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Genetic and non-genetic factors associated with growth curve parameters in lowland sheep

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Introduction

Growth curve parameters can be incorporated into breeding programs to achieve desired growth patterns in animals. Variation in growth curve parameters may result from both genetic and non-genetic factors (Abbas *et al.*, 2024), and a clear understanding of the influence of these factors can be important before incorporating the parameters into selection indexes. The fitting of a growth function and the estimation of its variance components also depend on several factors, including the number of available weight records and the intervals between which they are collected (Lambe *et al.*, 2006). Although several studies in sheep have estimated genetic parameters for growth curve parameters, there is still limited information on animals managed under grass based production systems. The Gompertz function was determined by Sharif *et al.* (2025) as the most appropriate model for describing the growth curves of female lowland grazing sheep. Accordingly, this study aimed to quantify the association between non-genetic factors and Gompertz function parameters (A, B, and K), to estimate their (co)variance components, and to evaluate the impact of the number of weight records collected after 730 days of age on these parameters in a female lowland sheep population.

Materials & Methods

Data on female lowland sheep were sourced from the national sheep database hosted by Sheep Ireland (www.sheep.ie). Animals that satisfied all the following criterion were considered in the analysis: known sire and dam; birth type (litter size) ≤4; rearing type (number of lambs reared by one dam in a lactation) ≤3; remained in flock of origin during their lifetime; and age at first lambing between 8 to 28 months. For each day of age, weight records outside two interquartile ranges from the first or third quartile were considered outliers and removed. Additionally, records exceeding three standard deviations from the mean daily weight were also excluded. Only animals with at least 1 weight record in the first 7 days of life, a minimum of 2 records between 7 and 240 days, at least 1 record between 365 and 730 days, and 4 records after 730 days, with a minimum interval of 60 days between consecutive records after 730 days were retained in the final dataset. After all edits, the dataset consisted of 40,403 weight records from 3,757 females born between 2010 and 2021.

Estimation of Gompertz function parameters. The Gompertz function, expressed as $Y = Ae^{-Be^{-Kt}}$ (Winsor, 1932), with Y representing observed weight at age t (in days), A the asymptotic weight, B the initial weight constant, and K the maturation rate, was fitted to each animal individually using four different scenarios. The scenarios explored were: (1) all pre-730 day weights and just the first post-730 day weight, (2) all pre-730 day weights and just the first two post-730 day weights, (3) all pre-730 day weights and just the first three post-730 day weights, and (4) all pre-730 day weights and just the first four post-730 day weights. Outliers for each estimated parameter within each scenario were defined as values more than 1.5 times

the interquartile range below the first quartile or above the third quartile. After the removal of outliers, the number of animals common to all four scenarios was 3,431; these were retained for the subsequent analysis. The goodness of fit of the function was evaluated based on mean coefficient of determination (R^2) across animals and the mean root mean square error (RMSE).

Analysis of non-genetic factors. The association between non-genetic factors and individual growth function parameter values (A, B, and K) was investigated using repeated measures analysis in SAS 9.4 (SAS Institute Inc., Cary, NC). Estimated values of each of the three growth function parameters obtained using varying numbers of post-730 day weight records were treated as repeated measures within animals. The fixed effects included the number of records post-730 days (1, 2, 3 or 4); birth type (1, 2, 3 or 4); rearing type (1, 2 or 3); dam parity (1, 2, 3, 4 or ≥5); animal age at first lambing (8–18 or >18–28 months); dam age at first lambing (8–18 or >18–28 months); contemporary group (flock by birth year); animal heterosis coefficient (0–49%, ≥50%, <100% or 100%); dam heterosis coefficient (0–49%, ≥50%, <100% or 100%); animal recombination loss coefficient (<10% or ≥10%); dam recombination loss coefficient (<10% or ≥10%); and breed proportions of six major breeds for both the animal and its dam (Easy Care, Belclare, Suffolk, Charollais, Vendeen and other). Texel was used as the reference breed. The interactions between dam parity and dam age at first lambing as well as the number of weight records post-730 day and all the other fixed effects were also evaluated.

Genetic analysis. (Co)variance components were estimated for all three growth curve parameters (i.e., A, B and K) for each of the four scenarios varying in the number of post-730 day weight records using an animal linear model in ASReml (Gilmour *et al.*, 2021). With the exception of a term representing the number of post-730 day weight records, all previously described fixed effects and breed composition covariates were included in the model. Random effects tested across all models included additive animal genetic effects modelled using a pedigree-based numerator relationship matrix, as well as maternal genetic, maternal permanent environmental, and common litter effects. The log-likelihood ratio tests were used to determine whether the addition of additional random terms improved the fit to the data. A series of bivariate analyses were performed to estimate genetic and phenotypic correlations between the growth curve parameters.

Results

Across all four scenarios (i.e., varying number of post-730 day weight records), the Gompertz function provided a good fit to the data, with a mean coefficient of determination ≥0.95.

The mean root mean square error (RMSE) across the four scenarios ranged from 3.41 kg, when only the first post-730 day weight included in addition to all pre-730 day weights, to 4.88 kg, when 4 post-730 day weights were included along with all pre-730 weights.

All three parameters (A, B and K) were associated with dam parity and number of post-730 day records ($P < 0.05$). The estimates for parameter A of animals that lambed for the first time between 9 and 18 months were 1.86 kg lower compared with those animals that lambed for the first time after 18 months, respectively ($P < 0.001$). Parameters A and B differed by animal birth type ($P < 0.001$), with animals born as quadruplets having the lowest parameter A value (64.25 kg) and the highest parameter B value (2.14). For parameter K, animals reared as singles had higher predicted marginal mean (0.0100 kg/day per kg asymptotic weight) compared to those reared as twins (0.0089 kg/day per kg asymptotic weight) and triplets (0.0085 kg/day per kg asymptotic weight) ($P <0.001$).

As the number of post-730 day weight records increased, the value of parameter A increased; the predicted marginal mean was 63.95 kg when only the first post-730 day record was used increasing to 69.90 kg when four such records were included. In contrast, the trends in values for parameters B and K were in the opposite direction; the mean of both parameters values

when only the first post-730 day record was considered in fitting the growth function was 2.12 and 0.0104 kg/day per kg of mature weight, respectively, but only 1.99 and 0.0081 kg/day per kg of mature weight, respectively, when four weights post-730 days were used (Table 1).

Table 1. Predicted marginal means (standard error in parenthesis), additive genetic standard deviation (σ_a), direct genetic heritability (h^2) and common litter effect for asymptotic weight (A), initial weight constant (B) and maturity rate (K)

Parameter[1]	Mean[2] (SE)	σ_a	h^2 (SE)	Common litter effect (SE)
A				
1	63.95 (0.30)[a]	3.25	0.31 (0.05)	0.17 (0.06)
2	66.30 (0.30)[b]	3.51	0.32 (0.05)	0.21 (0.06)
3	68.58 (0.30)[c]	3.90	0.36 (0.05)	0.18 (0.06)
4	69.90 (0.30)[d]	4.10	0.37 (0.05)	0.20 (0.06)
B				
1	2.12 (0.01)[a]	0.10	0.37 (0.04)	0.18 (0.06)
2	2.08 (0.01)[b]	0.10	0.34 (0.04)	0.09 (0.06)
3	2.03 (0.01)[c]	0.12	0.33 (0.05)	0.03 (0.07)
4	1.99 (0.01)[d]	0.12	0.34 (0.05)	0.02 (0.06)
K				
1	0.0104 (0.0001)[a]	0.0007	0.18 (0.04)	0.16 (0.07)
2	0.0095 (0.0001)[b]	0.0009	0.20 (0.04)	0.17 (0.06)
3	0.0087 (0.0001)[c]	0.0010	0.23 (0.04)	0.09 (0.07)
4	0.0081 (0.0001)[d]	0.0011	0.25 (0.04)	0.06 (0.07)

[1] Within each parameter (A, B and K), the numbers 1 to 4 indicate the number of post-730 day weight records included in the estimation of the corresponding components.

[2] Means, within each parameter, with different superscripts differed ($P < 0.05$) from each other.

The most parsimonious mixed model for the genetic analysis included just a direct additive genetic effect and common litter effect. Genetic standard deviations (SD) for parameters A and K increased with the number of weight records taken after 730 days, rising from 3.25 kg and 0.0007 kg/day per kg asymptotic weight, respectively, when only the first post-730 day record was used, to 4.10 kg and 0.0011 kg/day per kg asymptotic weight, respectively, when four such records were used (Table 1). Heritability for parameters A and K ranged from 0.31 (0.05) and 0.18 (0.04), respectively, when only the first post-730 day weight was included, to 0.37 (0.05) and 0.25 (0.04), respectively, when four post-730 day weights were incorporated. Heritability for parameter B ranged from 0.37 (0.04) with one post-730 day weight to 0.34 (0.04) when three post-730 day weights were included (Table 1). Increasing the number of weight records post-730 days from 1 to 4 reduced the proportion of common litter effects from 0.18 to 0.02 for parameter B and from 0.16 to 0.06 for parameter K, respectively (Table 1).

The strength of both the genetic and phenotypic correlations increased with the number of post-730 day weight records. As the number of records increased from one to four, genetic correlations strengthened between parameters A and B (from −0.01 to −0.37), A and K (from −0.50 to −0.66), and B and K (from 0.36 to 0.77). Similarly, phenotypic correlations increased between A and B (from 0.01 to −0.28), A and K (from −0.47 to −0.55), and B and K (from 0.41 to 0.76).

Discussion

Growth curve parameters can be more informative than body weight recorded at specific ages because they are derived from a series of repeated measurements rather than a single observation and therefore provide a more comprehensive representation of growth dynamics in

animals (Duan *et al.*, 2021). Understanding the factors that influence growth curve parameters can be useful for characterizing growth and for designing optimal strategies for feeding, breeding, and overall animal management.

Single born and single reared animals are generally heavier at preweaning and weaning than multiple born and multiple reared animals. In some cases, this early growth advantage may continue to be reflected in mature weight, as observed in the present study, where single born animals had higher mature weights (parameter A) compared to multiple-born animals.

The greater mean values of parameter A with the inclusion of additional weight records after 730 days indicates that excluding mature weight data may lead to an underestimation of mature weight, consistent with the findings of Lambe *et al.* (2006). The concurrent reductions in parameters B and K as the number of post-730 day records increased can be attributed to their negative correlations with parameter A; as estimates of parameter A become more reliable with the inclusion of mature weight records, the corresponding estimates of parameters B and K also improve in accuracy, despite their lower magnitudes.

The moderate heritability estimates for all three parameters in the current study are consistent with previous studies on sheep, in which heritability estimates for these parameters ranged from low to moderate (Lupi *et al.*, 2016; Mohammadi *et al.*, 2019).The increase in the magnitude of genetic standard deviation and heritability estimates for parameters A and K with the inclusion of additional post-730 day records suggested greater expressed genetic variation, indicating that estimates based on four post-730 day weight records can be reliable. The coefficient of genetic variation for parameters A and B was 6%, whereas for parameter K it was 13% when four post-730 day records were used. Although the heritability estimate for parameter K was slightly lower than those for parameters A and B, the higher genetic variation suggests that, despite requiring more records to achieve high selection accuracy, the potential genetic gain for parameter K may be greater. The high negative genetic correlation between parameters A and K indicates that selection for higher maturity rates may result in reduced mature weights.

Conclusions

Dam parity and number of weight records post-730 days were associated with all parameters (A, B and K). The moderate heritability of all three parameters highlights the need for extensive phenotypic records to obtain precise genetic evaluations.

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