

Research Application Summary

Random regression analyses using B-spline functions to model the growth of large white pigs

Ouko, V.O.,¹ Ilatsia, E.D.,² Rachuonyo, H.A.,¹ Kios, D. K.¹ & Oduho, G. O.¹.

¹Department of Animal Science, University of Eldoret, P.O. Box 1125-30100 Eldoret, Kenya

²Kenya Agricultural and Livestock Research Organization (KALRO), P.O. Box 25-20117,
Naivasha, Kenya

Corresponding author: ochieng.vincent@ymail.com

Abstract

The pigs industry in Kenya has faced many challenges, among them poor animal genetic resource base. To partly address this, genetic parameters were estimated using B-spline functions in random regression models for weight of Large White pigs measured between the 3rd and 36th week of age. The model accounted for contemporary groups, parity and sex as fixed effects while random effects modeled were; animal genetic effect, permanent environmental effect and maternal genetic effect along with heterogeneous residual variances. Heritability estimates decreased with age from 0.37 at 3 weeks to 0.27 at 36 weeks. Weight during the studied period showed initial positive genetic (0.20 – 0.91) and phenotypic correlations (0.25 – 0.91), which decreased with increase in age gap. The results from this study shows that body weight in Large White pigs is moderately heritable (0.27-0.37), especially prior to weaning, suggesting the potential for genetic gain from selection. The genetic correlations suggests that considerable genetic gain can be obtained by considering pre-weaning weight only, though the genetic correlation less than unity indicates that more genetic gain would be realized by including all the estimates of heritability throughout the growth period. In all cases, the estimates generated by this study were consistent with previous studies. This study suggests that random regression methods using B-spline are appropriate for estimating genetic parameters and genetic gain for weight in Large White pigs.

Key words: Body weight, B-spline function, genetic parameters, large white Pigs, random regression model

Résumé

L'industrie porcine au Kenya a fait face à de nombreux défis dont une faible base des ressources génétiques animales. Pour répondre en partie cela, les paramètres génétiques ont été estimés en utilisant les fonctions B-spline dans les modèles de régression aléatoires pour le poids des porcs Large White mesurés entre la 3^e et la 36^e semaine d'âge. Le modèle a considéré les groupes contemporains, la parité et le sexe comme des effets fixes tandis que les effets aléatoires modélisés étaient l'effet génétique animal, effet permanent de l'environnement et l'effet génétique maternel ainsi que des variances résiduelles hétérogènes. Les estimations de l'héritabilité ont diminué avec l'âge de 0,37 (3 semaines) à 0,27 (36 semaines). Le poids au cours de la période étudiée a initialement

montré des corrélations génétiques (0,20 - 0,91) et phénotypiques (0,25 - 0,91) positives qui ont ensuite diminué avec l'augmentation de l'écart d'âge. Les résultats de cette étude montrent que le poids corporel chez les porcs Large White est modérément héritable (0,27 - 0,37), en particulier avant le sevrage, suggérant le potentiel de gain génétique de la sélection. Les corrélations génétiques suggèrent que le gain génétique considérable peut être obtenu en considérant le poids avant sevrage seulement, bien que la corrélation génétique inférieure à l'unité indique que le gain plus génétique serait réalisé en incluant toutes les estimations de l'héritabilité pendant toute la période de croissance. Dans tous les cas, les estimations générées par cette étude sont cohérentes avec les études disponibles existantes dans la littérature. Cette étude suggère que les méthodes de régression aléatoire en utilisant B-spline sont appropriées pour l'estimation des paramètres génétiques dans les porcs Large White et le gain pondéral génétique.

Mot Clés: Le poids corporel, la fonction B-spline, les paramètres génétiques, les porcs Large White, modèle de régression aléatoire

Background

Random regression models based on Legendre polynomials have been used to study several farm animals in Kenya: Boran cattle (Wasike *et al.*, 2007) Dorper sheep (Kariuki *et al.*, 2010) and Holstein–Friesian cattle (Muasya *et al.*, 2014). Additionally, many countries have now incorporated the models in their breeding programs (Meyer, 2005a; Shirali *et al.*, 2015). These models have had the advantage of using all performance records from an animal, thereby excluding the need to adjust for standard ages. Moreover, more accurate estimates are realized in comparison to the conventional multi-trait models (Wolc *et al.*, 2013). B-splines have been recommended and adopted as an advanced alternative to Legendre polynomials with increased accuracy in estimation of genetic parameters (Meyer, 2005b; Misztal, 2006). This was to address undesirable properties associated with Legendre polynomials such as need to use high degrees of polynomials when small data sets are used and errors at the extremes of the curves due to oscillations therein (Meyer, 2005b; Köhn *et al.*, 2007). Even though there is limited information on estimation of pig genetic parameters using random regression models, spline functions were used to describe genetic variations using weights from 50 to 225 days by Huisman *et al.* (2002) and carcass weight by Zumbach *et al.* (2008). The objectives of this study were to estimate covariance functions for direct and maternal additive genetic effects, animal permanent environmental effects and successively, obtain genetic parameters for growth traits in Large White pigs, from 3rd to 36th weeks, using random regression models on B-splines of animal age.

Materials and methods

Data used in this study were obtained from the Non-ruminant Research Centre of Kenya Agricultural and Livestock Research Organization (KALRO) Naivasha, where the Pig Genetic Evaluation Program ran from 1982 to 1996. The animals were weighed

weekly from birth to 36 weeks when they were sold, while weaning was done at 8 weeks. The contemporary groups were divided into two (1982-1990 and 1990-1996) based on feeding regimes and feed quantities supplied per animal as described by Ilatsia *et al.* (2008). Weight at birth was not included to avoid implausible variance values at that age as reported by Köhn *et al.* (2007) and animals with less than three records were also excluded.

The data set was used to fit average growth trajectory using cubic B-spline after initial analysis indicated that linear and quadratic B-spline could not adequately model the data. The coefficients of the cubic B-spline were generated from the k interval defined by the points T_k and T_{k+1} with $T_k \leq T_{k+1}$, as described by Meyer (2005a), Misztal (2006) and Scalez *et al.* (2014). The partitions into m intervals requires the specification of $m - 1$ internal knots and two external knots (T_0 and T_m). This approach produces $m + 1$ knots and $m + p$ non-null functions $\phi_{k,p}$ (Scalez *et al.*, 2014).

The general random regression model with cubic B-spline used was as follows:

$$y_{ijm} = F_i + \sigma_{m=0}^{K_{A+3}} \beta_{k(ix)} \phi_{m,3}(t_{ij})_{ix} + \sigma_{m=0}^{K_{B+3}} \alpha_{im} \phi_{m,3}(t_{ij}) + \sigma_{m=0}^{K_{C+3}} \gamma_{im} \phi_{m,3}(t_{ij}) + \sigma_{m=0}^{K_{D+3}} \delta_{im} \phi_{m,3}(t_{ij}) + \epsilon_{ij} \quad (1)$$

where y_{ijm} is the j^{th} weight record taken at week t_{ij} from the m^{th} pig, F_i is the i^{th} random regression coefficient for the fixed effects (contemporary groups, parity and sex) and $\phi_{m,3}(t_{ij})$ represents the m^{th} cubic B-spline covariate at week t which was nested in fixed effect level i ; $\beta_{k(ix)}$ is the k^{th} coefficient of fixed regression nested in fixed effect i ; α_{im} is the i^{th} random regression coefficient for the additive genetic effect of pig m ; γ_{im} is the random regression coefficient for the permanent environmental effect of pig m ; δ_{im} is the random regression coefficient for the maternal genetic effect of pig m ; while K_{A+3} , K_{B+3} , K_{C+3} and K_{D+3} represents numbers of regular intervals in modelling the fixed average growth trajectories, random additive genetic, permanent environment and random maternal genetic effects, respectively. The covariance components and genetic parameters were estimated by the Restricted Maximum Likelihood method using the Wombat Software (Meyer, 2007), while the criteria AIC and BIC were used to compare the models.

Results and Discussion

Heritability decreased from the 3rd week (0.37) to the 36th week (0.27) while the proportion of animal permanent environmental variance increased gradually from 0.44 to a maximum of 0.71 during the studied period. On the other hand, proportion of maternal genetic variance reduced steadily to naught at the end of the trajectory (Figure 1).

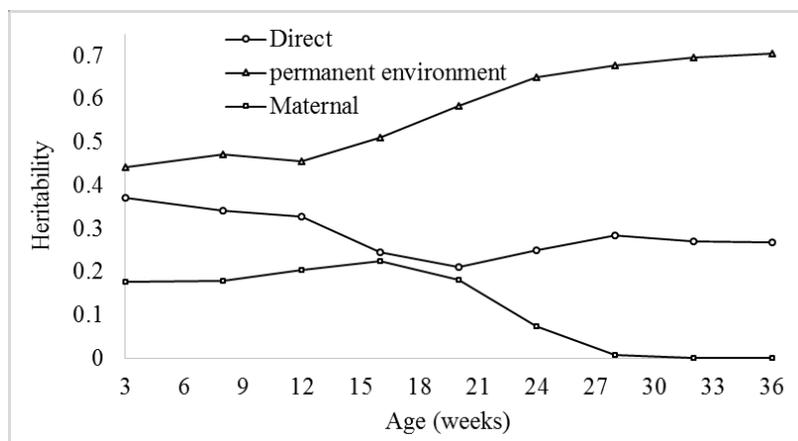


Figure 1: Estimates of direct and maternal heritability and estimates of Large White pigs' permanent environmental variance as a proportion of phenotypic variance at KALRO, Naivasha – Kenya.

The estimated heritability decreased with age from 0.37 to 0.27, along with increasing phenotypic variance signifying an increase in genetic variation. This indicates that weight is averagely heritable early in the pig's life before decreasing and is influenced by permanent environment and maternal genetic effects. A similar trend of heritability in pig weight was described by Huisman *et al.* (2002), Köhn *et al.* (2007) in Goettingen mini pigs and Ilatsia *et al.* (2008) in Large White pigs, though with lower estimates than findings of this study. Wetten *et al.* (2012) reported an increasing trend in heritability in Duroc and a decreasing one in Landrace between 80 and 160 days of growth. Norwegian Landrace sows had heritability estimates similar to this study, with the highest value observed at the 3rd week (Lundgren *et al.*, 2014).

Maternal heritability, though minimal, was significant and declined from the 20th week (0.22) to naught at the end of the growth period. This suggests that variations in weight observed up to the 20th week were partly determined by the condition of the rearing sow; including uterine nutrition and milk production capacity. However, the diminishing trend implies that selection for increased maternal ability is limited and genetic gains could only be realized before piglets get to 20 weeks old. Where weaning is done in three to four weeks, maternal genetic effect can be neglected due to its minimal influence (Köhn *et al.*, 2007). It was; however, important to include maternal genetic effect in this study since weaning was done at the 8th week; the same should apply to studies involving cattle, goats and sheep. Using the same data set, Ilatsia *et al.* (2008) reported a similar trend, though with higher estimates.

As expected, phenotypic and genetic correlations between body weights reduced with increase in distance (0.91-0.25) between age classes and ranged from moderate to high (Table 1). The low correlation between weight early in life and later in life indicates that they are different traits or affected by different genes altogether. Genetic

correlations were slightly higher than phenotypic correlations, signifying that individual pig performance is partly determined by their ability to tolerate stressful conditions imposed by the production environment (e.g crowding, confinement, ear tagging, heat stress, among others). High correlation between ages were recorded by Ilatsia *et al.* (2008) and Darfour-Oduro *et al.* (2009), though these authors used a multiple trait model unlike the current study. Similar estimates using random regression were reported by Huisman *et al.* (2002) and Haraldsen *et al.* (2009).

Table 1: Estimates of phenotypic (above diagonal) and genetic (below diagonal) correlations between Large White pig weights from week 3 to 36 of the B-Spline function at KALRO Naivasha

Age (weeks)	3	8	16	24	36
3		0.91	0.75	0.60	0.25
8	0.89		0.92	0.75	0.34
16	0.74	0.91		0.87	0.40
24	0.44	0.51	0.79		0.514
36	0.20	0.33	0.53	0.67	

Estimates of the first three eigen-functions were positive in all cases, accounting for 87.65% of the genetic variations. Proportion of genetic variation explained by the eigen-functions agrees with the scenario presented by the correlations. This implies that selection at any point within the growth period will lead to a positive change at other ages as was also reported by Köhn *et al.* (2007).

Conclusions and Recommendations

Random regression models employing cubic B-spline are effective at modeling the genetic variation for body weight among Large White pigs raised at KALRO, Naivasha. Estimates of heritability were moderate and can help in ranking and selection for increased genetic gain, in the current market that rewards for heavy pigs. Correlation estimates between the ages at recording were moderate to high, indicating that genetic selection at any point will lead to an indirect positive gain at all other ages. This study is of great value to pig breeding industry in Kenya, in light of the current absence of a national breeding scheme. It provides the required genetic information necessary for ranking and selection for weight gain at different pig ages to suit varying breeding objectives. It can be concluded that random regression models using cubic B-splines, could be used to regularly monitor Large White pig growth. Increased accuracy can be obtained by larger data set and performance records.

Acknowledgement

The authors thank the Kenya Agricultural and Livestock Organization of Naivasha for the pedigree and phenotypic data and University of Eldoret for facilitating the study. This paper is a contribution to the 2016 Fifth African Higher Education Week and RUFORUM Biennial Conference.

References

- Darfour-Oduro, K.A., Naazie, A., Ahunu, B.K. and Aboagye, G.S. 2009. Genetic parameter estimates of growth traits of indigenous pigs in Northern Nigeria. *Livestock Science* 125 (2): 187-191.
- Haraldsen, M., Odegard, J., Olsen, D., Vangen, O., Ranberg, I. M. and Meuwissen, T. H. 2009. Prediction of genetic growth curves in pigs. *Animal* 3 (4): 475-481.
- Huisman, A. E., Veerkamp, R. F. and Van Arendonk, J. A. 2002. Genetic parameters for various random regression models to describe the weight data of pigs. *Journal of Animal Science* 80 (3): 575-582.
- Ilatsia, E. D., Githinji, M. G., Muasya, T. K., Okeno, T. O. and Kahi, A. K. 2008. Genetic parameter estimates for growth traits of large white pigs in Kenya. *South African Journal of Animal Science* 38 (3): 166-173.
- Kariuki, C. M., Ilatsia, E. D., Wasike C. B., Kosgey, I. S. and Kahi, A. K. 2010b. Genetic evaluation of growth of Dorper sheep in semi-arid Kenya using random regression models. *Small Ruminant Research* 93(2): 126-134.
- Köhn, F., Sharifi, A. R., Malovrh, S. and Simianer, H. 2007. Estimation of genetic parameters for body weight of the Goettingen minipig with random regression models. *Journal of Animal Science* 85 (10): 2423-2428.
- Lundgren, H., Fikse, W. F., Grandinson, K., Lundeheim, N., Canario, L., Vangen, O. and Rydhmer, L. 2014. Genetic parameters for feed intake, litter weight, body condition and rebreeding success in primiparous Norwegian Landrace sows. *Animal* 8 (2): 175-183.
- Meyer, K. 2005a. Advances in methodology for random regression analyses. *Australian Journal of Experimental Agriculture* 45 (8): 487-585.
- Meyer, K. 2005b. Random regression analyses using B-splines to model growth of Australian Angus cattle. *Genetic Selection and Evolution* 37 (5): 473-500.
- Meyer, K. 2007. WOMBAT-a tool for mixed model analyses in quantitative genetics by Restricted Maximum Likelihood (REML). *Journal of Zhejiang University* 8(11): 815-821.
- Misztal, I. 2006. Properties of random regression models using linear splines. *Journal of Animal Breeding and Genetics* 123 (2): 74-80.
- Muasya, T. K., Peters, K. J., Magothe, T. M. and Kahi, A. K. 2014. Random regression test-day parameters for first lactation milk yield in selection and production environments in Kenya. *Livestock Science* 169: 27-34.
- Scalez, D. C., Fragomeni, B. O., Passafaro, T. L., Pereira, I. G. and Toral, F. L. 2014. Polynomials to model the growth of young bulls in performance tests. *The Animal Consortium* 8 (3): 370-378.
- Shirali, M., Nielsen, V. H., Møller, S. H. and Jensen, J. 2015. Longitudinal analysis of residual feed intake and BW in mink using random regression with heterogeneous residual variance. *The Animal Consortium* 1-8. doi:10.1017/S1751731115000956
- Wasike, C. B., Indetie, D., Pithford, W. S., Ojango, J. M. and Kahi, A. K. 2007. Genetic evaluation of growth of Kenya boran cattle using random regression models. *Tropical Animal Health Production* 39 (7): 493-505.

- Wetten, M., Odegard, J., Vangen, O. and Meuwissen, T. H. 2012. Simultaneous estimation of daily weight and feed intake curves for growing pigs by random regression. *Animal* 6 (3): 433-439.
- Wolc, A., Arango, J., Settar, P., Fulton, J. E., O'Sullivan, N. P., Preisinger, R. and Dekkers, J. C. 2013. Analysis of egg production in layer chickens using a random regression model with genomic relationships. *Poultry Science* 92 (6): 1486-1491.
- Zumbach, B., Misztal, I., Tsuruta, S., Sanchez, J. P., Azain, M., Herring, W. and Culbertson, M. 2008. Genetic components of heat stress in finishing pigs: Parameter estimation. *Journal of Animal Science* 86 (9): 2076–2081.