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# Putting flocks on the scales: evaluating flock performance for lamb liveweight using random regression models

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## Introduction

Lamb liveweight is an important indicator of profitability in meat sheep production systems (Bohan *et al.*, 2019). Many sheep genetic evaluation systems currently use single- or multi-trait models to estimate breeding values for liveweight at discrete timepoints. Given the increasing availability of on-farm weight data and the potential value of this additional information for both improving genetic evaluations and providing management feedback, investigation into methods that incorporate liveweight data across the growth trajectory of lambs is warranted. The use of random regression models to model serial measures of liveweight has been explored extensively across livestock species. Previously applied random regression studies in sheep have primarily focused on estimating variance components for liveweight, with little research focusing on their potential for informing on-farm management decisions. Random regression models offer potential as a benchmarking tool through the generation of producer-level performance profiles. Producer-level profiles generated through random regression models have been applied previously (Englishby *et al.*, 2017), though their application for benchmarking liveweight performance has not previously been explored. The objectives of the present study were to: 1) use a random regression model to estimate the (co)variance components for liveweight in growing lambs and, 2) evaluate the potential of flock-specific profiles derived from random regression models as a benchmarking tool. Results from this study will provide insights into the utility of random regression models for both the genetic evaluation of liveweight and on-farm management decisions in meat sheep production systems.

## Materials & Methods

A total 1,786,655 liveweight records from 517,580 lambs under 1 year of age, collected between the years 2015 and 2025, inclusive were available from the Irish national sheep database operated by Sheep Ireland (www.sheep.ie). Similar to the edits performed in the national genetic evaluations, liveweight records were retained if they fell within defined ranges: between 2 and 9 kg from 0 to 10 days of age, between 5 and 20 kg from 11 to 19 days, between 12 and 32 kg from 20 to 65 days, between 20 and 55 kg from 66 to 120 days, and between 25 and 70 kg from 121 to 150 days of age. All liveweights recorded after 150 days of age were excluded from all subsequent analysis.

Records were retained only for lambs with recorded parents, birth types between 1 (singles) and 4 (quadruplets), and rearing types between 1 and 3 lambs. Dam parity was classified into seven categories: 1, 2, 3, 4, 5, 6 and ≥7, and the age of the dam at first lambing was classified into two categories: 1) between 8 and 18 months of age, or 2) between 18 and 28 months of age. Lambs recorded as artificially reared, born by embryo transfer, or reared by a dam other than their genetic dam were also excluded from further analysis. The breed compositions of the seven most represented breeds (Suffolk, Texel, Charollais, Vendeen, Belclare, Lleyn and Easycare) were calculated for each lamb and dam. Heterosis and recombination loss coefficients were also calculated for each lamb and dam. Heterosis coefficients were grouped

into four distinct classes: <10%, 10 to <50%, 50% to <90% and ≥90%. Recombination loss coefficients were grouped into three classes: <10%, 10 to <30% and ≥30%.
Each record was allocated to a contemporary group of flock-week of weighing. An iterative procedure was then applied to retain only records from contemporary groups with at least five records, while ensuring that each lamb had at least one liveweight record at each of four key growth stages (birth, pre-weaning, weaning and post-weaning). This was repeated until both conditions were satisfied for all contemporary groups. After all edits were applied, a total of 159,627 records from 33,561 lambs spanning 461 flocks remained.
Variance components for lamb liveweight across ages were estimated using random regressions on age in ASReml. Legendre polynomials on age at weighing were fitted as a fixed effect interacting with sex, rearing type, and the interaction between dam parity and age at first lambing. Birth type, and heterosis and recombination classes of both the dam and lamb were fitted as fixed class effects, while the breed composition of both the dam and lamb were fitted as fixed covariates; these effects were not modelled as functions of age. The contemporary group of flock-week of weighing was included as a random class effect. Random regressions on age at weighing were used to model the direct genetic, permanent environmental, maternal genetic, maternal litter and flock-year effects, with the additive genetic variance components leveraging the available pedigree information. Seven residual variance blocks were fitted: 0 to 13, 14 to 34, 35 to 62, 63 to 76, 77 to 118, 119 to 132 and 133 to 150 days of age. A linear polynomial of age at weighing was deemed to be the best fit for all of the fixed effects interacting with age. Different orders of polynomial were then explored for the additive genetic, permanent environment, dam genetic, dam permanent environment, and flock-year effects. The most parsimonious order of the random regression to adequately model the data was decided on by comparing the Akaike information criterion and Bayesian information criterion of the higher order random regression model and the immediately lower order fit.
To evaluate the consistency of within flock-year growth profiles across age, the percentile rank of each flock was calculated within year at 40, 100 and 150 days of age from the random regression on age by flock-year. A secondary analysis was conducted to assess the stability of flock rankings across consecutive years, whereby only flocks with records in two consecutive years were retained. For each year pair, flock-year percentile ranks were calculated across all the retained flocks at 40, 100, and 150 days of age, and the consistency of flock rankings between consecutive years were then compared.

## Results

A quadratic Legendre polynomial provided the most parsimonious model to fit the data for all age-dependent random effects. The direct additive genetic standard deviation for liveweight increased across the age trajectory from 0.28 (SE = 0.02) kg at birth to 2.57 (SE = 0.10) kg at 150 days. The maternal genetic standard deviation increased from 0.30 (SE = 0.010) kg at birth up to a maximum of 1.44 (SE = 0.08) kg at 129 days. The animal permanent environment standard deviation, increased from 0.35 (SE = 0.01) kg at birth to 3.91 (SE = 0.05) kg at 150 days with a marked increase observed after 125 days. The standard deviation of the dam litter effect increased from 0.415 (SE = 0.007) kg at birth to 1.95 (SE = 0.05) kg at 100 days, with a reduced rate of increase thereafter, reaching a maximum of 2.19 (SE = 0.08) kg at 150 days. The contemporary group effect of flock-week-of-weighing had a standard deviation of 0.90 (SE = 0.012) kg. The direct heritability for liveweight was 0.06 (SE = 0.006) at birth, increasing to a maximum of 0.10 (SE = 0.007) at 76 days (Fig. 1), and then reducing slightly to 0.09 (SE = 0.007) at 150 days of age. At birth, the maternal heritability was 0.06 (SE = 0.004), peaking at 0.08 (SE = 0.006) at 11 days, and then reducing to 0.03 (SE = 0.004) at 150 days. The discrete jumps visible in the heritability trajectories in Fig. 1 reflect the boundaries between the seven residual variance classes fitted in the model.

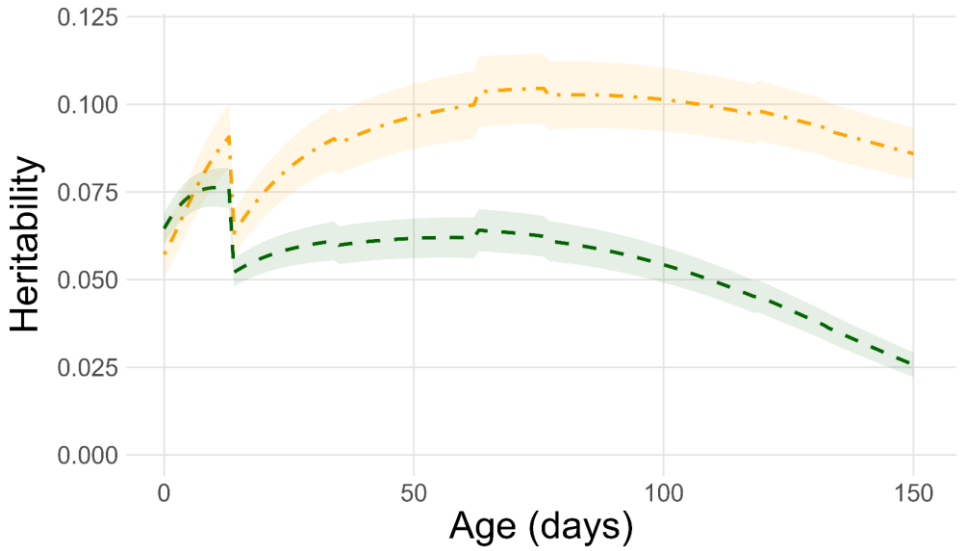


**Figure 1.** Direct (orange) and maternal (green) heritability for lamb liveweight across age. The shaded regions represent ±1 standard error around the estimate.

The proportion of total liveweight variance explained by flock-year increased with age, ranging from 0.04 at birth to 0.60 at day 150. When flocks were ranked within year and grouped into quintiles, 64% of flock-years remained in the same quintile at both day 40 and day 100, with the highest stability observed in the top and bottom quintiles. When comparing 40-day rankings with 150-day rankings, 45% of flock-years remained in the same quintile; of the flock-years initially ranked in the highest and lowest quintiles at 40 days, 65% and 57%, respectively, remained in the same quintile at 150 days. Only 14% of flock-years changed by more than one quintile in rank between 40 and 150 days, indicating that the majority of flock-years ranked similarly over the growth period.

Of the flocks with liveweight records in consecutive years, the proportion of flocks ranked in the top 20% in one year that remained in the top 20% for the same age in the following year ranged from 0.31 (day 40; 2021–2022) to 0.83 (day 100; 2016–2017) (Table 1). On average, flocks in the top 20% at day 40 in a given year had a 0.51 probability of remaining in the top 20% at day 40 in the following year; at day 150 the corresponding probability increased to 0.56.

**Table 1.** Year-to-year consistency of top 20% flocks at different ages[1]

| Years compared | No. of flocks | 40 days | 100 days | 150 days |
|---|---|---|---|---|
| 2015-2016 | 27 | 0.67 | 0.67 | 0.50 |
| 2016-2017 | 28 | 0.50 | 0.83 | 0.67 |
| 2017-2018 | 51 | 0.64 | 0.45 | 0.36 |
| 2018-2019 | 48 | 0.70 | 0.70 | 0.70 |
| 2019-2020 | 47 | 0.40 | 0.50 | 0.50 |
| 2020-2021 | 60 | 0.42 | 0.50 | 0.58 |
| 2021-2022 | 62 | 0.31 | 0.46 | 0.46 |
| 2022-2023 | 63 | 0.62 | 0.69 | 0.77 |
| 2023-2024 | 76 | 0.50 | 0.50 | 0.56 |
| 2024-2025 | 92 | 0.47 | 0.58 | 0.53 |

[1] Proportion of flocks in the top 20% in given year that remain in the top 20% in the following year

## Discussion

The application of genetic evaluations as decision-support tools for producers has been well documented (Kenny *et al.*, 2021), yet few studies have investigated the use of flock-level profiles of performance traits like liveweight as on-farm management aids. This study examined the potential to generate flock-level profiles for lamb liveweight to enable meaningful benchmarking of flocks across time. Estimates of both direct and maternal heritability for liveweight were generally lower than previously reported using univariate models in Irish sheep (McHugh *et al.*, 2023). Applying comparable univariate models to the present dataset also produced higher heritabilities than the random regression model, particularly at later growth stages. Modelling contemporary group as random instead of fixed in the univariate model reduced the heritabilities, demonstrating that the lower estimates from the random regression model were at least partly attributable to the treatment of contemporary group. The large permanent environmental variance for lamb liveweight, particularly later in life, is consistent with findings in other lamb populations (Paneru *et al.*, 2024) and likely reflects the cumulative effects of early-life conditions and individual parasite burden (Schaeffer, 2011). A key finding of the present study was the increasing importance of flock-year effects over the growth trajectory, accounting for up to 60% of the phenotypic variance by 150 days of age. This pattern suggests that management and environmental influences accumulate over time, with the proportion of phenotypic variance attributable to flock-year at 150 days of age being comparable to that reported for herd-year effects on carcass weight in cattle (Englishby *et al.*, 2017). By modelling flock-year effects as random regressions on age, this study generated flock-specific growth profiles to enable benchmarking of flocks across the production cycle. Due to shrinkage toward the population mean, these flock-level profiles may underestimate management differences, particularly at the extremes; however, using percentile ranks or similar relative metrics can still provide meaningful benchmarking. Incorporating flock-level growth profiles into benchmarking tools could enable producers to identify stages of the growth trajectory where flock performance deviates from expected growth patterns, enabling earlier and more targeted management interventions.

## Conclusions

The present study demonstrates how routinely collected liveweight records can be modelled using random regressions to generate both genetic evaluations and flock-specific profiles for liveweight. These results show the potential of this approach to better leverage all available liveweight data, support genetic evaluation, enable flock benchmarking and inform on-farm management decisions, disentangling management performance from genetic potential.

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