

# Across breed regression of traits on breed specific breeding values

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## Introduction

The New Zealand dairy industry produces around three million calves per annum not required as replacements for the dairy industry (Edwards *et al.*, 2021), and with the advent of technologies including sexed semen and heat detection using wearable devices there is significant opportunity to increase the use of superior beef bulls to improve the quality of these calves for beef production (Sneddon *et al.*, 2025). The New Zealand dairy industry uses across-breed genetic evaluations (DairyNZ, 2026), whereas the beef industry uses within-breed evaluations (BreedPlan, 2026). These industry structures mean that the beef and dairy industries can struggle to align their objectives or to directly compare the performance of animals. A national level progeny test programme the Dairy Beef Progeny Test (DBPT) was established to provide across-breed comparison of expected sire differences by including sires from beef breeds represented in New Zealand on multiple dairy herds to produce high quality data. This programme is used to identify sires with high genetic merit for the production of beef-on-dairy animals highly suited for the beef-finishing system, while still meeting the requirements of the dairy industry. Therefore, this study aims to test a means to compare the breeds on a common basis.

## Materials & Methods

Data used in this study was generated by the DBPT programme and from publicly (referred to as published) available information in the breed society reported estimated breeding values (EBV) for sires from Angus, Charolais, Hereford, Shorthorn and Simmental breeds. Estimated breeding values used in the analysis were those from the most recent BreedPlan run to the 15<sup>th</sup> of November 2025. Records from DBPT animals were collected from animals born between July and October each year from 2016 to 2024 (assigned as annual cohorts), records used included birthweight (measured within 24 hours of birth), 200-, 400- and 600-day weights and age at each of those events, calf sex, sire and dam as determined by genotypic parentage matching. Summary statistics of data are presented in Table 1. Contemporary groupings were determined using methods outlined in Weik *et al.*, (2021), where contemporary groups built on previous mobs, starting with birthyear, farm and sex, at each following event the recording mob at event was added to the end of the contemporary grouping.

**Table 1.** Number of sires, progeny, and mean estimated breeding values for birthweight (BWT), gestation length (GL), 200-, 400-, 600-day weight, and years of progeny test data included in regression analysis.

| Breed     | N sires | N Progeny | BWT   | GL    | 200-day | 400-day | 600-day | N years |
|-----------|---------|-----------|-------|-------|---------|---------|---------|---------|
| Angus     | 63      | 1393      | 2.27  | -6.37 | 45.06   | 83.93   | 106.28  | 9       |
| Charolais | 3       | 84        | -3.15 | -6.25 | 19.27   | 47.59   | 51.68   | 4       |
| Hereford  | 79      | 1972      | 1.77  | -2.63 | 34.03   | 60.58   | 81.61   | 9       |
| Shorthorn | 4       | 86        | 0.23  | -3.36 | 24.27   | 33.07   | 44.86   | 4       |
| Simmental | 10      | 370       | 1.48  | -4.48 | 72.04   | 107.43  | 118.66  | 6       |

Regression of EBVs on phenotype was done using Proc GLM in SAS 9.4, the models for the phenotype of interest (birthweight, gestation length, 200-, 400-, 600-day weights) included the

fixed effects of sire breed and contemporary grouping at event measurement, age at event and the respective published EBV fitted as a covariate. Genetic parameters and across breed internal EBVs were estimated using ASReml 4.2 (Butler *et al.*, 2023) with a univariate model for each trait and fitting the fixed effects of sire breed, contemporary group at event measurement, with age at event (for 200-, 400- and 600-day weights) fitted as a covariate, dam and animal were both fitted as random effects. The internal sire EBV predictions produced by the animal model were correlated with the published EBV using Prog CORR in SAS 9.4.

## Results & Discussion

Regression coefficient outputs are presented in table 2, a common slope was generated for all breeds with unique intercepts for each breed, where a EBV of 0 would be equivalent to the intercept for that breed. This means that using the intercept each breed can be compared and the expected phenotype could be estimated using the common slope. Due to differences in the trait definitions of EBVs for Simmental cattle it was not possible to obtain an intercept for the 200- or 400-day weights. The expected slope for all traits would be 0.5 if the population is under no form of bias or selection, is of sufficient size and the EBVs have a high accuracy. However, these slope coefficients deviated from the expected, with possible explanations including: the limited number of sires, selection process to select sires into the breeding programme, slight differences in trait definitions and the accuracies of the EBVs. This was most pronounced for 200- and 400-day weights, but due to the management processes (weaning determined on an individual weight basis rather than date) in dairy beef it is expected that these will deviate from the expected. While the slopes deviated from the expected values the estimations were in line with a previous study using similar data and analysis methodologies (Martín *et al.*, 2021)

**Table 2.** Regression coefficients, intercept (Int), r-squared and significance of the slope for estimated breeding values (EBV) for traits of interest regressed on phenotypic records for Angus (A), Charolais (Ch), Hereford (H), Shorthorn (Sh) and Simmental (Si) sires and breed average EBV for each trait and breed as of November 2025.

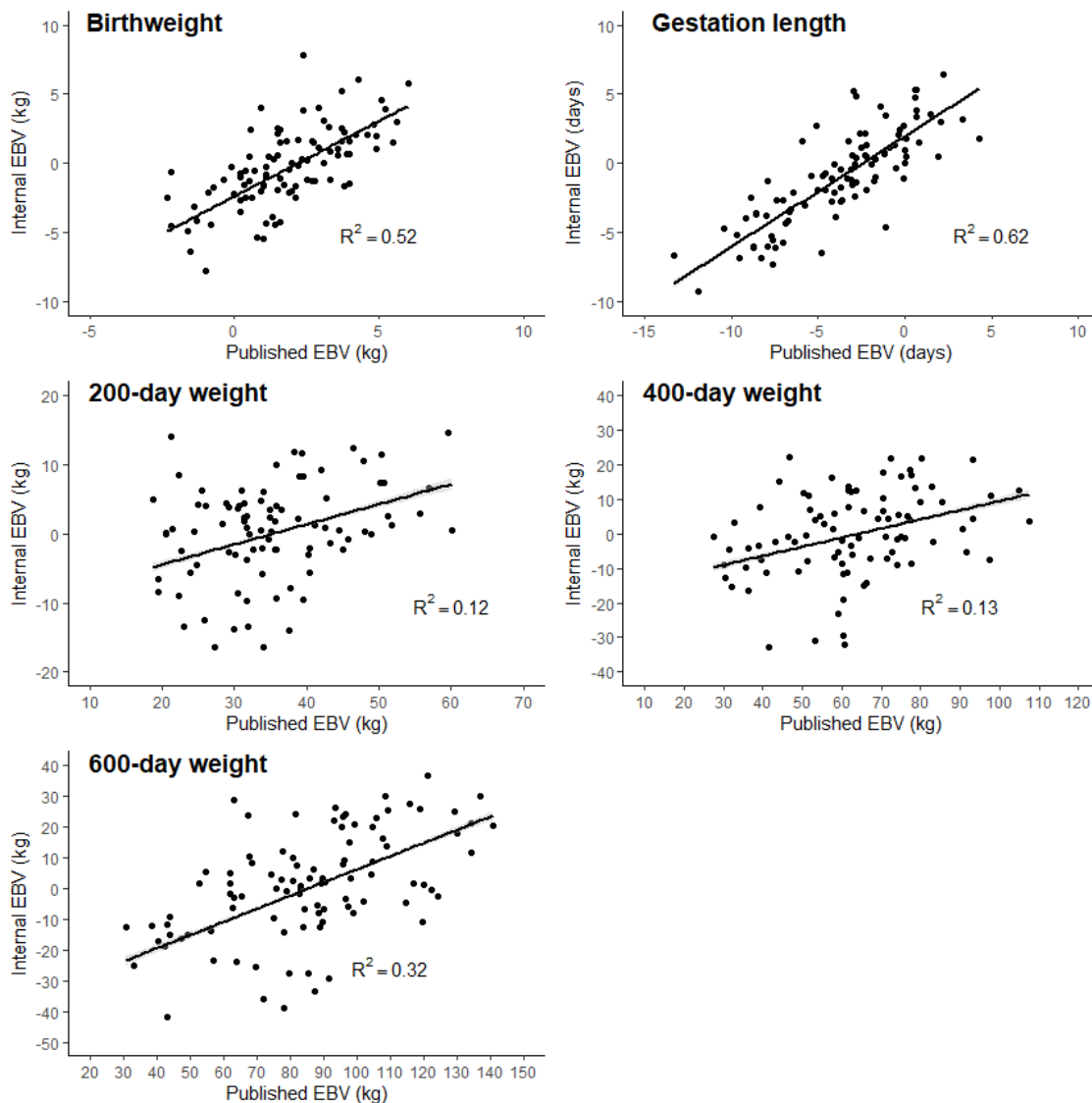
| Trait            | EBV slope    | A Int | Ch Int | H Int | Sh Int | Si Int | P-value | R <sup>2</sup> |
|------------------|--------------|-------|--------|-------|--------|--------|---------|----------------|
| Birthweight      | 0.675 ± 0.04 | 37.04 | 44.12  | 38.87 | 41.25  | 40.05  | <0.001  | 0.17           |
| Gestation length | 0.542 ± 0.03 | 281.2 | 283.9  | 281.7 | 281.9  | 283.4  | <0.001  | 0.19           |
| 200-day weight   | 0.254 ± 0.03 | 131.1 | 141.4  | 133.2 | 133.7  | 128.9  | <0.001  | 0.60           |
| 400-day weight   | 0.359 ± 0.03 | 223.5 | 253.7  | 232.7 | 236.7  | 222.3  | <0.001  | 0.70           |
| 600-day weight   | 0.396 ± 0.03 | 404.2 | 451.5  | 416.1 | 421.4  | 412.6  | <0.001  | 0.60           |
| Average EBV      | A            | Ch    | H      | Sh    | Si     |        |         |                |
| Birthweight      | 4.2          | 0.4   | 3.6    | 3.1   | 4.3    |        |         |                |
| Gestation length | -4.1         | -2.7  | -1.1   | -1.5  | -1.7   |        |         |                |
| 200-day weight   | 42           | 12    | 35     | 28    |        |        |         |                |
| 400-day weight   | 79           | 24    | 60     | 39    |        |        |         |                |
| 600-day weight   | 101          | 32    | 83     | 51    | 131    |        |         |                |

Heritability estimations ranged from 0.47±0.07 for 400-day weight to 0.54±0.08 for 600-day weight, the genetic parameter estimations in this study were within the range presented in previous studies using dairy beef animals (Coffey *et al.*, 2006; Brotherstone *et al.*, 2007; Martín *et al.*, 2018). The values produced in the estimation of genetic parameters were also used to produce new estimated breeding values for the traits of interest for all breeds, which were used to determine the correlations between publicly available EBVs and the EBVs generated by this study. A part of the explanation of this result is that the published EBVs are estimated using a multi-trait model, with a much deeper pedigree, and so have inbuilt correlations as priors vs the internal univariate EBV estimations. Correlations between these variables are presented in table

3. The correlations were greater between the published EBVs than internal EBV from this study. The correlations for the same trait were lowest for 200- and 400-day weights, this is most likely due to the difference in rearing system and in early life altering the growth trajectory of animals raised in a dairy system (artificial rearing) compared to those reared within the beef system (suckling from their dam).

**Table 3.** Correlations between published estimated breeding values (below the diagonal) and the internal estimated breeding values (above the diagonal) for traits of interest generated from the dairy beef progeny test dataset for animals born between 2016 and 2024.

| Trait                 | BWT   | GL     | 200d   | 400d  | 600d   |
|-----------------------|-------|--------|--------|-------|--------|
| Birthweight (BWT)     | 0.723 | 0.448  | 0.201  | 0.224 | 0.341  |
| Gestation length (GL) | 0.039 | 0.784  | -0.008 | 0.009 | -0.028 |
| 200-day weight (200d) | 0.477 | -0.269 | 0.353  | 0.801 | 0.703  |
| 400-day weight (400d) | 0.376 | -0.274 | 0.899  | 0.339 | 0.872  |
| 600-day weight (600d) | 0.409 | -0.231 | 0.905  | 0.965 | 0.599  |



**Figure 1.** Scatterplot of published and internally produced estimated breeding values (EBV) for birthweight, gestation length, 200-, 400-, 600-day weights from records from the dairy breed progeny test.

Figure 1 presents the relationship between the published and internal EBVs, indicating that the relationship between the values are lower for 200- and 400-day weights. This is explained by, the management of animals which have undergone artificial rearing and this reduces the relationship to the breeding values from beef origin animals. A similar trend was found in the research by Martín et al., (2021). Birth traits (birth weight and gestation length) were least affected by the system from which the EBVs are generated from.

## Conclusions

Within breed EBVs can be regressed on phenotypic records from progeny tests which incorporated all breeds and have good representation across years. These regression values will allow the within breed EBVs to be utilised within systems which are familiar with across breed evaluation. Slope coefficients were below the values expected for the half of EBV rule, which may be a reflection of the accuracy of the EBVs.

## Acknowledgements

The authors are grateful for the hard work and dedication of all of those who have been involved in the DBPT programme since its inception, from farm staff, and specific acknowledgement to Craig Foote for his technical expertise and oversight of data collection and management.

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