Length of beef performance test period at Tully, Ireland

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INTRODUCTION

An outbreak of a contagious disease at the beef performance station at Tully, Ireland in early 2007, followed by the necessity to vaccinate resulted in two intakes of bulls at the performance station being unsuitable for sale to Irish AI organisations. Why it impacted on two bull intake runs was because intakes are staggered at Tully by around 2 months (animals enter Tully around end of September and again in the end of November). This coupled with the labour cost and inconvenience associated with beef performance testing requires scrutiny of the optimal length of testing period for beef performance measurement with particular emphasis on feed intake and live-weight.

Therefore the objective of this study was to quantify the effect of alternative lengths of testing period on feed intake and live-weight measures and to make recommendations for the future running of Tully as a beef performance station as well as the type of analyses performed. Because the objective of Tully is to quantify genetic differences among animals being tested, the impact of alternative test period lengths will be evaluated at both the phenotypic and genetic level.

MATERIALS AND METHODS

Data

Live-weight and feed intake measures were obtained from the Irish Cattle Breeding Federation database for all animals performance tested in Tully performance station, Ireland between the years 1986 and 2007. In total 80,410 test-day records from 3,182 animals of 14 different breeds were obtained. Only purebred animals of the 8 most predominant breeds at Tully over that time period were retained. The breeds were Angus, Belgian Blue, Blonde d'Aquitaine, Charolaois, Hereford, Limousin, Saler and Simmental. Feed intake was measured approximately every 2 weeks from 1986 to 1991, inclusive and every 2 to 3 weeks from 1992 to 2004, inclusive. Thereafter feed intake was measured weekly as the total feed offered from Monday to Saturday less the total feed refused the following Monday; no feed was offered on Sundays. Live-weight was measured every 2 to 3 weeks across the entire period under analyses.

The start of the testing period for each animal was assumed to be the day of its first recorded feed intake. Age of the animal at this date was assumed to be its "age at start of test". Animals less than 100 days of age or greater than 350 days of age were removed. Feed intake records less than 1 kg/day and greater than 25 kg/day were set to missing. Similarly live-weight records less than 200 kg or greater than 850 kgs were set to missing. Subsequently test-day records with no information on either feed intake or live-weight were removed; a total of 67,206 test-day records remained. Animals with no known sire (n=12) and/or dam (n=10) were also removed from further analyses. The final edit required that all animals be present on test for at least 95 days. Furthermore, records greater than 250 days from the start of test were deleted and feed intake records greater than 207 days from the start of test were set to missing. Following all edits 52,172 test day records from 2,797 animals remained. Fortnight of the year was determined, based on calendar date for each test with the 1st of January each year initiating

the first fortnight. Dam parity number greater than five were grouped together and animals with a dam of unknown parity were coded into a separate class.

Phenotypic analysis

Because of the frequency of data recording across years, information was not available every week for all animals. Therefore, feed intake and live-weight was averaged within three weekly periods from the start of test. Least squares means after adjusting for dam parity number and age of calf at start of test were estimated across all data and within breed for each three weekly period from the start of the test. Only animals that had a record for each of the three weekly periods from the start of test to the 6th 3-week period (i.e., up to day 126 of test) were retained; a total of 2,463 animals were included in this analysis. Correlations between 3-weekly periods were also estimated using the animals with data for each time period.

Genetic analysis

Because one of the main objectives of Tully beef performance station is to identify genetically different animals it is important that the phenotypic data used in the estimation of genetic merit of animals reflects the true additive genetic merit (i.e., the performance driven by genes that can be passed on to their progeny) of the animal and is not largely clouded by maternal or previous herd environmental factors. For this reason it is important to quantify the contribution of maternal (e.g., milk yield/mothering ability of the dam) and previous herd environmental influences to the differences among animals observed in Tully and to remove these nuisance effects when estimating the additive genetic merit of each bull.

For animals where the herd of origin was not known (n=27) a unique herd number was given to these animals. Three herds supplied more than 250 animals each, over the period under analysis so each year within each of these herds was coded as a separate herd. Weekly average feed intake and live-weight was calculated for all animals although estimates for every week were not available on all animals. A total of 26,514 weekly records from 2,519 animals were included in the genetic analysis. These data were analysed using random regression methodology in ASREML (Gilmour et al., 2007) with the variance components modeled over weeks since start of test. A pedigree file four generations deep was generated. The methodology used is described in more detail in Appendix 1.

Additionally, feed intake and live-weight averaged within 3-weekly periods from the start of test were analysed using multi-trait analyses where each three weekly period was treated as a separate trait in the multi-trait analyses. Fixed effects adjusted for in the model were age at the mid-point of the three-weekly period (quadratic regression), an interaction between fortnight of the year and year, breed of the calf and dam parity number. Random effects included were an additive genetic, maternal, herd of origin and residual component; no covariance was assumed among random effects.

Genetic parameters were also estimated whereby the average feed intake and live-weight was determined across the entire test period to replicate what is currently done in the genetic evaluations. Fixed effects included in this model were year by fortnight of entry into Tully and a quadratic regression on age at entry into Tully. A random animal effect was also

fitted. This model is similar to that currently used in the genetic evaluations. In a subsequent analysis dam parity number was included as a fixed effect and maternal genetic and herd of origin were included as random effects.

RESULTS

Phenotypic analyses

Average feed intake and live-weight across all breeds is illustrated in Figure 1 across the test period. Feed intake rises considerably in the first 10 weeks of the measurement period and thereafter starts to plateau. In contrast, live-weight increased almost linearly from entry into Tully; a linear regression explained 99.6% of the variation in the six data points of live-weight in Figure 1.

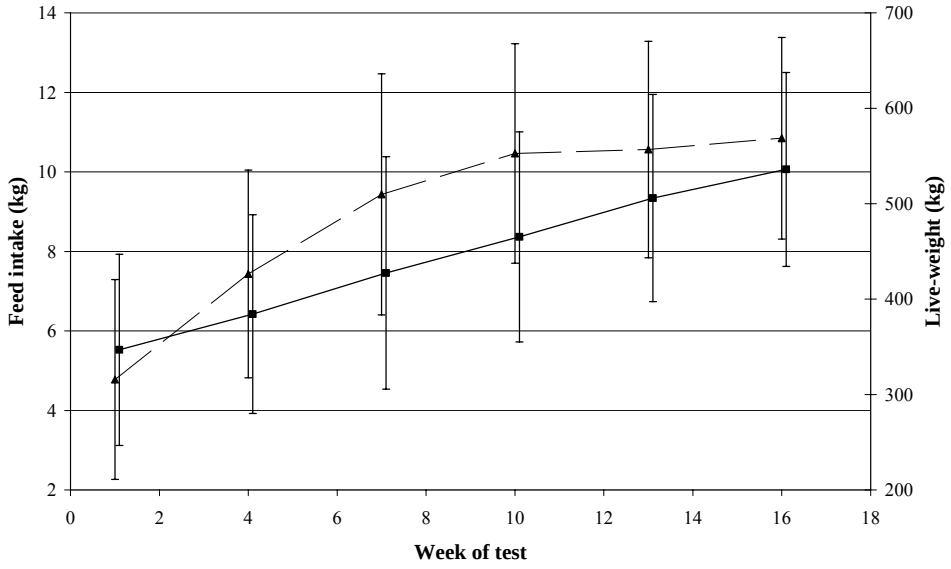

Figure 1. *Least squares means for feed intake (--▲--) and live-weight (—■—) averaged across 3-weekly periods for 2,463 animals across the test period. One standard deviation is represented above and below each value (i.e., 68% of the population will lie somewhere in between both error bars)*

Figure 2 and 3 illustrates the change in feed intake and live-weight, respectively across the test period for each breed separately. A total of 76 Angus, 77 Blonde d'Aquitaine, 44 Belgian Blue, 128 Hereford, 1,020 Limousin, 56 Salers and 763 Simmental animals were represented in the dataset. A similar trend across time was observed across all breeds with feed intake reaching a plateau at week 10 of test and live-weight increasing almost linearly across the test period.

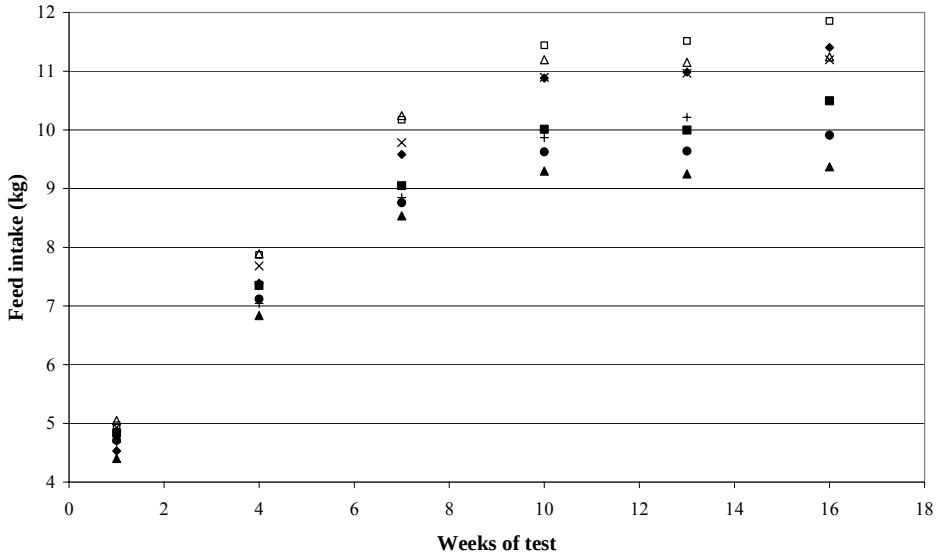

Figure 2. *Average feed intake for the Angus (Δ), Blonde d'Aquitaine, (■), Belgian Blue (▲), Charolais (x), Hereford (♦), Limousin (○), Saler (+), and Simmental (□).*

Correlations between feed intake at different stages of the testing period and between live-weight at difference stages of the testing period are summarised in Table 2. The correlations for live-weight were always stronger that the respective correlations for feed intake with the former correlations being greater than 0.92 and weakened as the interval between periods increased. Correlations between feed intake measured at different periods of the test varied from 0.06 to 0.80 suggesting that feed intake measured in the early test period (week 1 to 3 on test) was not a good indicator of intake in week 16 to 18 of test.

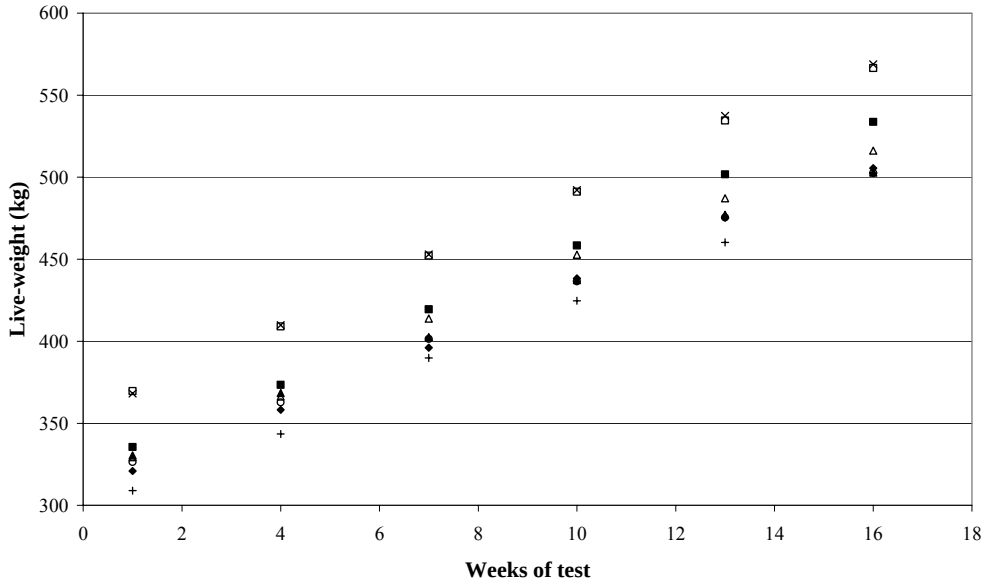

Figure 3. *Average live-weight for the Angus (Δ), Blonde d'Aquitaine, (■), Belgian Blue (▲), Charolais (x), Hereford (♦), Limousin (○), Saler (+), and Simmental (□).*

Table 1. *Correlations between feed intake (below diagonal) and live-weight (above diagonal) for different periods of the test.*

Week of test	1-3	4-6	7-9	10-12	13-15	16-18
1-3		0.98	0.97	0.95	0.94	0.93
4-6	0.80		0.98	0.96	0.96	0.95
7-9	0.50	0.70		0.98	0.97	0.97
10-12	0.39	0.48	0.75		0.97	0.98
13-15	0.28	0.45	0.67	0.76		0.99
16-18	0.06	0.18	0.48	0.62	0.75	

Genetic analyses

Heritability estimates of feed intake using the current model was 0.50 (SE=0.64). However, when maternal genetic and herd components were adjusted for as random effects the heritability was 0.31 (SE=0.064). The proportion of phenotypic variation explained by the maternal genetic and herd components were 0.12 (SE=0.036) and 0.08 (SE=0.019), respectively. Heritability estimates of live-weight using the current model was 0.64 (SE=0.062). However, when maternal genetic and herd components were adjusted for as random effects in the model the heritability was 0.24 (SE=0.059). The proportion of phenotypic variation explained by the maternal genetic and herd components were 0.20 (SE=0.037) and 0.18 (SE=0.025), respectively. Correlations between estimated breeding values estimated using the current procedure and the model with both maternal genetic and previous herd effects accounted for were 0.97 for feed intake and 0.91 for live-weight. This suggests some re-ranking of animals particularly for live-weight when adjusting for environmental factors prior to introduction to Tully.

Table 2 summaries the proportion of the observed phenotypic variation in feed intake explained by the additive direct genetic, maternal genetic and herd components. The proportion of variation explained by the animal component is equal to the narrow sense heritability. Therefore heritability of feed intake tended to increase with the period of the test from 0.07 to 0.30. There was no obvious trend in maternal variance as a proportion of the total variance but it was non-significant in the last period of the test. The herd variance as a proportion of the total variance was greatest in the first period of the test but halved thereafter. In the last period of the test, the dam and herd each contributed 4% to the total variation among animals.

Table 2. *Proportion of the phenotypic variation in feed intake explained by the animal direct, maternal genetic and herd components across different period of the test. Standard errors of the proportions are in parenthesis.*

Week of test	Animal	Maternal	Herd
1 to 3	0.07 (0.043)	0.00 (0.000)	0.10 (0.023)
4 to 6	0.12 (0.056)	0.20 (0.042)	0.04 (0.017)
7 to 9	0.19 (0.058)	0.09 (0.036)	0.06 (0.018)
10 to 12	0.18 (0.058)	0.11 (0.039)	0.05 (0.016)
13 to 15	0.24 (0.063)	0.16 (0.041)	0.04 (0.015)
16 to 18	0.30 (0.065)	0.04 (0.037)	0.04 (0.015)

Table 3 summaries the proportion of the observed phenotypic variation in live-weight explained by the additive direct genetic, maternal genetic and herd components. Heritability estimates (i.e., proportion of phenotypic variation explained by the animal component) did not vary much during test and ranged from 0.25 to 0.33. Furthermore, maternal variance and herd variance components as a proportion of the total phenotypic variation was relatively constant throughout the test period varying from 0.18 to 0.22 and from 0.14 to 0.17, respectively. However, even 16 to 18 weeks on test, the maternal and previous herd components comprised of 35% of the phenotypic variation in live-weight.

Table 3. *Proportion of the phenotypic variation in live-weight explained by the animal direct, maternal genetic and herd components across different period of the test. Standard errors of the proportions are in parenthesis.*

Week of test	Animal	Maternal	Herd
1 to 3	0.30 (0.069)	0.18 (0.041)	0.17 (0.027)
4 to 6	0.30 (0.069)	0.23 (0.041)	0.16 (0.026)
7 to 9	0.33 (0.071)	0.22 (0.042)	0.14 (0.025)
10 to 12	0.25 (0.063)	0.22 (0.040)	0.16 (0.026)
13 to 15	0.31 (0.067)	0.18 (0.040)	0.15 (0.025)
16 to 18	0.26 (0.064)	0.19 (0.040)	0.16 (0.026)

Figures 4 and 5 illustrate the proportion of phenotypic variation in feed intake and live-weight, respectively attributed to the direct genetic, maternal genetic and herd effects for each week of test estimated using random regression models. The variation between animals (i.e., phenotypic variance) increased with week of test for both traits. There are somewhat contrasting trends in variance components between the two traits. For feed intake there was no significant change in maternal genetic variance over the test period and remained low. The effect of herd prior to test, however, decreased in the first few weeks of test but increased thereafter although it rarely represented more than 10% of the total phenotypic variation. For live-weight the amount of variation observed among animals at Tully attributable to their dam's genetic effects (other than her direct genetic contribution) decreased week on week after week 7 of test while the contribution of herd although tended to decrease with time was not considerably different between the start and end of the test period.

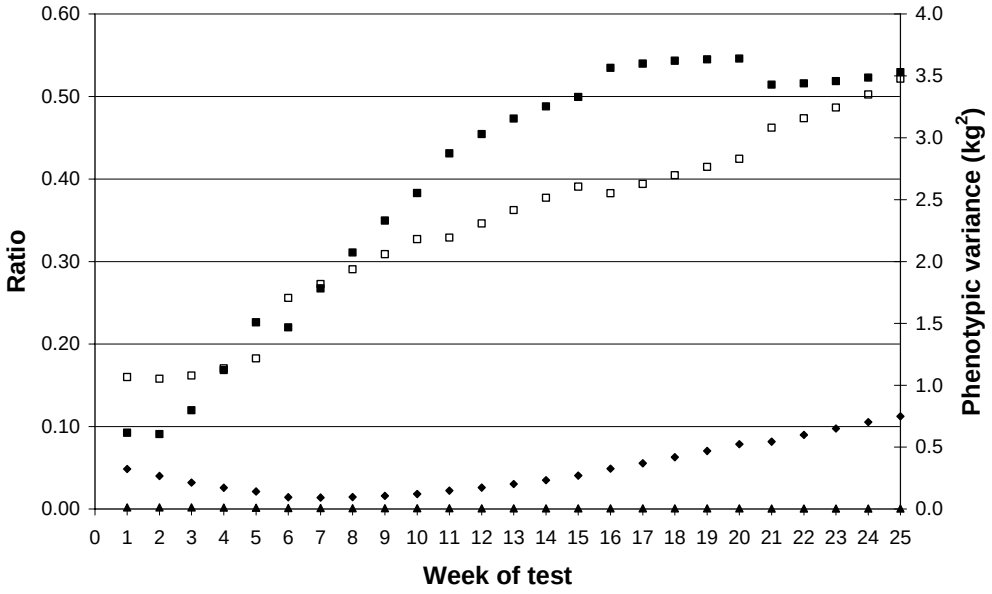

Figure 4. *Proportion of the phenotypic variation in feed intake explained by the direct genetic (■), maternal genetic (▲) and herd (♦) components across different period of the test. Actual phenotypic variance is also shown (□).*

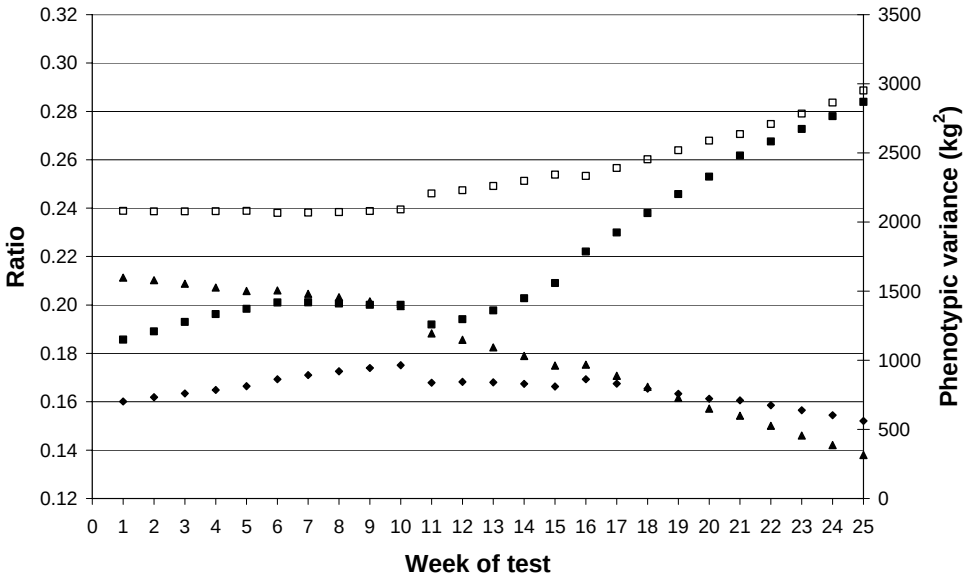

Figure 5. *Proportion of the phenotypic variation in live-weight explained by the direct genetic (■), maternal genetic (▲) and herd (♦) components across different period of the test. Actual phenotypic variance is also shown (□).*

Figure 6 shows the genetic correlation estimated using random regressions between different weeks of test with feed intake and live-weight measured at week 14 (i.e., around 100 days into test). Correlations estimated using the multi-trait analyses between different 3-weekly

stages of the test period are summarised in Table 4. Comparison of two types of analyses revealed similar conclusions that feed intake in the first few weeks (approximately first 4 weeks) of the test is under different genetic control to feed intake during the later stages of the test period. In contrast, live-weight at different periods of the test period was genetically a very similar trait.

Table 4. *Genetic correlations between different stages of the test period for feed intake (below the diagonal) and live-weight (above the diagonal)*

Weeks	1 to 3	4 to 6	7 to 9	10 to 12	13 to 15	16 to 18
1 to 3		0.99 (0.004)	0.98 (0.007)	0.96 (0.015)	0.94 (0.018)	0.90 (0.025)
4 to 6	0.67 (0.14)		0.99 (0.005)	0.98 (0.010)	0.96 (0.013)	0.93 (0.018)
7 to 9	0.40 (0.27)	0.84 (0.09)		0.99 (0.001)	0.98 (0.007)	0.96 (0.012)
10 to 12	0.15 (0.29)	0.84 (0.13)	0.95 (0.05)		0.99 (0.001)	0.99 (0.006)
13 to 15	0.14 (0.28)	0.81 (0.13)	0.99 (0.06)	0.99 (0.01)		0.99 (0.003)
16 to 18	0.44 (0.26)	0.74 (0.16)	0.84 (0.10)	0.97 (0.06)	0.99 (0.001)	

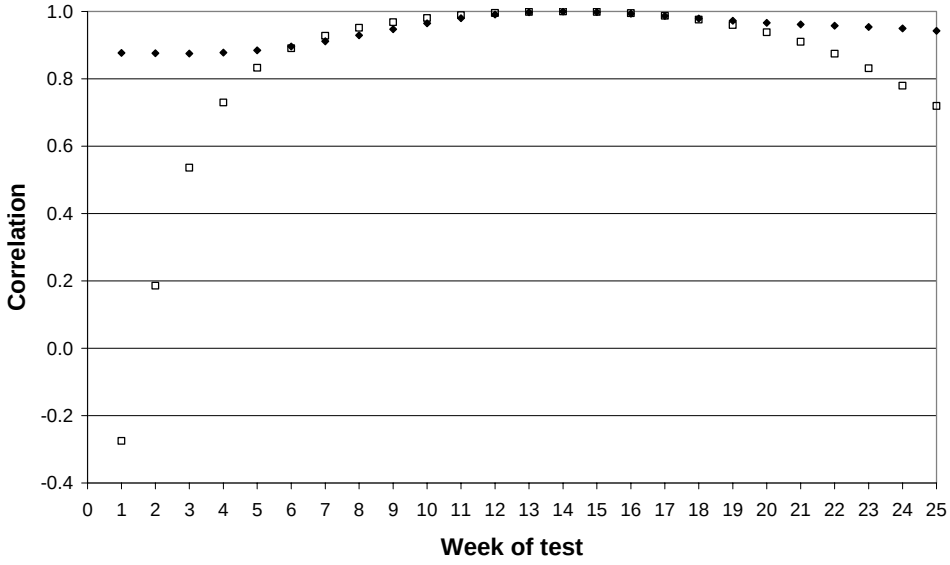

Figure 6. *Genetic correlation between different weeks of test with week 14 of test (i.e., approximately 100 days into test) for feed intake (□) and live-weight (♦).*

DISCUSSION

The motivation for this study was to determine the optimum test period length to be used at the beef performance station in Tully. Although profiles of feed intake and live-weight during the test period as well as phenotypic correlations between weeks of test provide an understanding of the change in these traits over time, the fundamental objective of beef performance testing is to identify genetic differences among animals. Hence, it is really the genetic parameters that are of interest when comparing different weeks of the test period. Although live-weight is genetically a similar trait irrespective of the time of its measurement during the test period, feed intake in the early test period appears to be governed by different genes compared to feed intake during the middle and towards then end of the test period.

Furthermore, a considerable amount of the variation in feed intake and live-weight observed among animals (irrespective of breed) at Tully can be attributed to their dam (over and above the genes the dam passed on to the calf) and the herd environment prior to coming to Tully. Hence, these components should be considered in future genetic evaluations of performance data, particularly live-weight and will lead to re-ranking of animals.

Feed intake profiles across the test period indicate that a plateau is not reached, on average, until around week 6 to 8. However, some of this may actually be due to the animal itself growing and feed intake increasing accordingly. In contrast, live-weight gain, on average, was constant across the test period. These phenotypic differences between the two trait is also reflected in the stronger correlations between live-weight at different stages of the test period compared to feed intake. Although the phenotypic correlations between feed intake in the early test period and later test period were low, they should be interpreted in combination with the correlations between adjacent stages. For example, the correlation between feed intake in weeks 1 to 3 and 13 to 15 was low (0.28) but the correlation between adjacent time periods week 10 to 12 and 13 to 15 was lower than unity (0.76). This indicates that the repeatability of feed intake across weeks is low (i.e., there is inherent variation in feed intake over time).

Genetic analyses revealed that maternal genetic and previous herd factors together account for as much phenotypic variation in feed intake and live-weight as the additive genetic effect. This is particularly true for live-weight and is most likely due to compensatory growth (or the opposite). A total of 56% of the herds included in the present study only had one animal in the dataset and therefore it is also important to note that the herd effect may include also some dam effects such as the permanent environmental effect of the dam with more than one progeny at Tully, as well as cytoplasmic and epigenetic effects; 384 dams had more than one progeny at Tully. Nonetheless, this analysis highlights the necessity to consider maternal and herd effects in the genetic evaluation of performance test data at Tully; this conclusion may also be applicable for other traits and should be investigated.

Heritability estimates and phenotypic variance estimates were lowest at the start of the test period for both feed intake and live-weight. This suggests a greater ability to more accurately quantify true differences between animals at later stages of the test period. When coupled with the low correlations, especially for feed intake, between measurements taken in the first 4 weeks of the test and later on in the test, a recommendation would be to remove the data from the first four weeks of the test period when genetically evaluating the animals. Heritability estimates from the random regression model were similar to those estimated from the multi-trait analysis as well as those estimated using the current approach with the inclusion of maternal genetic and herd random effects in the model. In the current approach all data across the test period is averaged and genetic parameters are estimated using a linear model.

Furthermore, the strong genetic correlations between the week 5 to 25 of the test suggest little additional benefit in collecting data beyond this time period (day 175). Additionally, if intake is going to be measured weekly, as it is envisaged in the future, there appears to be minimal benefit in measuring feed intake after 105 days of test with the first 28 days removed. Using this approach there is still 10 weeks data points for feed intake and one could argue that this could even be reduced further to 4 weeks acclimatization and 8 weeks

measurement. If live-weight was measured every 2½ weeks, starting on week 4 of test, then 4 live-weight measures are also possible.

RECOMMENDATIONS

- Date of entry into Tully should be provided in the data extract as should the run and preferably pen the animal was in
- Maternal and herd variance components should be accounted for in the genetic evaluation of feed intake but in particular live-weight at Tully
- Data from the first four weeks of the test period should be removed for genetic evaluations since it is genetically a different trait to measurements taken during later periods of the test
- It is possible to reduce the testing period to 15 weeks of which the first 4 weeks would be an "acclimatization period" when measurements are not necessary
- Feed intake should continue to be measured weekly and live-weight every 2½ to 3 weeks starting on week 4 of test and ending immediately prior to sale. this will ensure 8 to 10 feed intake measures and 4 to 5 live-weight measures.

APPENDIX 1.

Random regression models facilitate the quantification of variance components along a trajectory where data on each point on the trajectory may not be available on all animals. In the present study five random components were fitted: additive genetic, permanent environmental, maternal, herd and residual. The test period was divided into 5 blocks, weeks 1 to 5, 6 to 10, 11 to 15, 16 to 20, >20 and residual variances were estimated within each block. Therefore residual variances were assumed homogenous within block but heterogenous between block; no residual covariance between period was assumed. The following random regression model was fitted

$$Y = Fortnight * year + Parity + breed * \sum_{i=1}^{2} age_i + breed * \sum_{j=1}^{2} week_j + \sum_{k=1}^{n} a_k * week + \sum_{k=1}^{n} p_k * week +$$

$$\sum_{l=1}^{n} dam_l * week + \sum_{m=1}^{n} herd_m * week + e$$

Where Y = average weekly feed intake or live-weight; *fortnight*year* = two-way fixed effect interaction between the fortnight of the calendar year at test by year of test; *parity* = fixed effect parity of dam; $breed * \sum_{i=1}^{2} age_i$ = fixed quadratic regression on age at start of test interacted with breed; $breed * \sum_{j=1}^{2} week_j$ = fixed quadratic regression on the week of test interacted with breed; $\sum_{k=1}^{n} a_k * week$ = random additive genetic component across week of test modeled using Legrende polynomials; $\sum_{k=1}^{n} perm_k * week$ = permanent environmental component modeled using Legrende polynomials; $\sum_{l=1}^{n} dam_l * week$ = maternal component across week of test modeled using Legrende polynomials; $\sum_{m=1}^{n} herd_m * week$ = herd component across week of test modeled using Legrende polynomials; e = residual