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Random regression analysis to determine herd profiles for carcass weight in UK beef cattle

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Application Knowledge of the variability in herd performance across years, by drawing inferences from carcass weight at slaughter, could be used as a management tool to monitor herd performance.

Introduction Random regression models can provide information of the genetic variability in carcass weight across a given time trajectory defined by age at slaughter. Random regression models also allow for modelling of herd-specific deviations to describe differences in growth curves across herds (De Roos *et al.*, 2004). The objective of the present study was to determine growth curve and herd curve parameters, using a random regression model, for carcass weight measured on young bulls across multiple breeds.

Material and methods Carcass trait information was available on 58,655 bulls from 2,387 UK herds slaughtered between 2002 and 2012. Records from bulls slaughtered <12 months or >24 months of age were discarded as were bulls with no known sire or dam. Records outside ± 4 standard deviations from the mean carcass weight or age at slaughter were discarded. Dam records were restricted to parity 1 to 10, and parity was categorised as 1, 2, 3, 4, and ≥ 5 . Only records from sires with at least 5 progeny records were retained. Two contemporary groups were defined 1) abattoir-date of slaughter, and 2) finishing herd-year of slaughter; only contemporary groups with five or more records were retained. Following edits, 22,971 young bulls from 2,239 sires remained. A random regression model was fitted in ASReml (Gilmour *et al.*, 2009). A fixed effect of age at slaughter was modelled with a Legendre polynomial and reflected the fixed curve. Other fixed effects included breed of sire and breed of dam, parity of the dam, contemporary group of abattoir-date of slaughter as well as heterosis and recombination coefficients of the animal. Random effects included the sire of the animal and the contemporary group of finishing herd-year of slaughter; both were modelled across age at slaughter with Legendre polynomials. Random effects reflected individual deviations from the fixed curve. The random residual term was modelled as heterogeneous across age at slaughter classes. Covariance function coefficients were estimated using the variance covariance matrix and the matrix of Legendre polynomials: $G = \Phi'K\Phi$ where G is the variance covariance matrix for slaughter ages, Φ is the matrix of Legendre polynomial age regression coefficients, and K is the estimated variance covariance matrix of the random polynomial coefficients K_a or K_{hy} ; K_{hy} is the estimated finishing herd-year of slaughter variance covariance matrix; K_a is the estimated genetic variance covariance matrix multiplied by four to transform from a sire variance to a genetic variance.

Results The average (standard deviation in parentheses) carcass weight and age at slaughter across the data was 354.3 (52.2) kg and 454.8 (51.4) days, respectively. A random quadratic Legendre polynomial on sire and a random linear Legendre polynomial on finishing herd-year of slaughter fitted the data best. The heritability of carcass weight (standard error in parentheses) was least (i.e., 0.19; se=0.04) at 673 days of age and greatest (0.25; se=0.02) at 536 days of age indicating that sufficient genetic variation exists for selection on this trait (Fig. 1). Finishing herd curve variance (standard error in parentheses) ranged from 802.63 (70.98) units² to 1594.90 (172.19) units² for carcass weight (Fig. 2). Analysis of eigenvalues of finishing herd-year covariance across age at slaughter, revealed considerable variation between herds in their growth curve parameters for carcass weight.

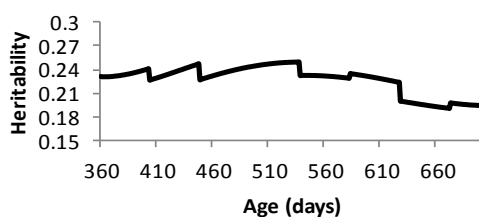


Figure 1 Estimated animal genetic variances for carcass weight across age at slaughter. Standard errors ranged from 0.02 to 0.06.

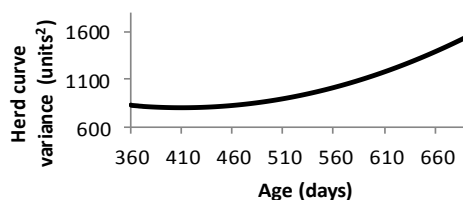


Figure 2 Herd curve variance estimates for carcass weight across age at slaughter. Standard errors ranged from 68.93 to 172.19.

Conclusion Random regression models can be used to model herd variance in carcass weight across an age trajectory. Considerable variation exists between herds in their growth curve parameters for carcass weight, reflecting different management practices.

References

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