adjustment method were divided into 10 classes based on the variance of the *k* values: variance below the 10th percentile, variance between the 10th and 20th percentile, and so on up to variance between the 90th and 99th percentile (extreme values were ignored). So, there were 10 groups of similar size for which the MSE of the prediction was calculated (**Figure 1**).

For all four traits, the MSE increases with the variance of the set of generated values, which implies that it is possible to get an indication of the reliability of the prediction with the proposed method. However, even if there is a correlation, the MSE is significantly higher than the variance of all generated values. This difference could be caused by (i) bias in the models or (ii) under-dispersion generated by the Bayesian approach (i.e. the Bayesian approach does not reproduce the true variability in the data). Since bias in the models is relatively low (**table 3**), under-dispersion is the most probable cause, which is confirmed by the Talagrand diagram (**Figure 2**). For the four traits, the true value to predict is too often outside or at the limit of the set generated by the Bayesian approach.

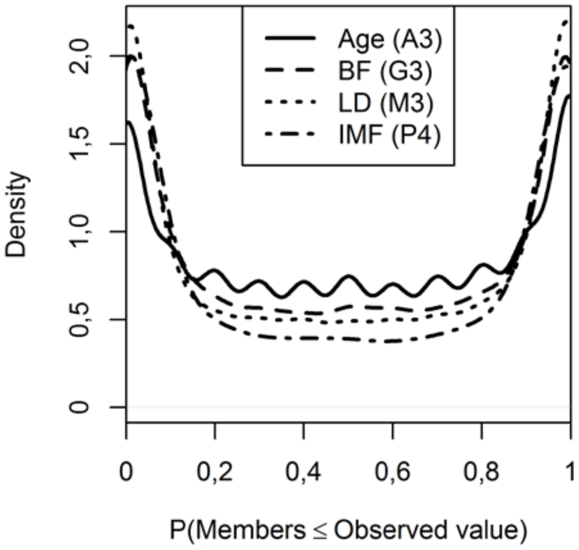

Figure 2 –Talagrand diagram for the four traits. A perfect model would have a constant density of 1.

3. DISCUSSION

This study allowed for updates to the equations in the CSIP. For age and LD, growth curves (2-parameter Gompertz function) have been selected. For age, the reduction in bias is major: around 4.5 days on average across all weight classes (**Table 3**) and around 10 days when the target weight is between 75 and 90 kg and the observed weight is between 140 to 160 kg. The reduction in bias is much less for LD, but the results still detected non-linearity with only five observations per animal.

The linear equation, already used in the CSIP, was selected for BF. This result does not necessarily imply linearity, but rather that the non-linearity, if present, was not important enough to improve the results from five observations per animal.

For IMF, the correlation is much stronger with BF than with weight. More individuals with multiple observations would be necessary to refine the models; for now, barrows are excluded and the majority of the data comes from the Duroc breed.

The Bayesian adjustment approach has shown very interesting results. For IMF, the bias has decreased slightly compared to use of the deterministic approach (multiplication factor) from the same reference population (**Table 3**). But the main advantage of using such an approach is the assessment of the variability of the prediction. At this stage, the results show some potential to have an appreciation for the reliability of the predictions (**Figure 1**), however the full potential of the approach has not yet been realized.

The main factor that would improve predictions would be to increase the size of the dataset. The size of the dataset acquired during this study allowed for some interesting advancements, but it did not allow for the creation of homogenous groups precise enough to get a targeted prediction for the animal. This was the case for age, where the model by sex and by breed (A4) had slightly poorer performance compared to the models by sex (A2 and A3), and for IMF, where the amount of data did not allow for consideration of a model by breed and by sex.

An increase in the size of the dataset would improve the objective function *L* by refining the definitions of the groups and integrating several performance criteria. For example, the selection of *k* animals in the reference population could be done by considering groups of traits (e.g. use BF, LD, IMF and ultimately feed intake to predict age at a given weight). Regarding the definition of groups, it does not need to be limited to sex and breed, but can take into account any information such as, for example, the barn, the technician, the year (to take genetic evolution into account), the dates (to take the effect of the environment into account), etc.

With the objective of increasing the size of the reference dataset and adding criteria for consideration, other machine learning approaches could be considered. Also, the selection of animals in the reference population could be done based on the raw data, without going through a reference equation. It should be noted that, in this study, the reference animals were characterised by the parameters of the reference equation and not by their raw data. The prediction of performance without a reference equation would represent a major change in the approach for data standardization. It would undoubtedly require training efforts among breeders and users of adjusted performances and breeding values. A real advantage, however, would be the ability to exploit the full potential of the raw data, notably in terms of variability, which the current approach, based on parameters of the equation, underestimates (**Figure 2**).

In addition, the proposed approach requires that trials be carried out periodically by breeders. The protocol for the implementation of the trials (frequency of trials by breeder, number of animals by sex and by breed, number of measurements by animal, collection of new data, etc.) remains to be planned with the breeders. It depends particularly on the adjustment approach that is adopted.

CONCLUSION

The objective of the study was to propose more flexible adjustment models for the CSIP, particularly those that adapt to different weights. The two-parameter Gompertz equation, which conceptually represents the nonlinear growth of the animal, was selected for weight and LD. Improvement in prediction of age at a given weight is very important compared to the previously used standard equation, developed based on lighter animals. For BF, the linear equation may still apply and for IMF, models based on BF have shown good results, however more data is needed to refine the model.

Beyond the selection of new models, this study aimed to evaluate a new, evolutionary standardization approach for the CSIP. The new Bayesian approach shows interesting results, especially with regards to the visualization of variability. However, the full potential of this approach can be expressed by taking new repeated measurements periodically. It could also be enhanced by the inclusion of new variables from new sensors and if necessary, by new big data analysis approaches. The implementation strategy remains to be developed with the breeders.

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BIOGRAPHICAL REFERENCES

- Agriculture et Agroalimentaire Canada, 2020. Information sur le marché des viandes rouges. Rapport des poids moyens de carcasses chaudes dans les abattoirs inspectés fédéralement (009D).
- Alonso J., Villa A., Bahamonde A., 2015. Improved estimation of bovine weight trajectories using Super Vector Machine Classification. Computers and Electronics in Agriculture, 110, 36-41.
- Alsahaf A., Azzopardi G., Ducro B., Hanenberg E. Veerkamp R.F., Petkov N., 2018. Prediction of slaughter age in pigs and assessment of the predictive value of phenotypic and genetic information using random forest. J. Anim. Sci., 96, 4935-4943.
- France, J., Dijkstra, J., Dhanoa, M. S., 1996. Growth functions and their application in animal science. *Annales de Zootechnie*, 45(Suppl1),165-174.
- Kennedy B.W. & Uribe H., 1994. Adjustments for weight at probing to 105 kg. Report to CCSI Genetics Committee, September 1994. 7 pages.
- Lonergan M., Topel D.G., & Marple D.N, 2019. Growth curves and growth patterns. *In The Science of Animal Growth and Meat Technology (Second Edition)* p71-109.
- Schinckel A. P. & de Lange C.F., 1996. Characterization of growth paremeters needed as inputs for pig growth models. *J. Anim. Sci.* 74, 2021-2036.
- Schinckel A. P., Mahan D. C., Wiseman T. G., & Einstein M. E., 2008. Growth of protein, moisture, lipid, and ash of two genetic lines of barrows and gilts from twenty to one hundred twenty-five kilograms of body weight. *J. Anim. Sci.* 86, 460-471.
- Schull C.M., 2013. Modeling growth of pigs reared to heavy weights. PhD Thesis, University of Illinois at Urbana-Champaign, 143 pages.
- Teleken J.T., Cazonatto Galvão A., da Silva Robazza W., 2017. Comparing non-linear mathematical models to describe growth of different animals. *Acta Scientiarum. Animal Sciences*, 39, 73-81.
- Wellock I. J., Emmans G.C., & Kyriazakis I., 2004. Describing and predicting potential growth in the pig. *Anim. Sci.* 78, 379-388.