McNaughton, L., Ismael, A., Sherlock, R., Boerner, V., Harris, B., Spelman, R. (2026) The genetic relationship between liveweight in dairy youngstock and lactating cows in New Zealand dairy cattle, *Proceedings 13th World Congress on Genetics Applied to Livestock Production* 23574: https://doi.org/10.31274/wcgalp.23574 ©2026 McNaughton, et al. CC BY-NC-ND

The genetic relationship between liveweight in dairy youngstock and lactating cows in New Zealand dairy cattle

L.R. McNaughton*[1], A. Ismael[1], R.G. Sherlock[1], V. Boerner[2], B.L. Harris[1] and R.J. Spelman[1]

[1]*Livestock Improvement Corporation, 605 Ruakura Road, Hamilton 3286, New Zealand.*
[2]*GHPC Consulting and Services Pty. Ltd., Armidale 2351, Australia; *Corresponding author: lorna.mcnaughton@lic.co.nz*

Introduction

Regular live weight (LWT) recording of growing beef and dairy animals is a common management practice in New Zealand. In seasonal, pasture-based systems individual feed intake recording at grazing is currently not feasible at the required scale for phenotyping purposes. LWT can be used as a proxy for efficiency (Harris, 1998). Previous studies have indicated that incorporating LWT into a selection index in New Zealand grazing systems, alongside milk, fat, and protein, resulted in an additional economic gain of 3-5% compared to selection based on an index without LWT (Spelman and Garrick, 1997). LWT was introduced into New Zealand's dairy cattle selection index in 1996, with a negative economic value. In the genomic age, phenotypes remain a key part of genetic evaluation systems. In New Zealand more than 60% of cows are crossbred (DairyNZ, 2025), requiring larger populations of phenotyped and genotyped animals for accurate genomic evaluations. Phenotypic records of LWT from lactating dairy cattle are limited (approximately 40,000 animals/yr); most records are collected from first-lactation heifers in sire-proving scheme herds, during classification for type traits. The genetic correlation between LWT and milk yield varies by stage of lactation. For example, the genetic correlation between LWT and milk yield changed from 0.29 in lactation week 3 to -0.25 in week 13, meaning cows genetically superior for milk yield might grow less during lactation due to the negative energy balance and the mobilization of body tissues (Veerkamp, 1998). LWT has been demonstrated to be correlated with improved milk production, reproductive performance, and stayability in dairy heifers (Handcock *et al*., 2020). More than one million youngstock LWTs are recorded into LIC's animal database annually, providing a potential source of phenotypes for genetic evaluation. This study aimed to estimate variance components and genetic parameters for LWT in the New Zealand multi-breed dairy heifer population, to determine if youngstock LWT could be used as a source of phenotypes for the genetic evaluation of mature LWT.

Materials & Methods

Pedigree and phenotype data were extracted from the Livestock Improvement Corporation (LIC, Hamilton, New Zealand) database in July 2023. Animals with a minimum of 2 LWT records between birth and 365 days of age and 2 LWT records between 366 and 700 days were included. In each month of age and for each breed, records that deviated from their breed-age mean by more than four standard deviations were removed. Contemporary groups were defined by herd-year-month of weight record, with records excluded if their contemporary group size was less than ten animals. After filtering a total of 10,949,191 LWT records from birth to 24 months for 1.3m dairy heifers and 30,000 dairy bulls born between 2008 and 2022 remained. The pedigree file included 4,183,131 animals. LWT at different ages was defined: LWT1 (birth to 100 days), LWT2 (101 – 300 days), LWT3 (301-500 days), LWT4 (501-700 days), and LWT5 (730-1200 days). The analysis was conducted using APEX – Linear Model

Suite with a single-trait model to estimate variance components and heritability for each trait, followed by a multi-trait model to estimate the genetic correlation between traits. These models incorporated the fixed effects of sex, contemporary group of herd-year-month of weight, the individual inbreeding coefficients calculated from pedigree, regressions on age in days using cubic Legendre polynomials, breed proportion of the animal (Jersey, Holstein, Friesian, Red Dairy Cattle), regressions on age in days using cubic Legendre polynomials nested within breed proportions, heterosis effects, an individual's (pedigree-based) inbreeding coefficient, genetic group covariates, random genetic effects and random residuals. The genetic groups were assigned for males and females with missing parent(s), separately in five-year windows based on the individual's birth year. The male genetic groups were divided into two sub-groups, based on whether an individual was sired by an unrecorded male or by artificial insemination where the actual sire could not be determined. Genetic groups containing fewer than 2,000 observations were combined with the preceding genetic group. The genetic groups were assigned to all individuals using Westell grouping procedures (Westell *et al*., 1988). Heterogeneous residual variances were assumed across weighing age for the following time intervals; LWT2:101-150, 151-200, 201-250, and 251-300 days; LWT3: 301-350, 351-400, 401-450, and 451-500 days; LWT4: 501-550, 551-600, 601-650, and 651-700 days; LWT5: 730-830, 831-930, 931-1030, and 1031-1200 days. LWT1 was assumed to exhibit homogeneous residual variance across all age intervals.

A subset of 70,063 females had both youngstock LWT records and at least one LWT record during lactation between 730 and 1200 days of age (LWT5) (96,397 records). Bivariate repeatability animal models were used to estimate the genetic correlations between LWT5 and each of LWT1, LWT2, LWT3, and LWT4. The improvement of model reliability from single-trait model to multi-trait model was evaluated using the predicted error variance (PEV) of the breeding value as 1-PEV/σ_a^2 , where PEV is the predicted error variance of animals which was calculated by inverting the coefficient matrix of the mixed model equations (Henderson, 1975) and σ_a^2 is the additive genetic variance for each trait.

Results & Discussion

The incorporation of youngstock LWT into the genetic evaluation system would result in a large increase in the volume of LWT phenotypes available for evaluation. The number of LWT records, animals with LWTs and descriptive statistics used in this study are presented in Table 1.

Table 1. Number of records, number of animals and the summary statistics of liveweight traits.

Traits	N records	N animals	Mean (kg)	SD	CV%	Age (d)
LWT1	1,477,474	730,668	79.6	17.6	22.14	0-100
LWT2	5,052,529	1,290,678	156.1	41.1	26.35	101-300
LWT3	2,685,123	990,703	269.2	53.4	19.84	301-500
LWT4	1,734,065	803,188	400.6	54.0	13.48	501-700
LWT5	96,397	70,063	419.7	53.5	12.74	730-1200

LWT2 had the largest number of records and animals with LWT records. This period encompasses the post-weaning period, when many heifers move from the dairy farm to a dedicated youngstock facility. Mean LWT increased from 79.6 kg at LWT1 to 400.6 kg at LWT4 and 419.7 kg at LWT5. Average LWTs for the genetic base cow in New Zealand are 398 kg for two-year-olds, 458 kg for three-year-olds, 492kg for four-year-olds and 526 kg for five- to eight-year-olds (DairyNZ, 2026). Lactanet reports mature Canadian Holstein dairy cows average 771kg, and are over 80kg heavier compared to 20 years ago (Molano, 2022). Selection against LWT has limited LWT increase in New Zealand. LWT breeding values for

Holstein Friesian x Jersey animals (>60% of the dairy population) on the LIC database have increased by 23kg between 1996 and 2025.
Heritabilities ranged between 0.40 for LWT2 and 0.65 for LWT5 (Table 2), similarly to estimates reported in literature (Koenen and Groen, 1998; Berry *et al*., 2003). Genetic correlations between LWT5 and the other LWT traits were of particular interest and were all strong (>0.70). Repeatabilities ranged from 0.75 to 0.86, indicating that LWT is stable within animals over time across repeated measurements, and early LWT records can be used to generate breeding values. LWT1 had the weakest genetic correlation with LWT5 (0.77), a similar result to previous studies where birthweight had the lowest genetic correlation with other LWTs (Yin and König, 2018; Feng *et al*., 2025). The strongest genetic correlation (0.96) was between LWT3 and LWT4. LWT4 had the highest genetic correlation with LWT5 (0.91). The strong (≥0.88) genetic correlations between LWT5 and both LWT3 and LWT4 suggest that LWT records from animals of >12 months of age are the best predictors of mature LWT breeding values.

Table 2. Heritabilities (bold, on the diagonal, with SE), genetic (above diagonal, with SE) and permanent environmental (below diagonal) correlations between liveweight (LWT) traits. LWT1 (birth to 100 days), LWT2 (101 – 300 days), LWT3 (301-500 days)), LWT4 (501-700 days) and LWT5 (730 – 1200 days).

Traits	LWT1	LWT2	LWT3	LWT4	LWT5
LWT1	**0.52 (0.003)**	0.92 (0.001)	0.81 (0.003)	0.78 (0.003)	0.77 (0.007)
LWT2	0.79	**0.40 (0.002)**	0.91 (0.001)	0.87 (0.002)	0.84 (0.015)
LWT3	0.53	0.74	**0.46 (0.002)**	0.96 (0.001)	0.88 (0.009)
LWT4	0.49	0.65	0.88	**0.53 (0.002)**	0.91 (0.007)
LWT5	0.32	0.55	0.69	0.77	**0.65 (0.010)**

The impact of the incorporation of youngstock LWTs on the reliability of estimated breeding values are presented in Table 3. The single trait evaluation of sires (ST(sires)) is the closest comparison to the current evaluation system. The multi-trait evaluation provides an 11% increase in the reliability of breeding values. Moreover, although LWT5 records were only available on a relatively small number of animals (~70k cows with LWT5 records) compared to younger LWT traits, the multi-trait model was able to predict the estimated breeding values (EBV) for non-phenotyped animals with 0.49 reliability; a substantial increase compared to a reliability of 0.28 for animals without a phenotype nor genotype in the current evaluation system. A further simulation of ungenotyped cows in the current LIC animal evaluation system was run to estimate the increase in reliability of LWT EBVs of the current animal evaluation model if LWT2 were added to the model. The current model reliability for animals with a mature LWT phenotype is 0.74. Adding LWT2 records to the evaluation would increase the reliability to 0.77. Similarly, for animals without phenotypes the reliability of LWT EBV increased from 0.31 to 0.53. LWT EBVs are used in the Breeding Worth (BW) and Production Worth (PW) indexes, with PW used to make culling decisions and to set growth targets for youngstock (Bryant *et al*., 2004). Such an increase in reliability would allow farmers to make more accurate breeding and culling decisions.
The current animal evaluation LWT trait is defined as mature cow LWT, although in practice most of the measurements are derived from first lactation animals, in early to mid-lactation. Stage of lactation affects LWT and the genetic correlation between milk production and LWT changes over the lactation (Veerkamp, 1998). Youngstock LWTs are not subject to a stage of lactation effect, potentially making them a better phenotype than mature LWT. The genetic

correlation between youngstock LWT and the traits included in New Zealand's animal evaluation system should be estimated in future work.

Table 3. Reliability of breeding values estimated from single-trait (ST) vs multi-trait (MT) model. LWT1 (birth to 100 days), LWT2 (101 – 300 days), LWT3 (301-500 days)), LWT4 (501-700 days) and LWT5 (730 – 1200 days).

Trait	ST (All- animals)	MT (All animals)	ST (Sires)	MT (Sires)	Non-Phenotyped
LWT1	0.36	0.38	0.65	0.68	0.58
LWT2	0.36	0.39	0.63	0.65	0.60
LWT3	0.35	0.38	0.62	0.67	0.58
LWT4	0.37	0.38	0.65	0.70	0.57
LWT5	0.28	0.32	0.69	0.77	0.49

Conclusion

Estimated heritabilities for youngstock LWT were moderate to high and ranged from 0.4 to 0.65. Genetic correlations between all youngstock LWT traits and mature LWT were all greater than 0.70. The reliability of estimated breeding values for LWT was substantially increased by the inclusion of youngstock LWTS, allowing farmers to make more accurate breeding and culling decisions. Youngstock LWT records should be incorporated into the New Zealand animal evaluation system.

References

Berry, D. P., F. Buckley, P. Dillon, R. D. *et al*. (2003) J. Dairy Sci. 86:2193–2204. doi:10.3168/jds.S0022-0302(03)73809-0.

Bryant, J. R., C. W. Holmes, N. Lopez-Villalobos, *et al*. (2004) Proc. NZSAP. Vol. 64. Hamilton. New Zealand.

DairyNZ. (2025) New Zealand Dairy Statistics 2024-25. Available at: https://www.dairynz.co.nz/resources/resource-list/new-zealand-dairy-statistics-2024-25-pdf/ ,visited on: 28 01-2026

DairyNZ, (2026) Genetic Base Cow. Available at: https://www.dairynz.co.nz/animal/breeding-decisions/genetic-base-cow/, visited on: 20-01-2026

Feng, X., Y. Wang, J. Zhao, *et al*. (2025) Agricult. 15. doi:10.3390/agriculture15111216.

Handcock, R. C., N. Lopez-Villalobos, L. R. McNaughton, *et al*. (2020) J. Dairy Sci. 103:4466–4474. doi:10.3168/jds.2019-17545.

Harris, B., L. (1998) Proc. 6th WCGALP. Vol. 1.

Henderson, C. R. (1975) Biometrics. 31:423–447. doi:10.2307/2529430.

Koenen, E. P. C., and A. F. Groen. (1998) J. Dairy Sci. 81:1709–1713. doi:10.3168/jds.S0022-0302(98)75738-8.

Molano, R. (2022) Your Mature Cows: Your Heifers' Best Unit of Measure. Available at: Your Mature Cows: Your Heifers' Best Unit of Measure - Lactanet

Spelman, R. J., and D. J. Garrick. (1997) J. Dairy Sci. 80:2557–2562. doi:10.3168/jds.S0022-0302(97)76211-8.

Veerkamp, R. F. (1998) J. Dairy Sci. 81:1109–1119. doi:10.3168/jds.S0022-0302(98)75673-5.

Westell, R. A., R. L. Quaas, and L. D. Van Vleck. (1988) Journal of Dairy Science. 71:1310–1318. doi:10.3168/jds.S0022-0302(88)79688-5.

Yin, T., and S. König. (2018) J. Dairy Sci. 101:2158–2170. doi:10.3168/jds.2017-13835.