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HERD LEVEL PROFILES FOR CARCASS TRAITS

Herd-specific random regression carcass profiles for beef cattle after adjustment for animal genetic merit**Tanya M. Englishby^{a, b, *}, Kirsty L. Moore^a, Donagh P. Berry^b, Mike P. Coffey^a, Georgios Banos^{a, c}**^a*Scotland's Rural College (SRUC), Easter Bush, Midlothian, Scotland, EH25 9RG, UK.*^b*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Co. Cork, Ireland.*^c*The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Easter Bush, Midlothian EH25 9RG, UK.*

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Abstract:

Abattoir data are an important source of information for the genetic evaluation of carcass traits, but also for on-farm management purposes. The present study aimed to quantify the contribution of herd environment to beef carcass characteristics (weight, conformation score and fat score) with particular emphasis on generating finishing herd-specific profiles for these traits across different ages at slaughter. Abattoir records from 46,115 heifers and 78,790 steers aged between 360 and 900 days, and from 22,971 young bulls aged between 360 and 720 days, were analysed. Finishing herd-year and animal genetic (co)variance components for each trait were estimated using random regression models. Across slaughter age and gender, the ratio of finishing herd-year to total phenotypic variance ranged from 0.31 to 0.72 for carcass weight, 0.21 to 0.57 for carcass conformation and 0.11 to 0.44 for carcass fat

score. These parameters indicate that the finishing herd environment is an important contributor to carcass trait variability and amenable to improvement with management practices.

Keywords: cattle, carcass traits, herd management, random regression

1. Introduction

Routinely collected abattoir data is an important source of information for genetic evaluations of beef carcass traits in many countries including Ireland (Pabiou et al., 2009), France (Laloë, Fouilloux, & Guerrier, 2007) Sweden (Eriksson, Nasholm, Johansson, & Philipsson, 2003) and the UK (Moore et al., 2014). Best Linear Unbiased Prediction is traditionally used to estimate genetic evaluations adjusted for systematic management effects. Geneticists are mainly interested in the genetic evaluations themselves with the environmental effects usually being fitted to simply account for systematic variation. These systematic environmental effects could, however, be useful for management purposes in decision support tools (Caccamo et al., 2008).

Random regression is a useful technique for the study of trait profiles across a time trajectory (Olori, Hill, McGuirk, & Brotherstone, 1999) and is widely used in dairy cattle to model milk lactation profiles (Cobuci et al., 2005; Jamrozik, Jansen, Schaeffer, & Liu, 1998). Measurements need not necessarily originate from the same animal but an underlying covariance structure, such as pedigree linkages, could connect individual animals measured over time. It is therefore possible to longitudinally model a trait for different sires exploiting information on the genetic relatedness among progeny slaughtered at different ages, thereby providing several effective measurements per sire across a time trajectory (Englishby et al., 2016; Jones, White & Brotherstone, 1999). In addition to producing genetic trait profiles for

beef carcass traits (Englishby et al., 2016), random regression models may also be used to model herd-specific trait profiles after accounting for differences in animal genetic merit (de Roos, Harbers, & de Jong, 2004). These herd-specific trait profiles provide information on how animals within a herd perform compared to their respective performance under average management conditions (Caccamo et al., 2008). The inclusion of herd-specific regression curves was first proposed by Gengler, Tijani, & Wiggans (2000) and has since been applied to test-day models for management purposes in dairy cattle (Bastin et al., 2009; Caccamo et al., 2010; Mayeres, Stoll, Bormann, Reents, & Gengler, 2004).

The objective of the present study was to quantify the contribution of finishing herd-year environment to the variability in carcass characteristics in beef cattle with particular emphasis on generating herd-specific profiles for carcass traits across age at slaughter. Genetic components were also considered in the statistical model to account for their effect on the studied carcass traits. Results will be useful in the development of management tools that provide information to producers on their herd performance over years.

2. Materials and methods

All data used in the present study were obtained from the UK national beef carcass database.

2.1. Data

Carcass weight (kg), carcass conformation score (scale 1 to 15) and carcass fat score (scale 1 to 15) records from 2,964,387 beef cattle slaughtered between the years 2002 and 2014 were available. Carcass weight is measured on average two hours after slaughter following the removal of the head, legs, thoracic and abdominal organs, and internal fats and hide. Carcass classification (conformation and fat scores) is estimated using the European EUROP grid method, via visual inspection of the carcass by trained graders (Craigie et al.,

2012). For the purposes of the present study, the resulting EUROP classification grades were transformed into a 15-point numeric scale in line with national genetic evaluations for conformation and fat scores as described in Englishby et al (2016).

Animals without a recorded sire or dam were discarded. Records were restricted to animals that moved herd no more than three times during their lifetime in order to reduce noise accruing from the effects of multiple herd environments. Cows (i.e., females that had at least one recorded calving date) and bulls >720 days of age at slaughter were not further considered. The remaining 1,050,832 records were restricted to prime slaughter heifers and steers (castrated) slaughtered between 360 and 900 days of age, and young bulls <720 days of age at slaughter. Further edits removed animal records more than four standard deviations from the within gender (heifer, steer, or young bull) population mean carcass weight and age at slaughter. Furthermore, dam parity was restricted to 1 to 10 and parity was subsequently categorised as 1, 2, 3, 4, and ≥ 5 . Only progeny from sires with at least 5 paternal half-sibs were retained in order to achieve sufficient genetic linkage among herds. Following these edits, 258,875 carcass records remained.

Two contemporary groups were generated: 1) abattoir by date of slaughter and 2) finishing herd-year of slaughter. Contemporary groups with less than five records were omitted. Following these final edits, 147,876 animals from 7,742 contemporary groups of finishing herd-year of slaughter remained. Of these data, 46,115 were heifers, 78,790 were steers and 22,971 were young bulls. Animals included in the analysis were progeny of 8,817 sires.

2.2. Data analysis

Carcass weight, conformation score and fat score were analysed within gender using the following random regression model:

$$Y_{dhjklqnz} = \mu + Parity_d + Abattoir_DoS_h$$

$$\begin{aligned}
& +Dambreed_j + Sirebreed_k + a_1.Het + a_2.Rec + \\
& \sum_{i=1}^n b_n P_n Age + \sum_{i=1}^n HY_{ln} P_n Age + \\
& \sum_{i=1}^n Sire_{qn} P_n Age + e_{dhjklqnz}
\end{aligned}$$

(1)

Where $Y_{dhjklqnz}$ = the observed record for carcass weight, carcass conformation score or carcass fatness score on animal z ; μ = the population mean; $Parity_d$ = fixed effect of the d^{th} parity of the dam of animal z (5 levels); $Abattoir_DoS_h$ = fixed effect of abattoir by date of slaughter interaction h (9,154 levels); $Dambreed_j$ = fixed effect of breed j of dam of animal z (56 levels); $Sirebreed_k$ = fixed effect of breed k of sire of animal z (52 levels); a_1 = linear regression coefficient on heterosis (Het) in animal z ; a_2 = linear regression coefficient on recombination loss (Rec) in animal z ; b_n = fixed regression coefficient on age at slaughter (Age) modelled with n^{th} order Legendre polynomial (Pn); HY_{ln} = random regression coefficient on age at slaughter associated with the effect of finishing herd-year l , representing management practices; $Sire_{qn}$ = random regression coefficient on age at slaughter associated with the genetic effect of sire q of animal z , including all available pedigree data (42,773 additional non-founder animals); $e_{dhjklqnz}$ = residual error term for age class.

Coefficients of heterosis and recombination loss were calculated for each animal as follows (Van der Werf and de Boer 1989):

$$Heterosis (Het) = P_S (1 - P_D) + P_D (1 - P_S)$$

$$Recombination (Rec) = P_D (1 - P_D) + P_S (1 - P_S)$$

Where P_S and P_D = the proportions of the primary genetic group in the sire and the dam, respectively. The genetic groups were formed by the compression of 56 breed types into 4 genetic groups based on pedigree information and the assumption of some common ancestry among the breeds of each genetic group (continental beef breeds, dual purpose breeds, native UK breeds, and all other breeds). As there were 4 genetic groups defined this resulted in 6 heterosis and 6 recombination loss terms which were summed to produce an overall heterosis value and an overall recombination loss value for each animal.

Residual errors across age at slaughter were expected to have heterogeneous variances, possibly due to different management practices; therefore, different residual error classes associated with different ages at slaughter were modelled. The data of heifers and steers was divided into 12 classes and the young bull data into 8 classes as described in Table 1. Within class, residual variances were assumed to be homogenous and co-variances between classes were assumed to be zero.

In model (1), the fixed regression coefficient on age at slaughter was associated with an overall curve for each trait and gender, whereas the random regressions modelled both individual finishing herd-year contemporary group deviations and individual animal deviations from the overall curve.

Univariate and bivariate analyses based on model (1) were used to estimate variance and covariance components for each of the carcass traits. For the bivariate analyses, the same fixed and random effects were fitted for all traits. Different orders of Legendre polynomials were tested. Model building and the goodness of fit was determined as described by Englishby et al (2016).

All analyses were conducted using the AsReml software (Gilmour, Gogel, Cullis, & Thompson, 2009)

2.3. (Co)variance components

Finishing herd-year and genetic (co)variance function coefficients for each trait were fitted using the model suggested by Kirkpatrick & Heckman (1989):

$$\mathbf{G} = \Phi' \mathbf{K} \Phi$$

Where \mathbf{G} is the (co)variance matrix for slaughter ages, Φ is the matrix of Legendre polynomial age regression coefficients, and \mathbf{K} is the estimated (co)variance matrix of the random polynomial coefficients (finishing herd-year or sire; in the latter case, variance was multiplied by four to convert to a genetic variance estimate (Huisman, Veerkamp, & Arendonk, 2002). Model solutions for the random effects were used to derive two sets of curve coefficients, one per finishing herd-year and one per sire, facilitating estimates and inference to be made about environmental and genetic effects, respectively, across the trajectory.

The estimates of (co)variance components were used to calculate variance ratios for each trait at different ages at slaughter as well as correlations between finishing herd-year effects and between carcass traits at different ages at slaughter. Approximate standard errors of the variance ratios were derived using a Taylor series expansion (Fischer, Gilmour, & van der Werf, 2004); approximate standard errors of correlations were calculated using the methodology described in Falconer & MacKay (1996). Eigenvalues and eigenfunctions of the finishing herd-year and genetic (co)variance matrices of polynomial coefficients were calculated to determine their overall contribution to the trait curves.

3. Results

Phenotypic statistics for carcass weight, conformation and fat scores in each gender are in Table 2. Heifers were slaughtered at an average age of 676 days and were the fattest of the three genders. Young bulls had the heaviest mean carcass weight, highest conformation score and lowest fat score of the three genders.

There were 1,582 finishing herds containing heifers, 1,278 finishing herds containing steers, and 525 finishing herds containing young bulls, and each with an average of 43, 59 and 44 animals, respectively. An average of approximately 4 sires was used per herd.

The fixed regression trajectories were best modelled as cubic regressions in all instances. Third order Legendre polynomials had the best parsimony to account for random finishing herd-year and sire variances across all traits and genders except for sire variances in young bulls which was best modelled with a second order Legendre polynomial.

3.1. Finishing herd-year parameters

The pattern of the ratio of finishing herd-year variance to total phenotypic variance across different ages at slaughter is presented in Figure 1. Average estimates across all ages at slaughter are shown in Table 2, along with corresponding trait average heritability estimates for comparison. All estimates of finishing herd-year variance to total phenotypic variance ratios and estimates of heritability (genetic to phenotypic variance ratios) were greater ($P < 0.05$) than zero. Estimates of finishing herd-year variance to total phenotypic variance and estimates of heritability for ages at slaughter between 360 to 405 days in heifers and steers, and those for ages between 631 to 720 days in young bulls, were not reported due to the low numbers of records and large associated standard errors in these age groupings. Across gender, finishing herd-year variance for carcass weight accounted for between 30.83% and 71.48% of the total phenotypic variation (Figure 1). Finishing herd-year variance estimates for conformation score (Figure 1) accounted for less phenotypic variation across age at slaughter in young bulls (21.68%-26.29%) than in heifers (25.06%-32.51%) or steers (30.83%-56.22%). The lowest finishing herd-year variance ratios were observed for fat score (Figure 1) across gender explaining between 10.88% (fat at 628 days of age at slaughter in young bulls) and 44.04% (fat at 405 days of age at slaughter in heifers) of the total phenotypic variance. As young bulls aged, the influence of herd management on carcass

weight and conformation score remained constant, whereas the influence of management on fat score decreased. In steers and heifers, management effects across age at slaughter decreased as animals aged for all carcass traits except for the influence of management on conformation score in heifers which remained constant across age at slaughter.

Eigenvalues and eigenfunctions derived from the finishing herd-year (co)variance matrices are shown in Table 3 and Figure 2 (steers only), respectively. Each eigenvalue was expressed as a percentage of the sum of all eigenvalues to determine its relative importance. The largest proportion of the variance in finishing herd-year was explained by the first eigenvalue, which ranged from 48.63% for fat score in heifers to 93.30% for fat score in young bulls. The largest eigenvalue corresponded to the intercept term in all models, which represents the height of the finishing herd-year profiles for each carcass trait. The second and third eigenvalues combined, which represent the shape of the finishing herd-year profiles accounted for between 6.70% (fat score in young bulls) and 51.37% (fat score in heifers) of the variation in carcass traits across ages at slaughter.

In steers, the direction of the largest eigenfunction associated with the leading eigenvalues was constant across ages at slaughter, whereas the sign changes across age at slaughter were associated with the eigenfunctions of the second and third eigenvalues for all traits (Figure 2). Similar trends in the direction of eigenfunctions existed for all carcass traits in young bulls and heifers (results not shown) with the exception of fat score in heifers where the direction of the largest eigenfunction changed from negative to positive as age at slaughter increased.

3.2. Finishing herd-year correlations within trait

Correlations between the herd-year effects in the youngest and all subsequent ages at slaughter varied from -0.28 (± 0.03) to 1.00 (± 0.00) in heifers, from 0.01 (± 0.03) to 1.00 (± 0.00) in steers, and from 0.13 (± 0.05) to 1.00 (± 0.00) in young bulls (Figure 3). Within trait

correlations weakened with increasing interval between ages at slaughter. Irrespective of gender, finishing herd-year correlations between youngest and oldest ages at slaughter were strongest for conformation score. Negative correlations between herd-years effects were observed in heifers between fat score at 405 days and all ages at slaughter beyond 632 days, and between carcass weights at 405 days and all slaughter ages beyond 777 days (Figure 3).

3.3. Correlations between herd-year effects on different carcass traits

The strongest correlations between traits at the same age at slaughter were between carcass weight and conformation score in all genders, ranging from 0.67 (± 0.04) at 594 days in young bulls to 0.77 (± 0.01) at 769 days in steers (Figure 4). Regardless of gender, positive correlations also existed between carcass weight and fat score across age at slaughter. The weakest correlations across age at slaughter occurred between conformation and fat score in all genders. A practically zero correlation of 0.04 (± 0.12) existed between these two traits at 561 days of age at slaughter in young bulls.

3.3. Finishing herd-year curves for carcass traits

The herd-year solution curves for young bulls slaughtered in three example finishing herds in the year 2011 relative to the mean (fixed) curve are shown in Figure 5. The management practices in herds A and B resulted in carcass weights that were similar to those of young bulls reared under average management conditions at younger age of slaughter (until 451 and 448 days, respectively) (Figure 5). Older bulls in herd A performed better than in the average herd whereas bulls in herd B had a below average performance when slaughtered at older ages. In contrast, herd C, had excellent management conditions for early slaughter ages but relatively poor performance at older ages at slaughter. For conformation, the management practices of herd C produced better shaped carcasses across all slaughter ages compared to the population average whereas the opposite was true for herd A (Figure 5). Herds A and C produced carcasses that were leaner compared to average management

conditions across all slaughter ages, whereas herd B performed close to the average (Figure 5).

3.4. Within finishing herd deviations across year of slaughter

Clear variability in the influence of the herd management practices on carcass traits existed across year of slaughter. Figure 6 illustrates variability in herd management effects on carcass traits at two distinct slaughter ages (540 and 840 days), across year in two example herds of steers compared to the respective population average. The overall fixed curve demonstrates average management practices per age at slaughter across years whereas individual herd curves reflect management deviations from this average. The influence of management practices on carcass traits in these herds fluctuated greatly across year, in comparison to the average herd performance. The pattern of the management impact on carcass weight at the early slaughter age was not necessarily reflective of changes at older ages at slaughter (Figure 6). In general, similar trends were observed between carcass conformation and fat score (Figure 6) across the year of slaughter trajectory. The corresponding patterns in the two other genders (heifers and young bulls) were similar (results not shown).

4. Discussion

4.1. Finishing herd-year parameters

The contribution of genetic variability to phenotypic variation in carcass traits of cattle has been well documented elsewhere (Englishby et al., 2016; Hickey, Keane, Kenny, Cromie, & Veerkamp, 2007; Pabiou et al., 2009 and 2011; Reverter et al., 2000). However, little attention has been given to the examination of the environmental effect estimates simultaneously generated in the genetic evaluation process. Modelling a random finishing herd-year effect across age at slaughter provides information on how environmental, mainly management, conditions may affect beef carcass trait profiles (Bormann, Wiggans, Druet, &

Gengler, 2003). Therefore, finishing herd-year profiles, which are analogous to estimates of genetic merit for individual animals commonly used by animal breeders, can potentially be used as a management tool to monitor herd performance across years (Windig, Calus, & Veerkamp, 2005). Such information can also facilitate more informed management decisions through better modelling of environmental effects (Druet, Jaffrezic, & Ducrocq, 2005; Mrode, Swanson, & Paget, 2003).

In conventional carcass trait genetic evaluations, the genetic effect estimates of the animals are adjusted to average management conditions. An advantage of the present study was that the model included random effects for both animal genetic merit and finishing herd-year, thereby making it possible to assess management practices independently of the genetic merit of the animals (Caccamo et al., 2010). The performance and, consequently, profitability of the herd is related to both its genetic make-up and the environment in which the animals are finished (Wilton & Goddard, 1996); therefore, breeding decisions may be suboptimal if not combined with optimum management practices and vice versa. For instance, some sires with high genetic merit for carcass traits may produce progeny that do not reach premium grades at the abattoir due to sub-optimum management of the finishing herd, or produce premium grades but at a higher cost to the farmer than necessary.

The finishing herd environment evidently has an important influence on carcass characteristics, as, in the present study, a large proportion of total phenotypic variance in the three studied carcass traits was attributable to finishing herd-year variance. Estimates ranged from 30.83% and 71.48% for carcass weight, from 21.68% to 56.22% for conformation score and from 10.88% to 44.04% for fat score (Figure 1) and in some cases were higher than the corresponding trait heritability estimates (Table 2). Even so, the average heritability estimates for carcass weight, conformation and fat score across all ages at slaughter and gender were moderate to strong (Table 2), and given the large genetic variance also estimated, genetic

selection on carcass traits at any age at slaughter would be feasible and further improve animal performance.

Regardless of gender, the finishing herd environment contributed more to the phenotypic variance of carcass weight than either carcass conformation score or fat score, indicating that improving carcass weight across ages at slaughter could potentially be easier to achieve than improvements in the other two traits. Nonetheless, the finishing herd-year correlations between carcass weight and conformation score were favourable (Figure 4) meaning that altering management conditions to increase the value of one will also lead to superior values of the other trait. On the other hand, the positive finishing herd-year correlations between carcass weight and fat score, and between conformation and fat scores were not favourable, suggesting that management practices leading to large and well-shaped carcasses will also lead to greater fat content. Nevertheless, as these correlations were less than unity, management practices may be manipulated in order to produce animals with well conformed but lean carcasses. The most efficient use of these correlations would be their incorporation into finishing herd management indexes, similar to genetic indexes (Hazel, 1943), with appropriate weighting given to each trait depending on their respective economic values.

An example of how specific finishing herd environments may influence the performance of carcass traits is illustrated in Figure 5 through the graphical interpretation of finishing herd-year of slaughter solutions across age at slaughter. In general, deviations above the fixed curve for carcass weight or conformation score confirm that the management of a particular finishing herd may result in better performing animals than those on farms under average management conditions. In contrast, deviations below the fixed curve indicates that improvements in management be warranted (Figure 5). Furthermore, individual finishing herd deviations above the fixed curve for fat score may not be favourable as they are

associated with fatter carcasses. Although some finishing herd management practices have the propensity to produce desirable carcass traits at younger ages, the same finishing herd may perform below average at older ages or vice versa. Therefore, knowledge of individual finishing herd performance for carcass traits is important so that procedures to rectify persistent unfavourable deviations can be implemented and herds can adopt practices to improve performance.

4.2. Variation in finishing herd-year effects across age at slaughter

The within-gender variability observed among finishing herd-years for different ages at slaughter suggests that different management practices may be more applicable for differently aged cattle within finishing herds (Figure 1). For example, for carcass weight in heifers and steers, the finishing herd environment had a greater influence at early ages of slaughter. Therefore, a greater opportunity potentially exists for management practices to alter carcass weight in younger than in older heifers or steers. The opposite was evident for young bulls, where for the influence of finishing herd-year on carcass weight was greatest at older ages at slaughter.

The presence of variability in finishing herd-year effects across traits and genders was further investigated through the examination of the respective (co)variance matrices. The resulting eigenvalues and eigenfunctions confirmed significant variability among finishing herds in the shape of the carcass trait profiles. The direction of the largest eigenfunctions associated with the leading eigenvalues for all traits and genders was consistent across age at slaughter, suggesting that the corresponding proportion of finishing herd-year variation was explained by environmental factors acting similarly in all ages. However, as the second and third eigenvalues combined accounted for between 6.70% (fat score in young bulls) and 51.37% (fat score in heifers) of the total phenotypic variation, this suggests that a substantial proportion of management effects may not be the same across all ages at slaughter. All

second and third eigenfunctions for the three traits had steep trends and sign changes across ages at slaughter, in agreement with the weakening of finishing herd-year correlations with increasing age distance (Figure 3); this therefore suggests that beef carcass traits at younger and older ages at slaughter are influenced by different management factors. The less than unity correlations between herd-year effects across different ages at slaughter for all traits and genders (Figure 3) also imply that modifying on-farm conditions to alter carcass traits at young ages will have lesser effect on carcass traits at older slaughter ages. This highlights the potential for farmers to focus on finishing beef for a particular end point. Indeed, the negative finishing-herd-year correlations between heifers carcass weight and fat score at very young versus very old age at slaughter suggests that management practices that alter carcass weight or fat score in heifers at youngest ages will have an antagonistic effect on these traits at older slaughter ages.

In addition to variability in finishing herd-year effects across herds, within-herd variability across years was also evident (Figure 6). Indeed the performance of animals from the same finishing herd, slaughtered at the same age across different years varied greatly, emphasizing the need for accurate and continuous evaluations of environmental effects in order to enhance management practices and performance across years. Such information could also allow producers to identify the ages at slaughter that are most profitable based on their current management systems, further enabling them to focus on finishing beef for a particular end point. For example, they may decide to adopt management practices that are more conducive to slaughtering at an earlier age.

4.3. Practical implications - Finishing herd-year solutions as a management tool

Commercial cattle are generally determined as ready for slaughter by visual inspection of the degree of fatness within the appropriate range of live weight (Van Groningen, Devitt, Wilton, & Cranfield, 2006). With the implementation of herd-specific trait

profiles described in the present study, more informed decisions on the appropriate time to slaughter may be made in order to achieve maximum returns at the abattoir. For example, if the shape of the growth profile for a finishing herd is below average at younger ages at slaughter but above average at older ages at slaughter then this finishing herd in subsequent years should perhaps focus on slaughtering as many animals as possible at older ages and streamline its management practice accordingly. Thus finishing herds specializing in specific slaughter ages may be established. As management practices tend to have greater effects on younger ages at slaughter, finishing herds aiming to improve carcass traits at these ages may see greater progress than those with objectives to slaughter at older ages. Moreover, the herd-specific growth profiles in the present study were relative to the population average. It may however also be possible to describe the herd-specific to any given profile.

The present study illustrates that the output from random regression models is a suitable continuous herd management tool for carcass traits across ages at slaughter (Figures 5 and 6). Potentially, the outputs from such analyses could be incorporated into a beef herd management web application that graphically displays individual herd management levels across ages at slaughter in addition to trends across years. There is also the potential for the incorporation of such analyses into prediction algorithms of likely future performance, which in turn could also be graphically displayed to identify the most optimal age at slaughter for a given genetic merit in a given herd. Such web applications have previously been developed for dairy herd management purposes (Koivula, Nousiainen, Nousiainen, & Mäntysaari, 2007). Finishing herd management levels may be displayed in a variety of formats to assess herd performance compared to the average, for example as the performance across finishing herds within a certain year (Figure 5), or within finishing herd across different years (Figure 6). Such information reflecting on-farm management across time coupled with breeding information and the knowledge of actual on-farm activities may highlight practices or

environmental issues that resulted in poor or improved performance, thereby offering useful insights to forecast future performance. For example, consistently inferior performance relative to expectations may reflect underlying compromised health status of the herd requiring remedial action such as vaccination. Thus, management practices may be altered accordingly and/or contingency plans implemented for the following years. This may consequently result in fewer unfavourable deviations in finishing herd performance across subsequent years as farmers make more informed decisions to improve performance at an earlier point in time. Additionally, individual finishing herd-year solutions from a random regression model could be compared between finishing herds from similar geographical regions or herds whose animals are slaughtered at the same abattoir for benchmarking purposes.

Market trends and abattoir specifications fluctuate across time in terms of carcass classification (Grunert 2006; Hornibrook & Fearn 2001); consequently, finishing herd-year solutions can aid farmers in altering their breeding goals and on-farm conditions to produce animals more in line with the anticipated changes. Further investigation into the sources of finishing herd-year variation regarding specific conditions such as differences in pasture quality, feed allocation, herd health status, stocking rates or weather fluctuations, is desirable and results could be also incorporated into enhanced management tools creating more informed, comprehensive and efficient production systems.

5. Conclusions

The present study demonstrates how the analysis of routinely collected abattoir data for the genetic evaluation of beef carcass traits can yield useful information for consideration in farm management and decision support tools. Knowledge of the variability in herd

performance across ages at slaughter and years of slaughter is a useful indicator of management and facilitates the enhancement of best on-farm practices.

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References

- Bastin, C., Laloux, L., Gillon, A., Miglior, F., Soyeurt, H., Hammami, H., ... Gengler, N. (2009). Modeling milk urea of Walloon dairy cows in management perspectives. *Journal of Dairy Science*, *92*(7), 3529–3540.
- Bormann, J., Wiggans, G. R., Druet, T., & Gengler, N. (2003). Within-Herd Effects of Age at Test Day and Lactation Stage on Test-Day Yields. *Journal of Dairy Science*, *86*(11), 3765–3774.
- Caccamo, M., Veerkamp, R. F., de Jong, G., Pool, M. H., Petriglieri, R., & Licitra, G. (2008). Variance Components for Test-Day Milk, Fat, and Protein Yield, and Somatic Cell Score for Analyzing Management Information. *Journal of Dairy Science*, *91*(8), 3268–3276.
- Caccamo, M., Veerkamp, R. F., Ferguson, J. D., Petriglieri, R., La Terra, F., & Licitra, G. (2010). Associations of breed and feeding management with milk production curves at herd level using a random regression test-day model. *Journal of Dairy Science*, *93*(10), 4986–95.
- Cobuci, J. A., Euclides, R. F., Lopes, P. S., Costa, C. N., Torres, R. D. A., & Pereira, C. S. (2005). Estimation of genetic parameters for test-day milk yield in Holstein cows using a random regression model. *Genetics and Molecular Biology*, *28*(1), 75–83.
- Craigie, C. R., Navajas, E. A., Purchas, R. W., Maltin, C. A., Bünger, L., Hoskin, S. O., ... Roehe, R. (2012). A review of the development and use of video image analysis (VIA) for beef carcass evaluation as an alternative to the current EUROP system and other subjective systems. *Meat Science*, *92*(4), 307–18.

De Roos, A. P. W., Harbers, A. G. F., & de Jong, G. (2004). Random Herd Curves in a Test-Day Model for Milk, Fat, and Protein Production of Dairy Cattle in The Netherlands. *Journal of Dairy Science*, 87(8), 2693–2701.

Druet, T., Jaffrezic, F., & Ducrocq, V. (2005). Estimation of genetic parameters for test day records of dairy traits in the first three lactations. *Genetics Selection Evolution*, 37(3), 257–271.

Englishby, T. M., Banos, G., Moore, K. L., Coffey, M. P., Evans, R. D., & Berry, D. P. (2016). Genetic analysis of carcass traits in beef cattle using random regression models. *Journal of Animal Science*, 94(4), 1354–1364.

Eriksson, S., Nasholm, A., Johansson, K., & Philipsson, J. (2003). Genetic analyses of field-recorded growth and carcass traits for Swedish beef cattle. *Livestock Production Science*, 84(1), 53–62.

Falconer, D.S., & MacKay, T. F. C. (1996). *Introduction to Quantitative Genetics* (4th ed.edi.). Essex U.K.: Longman.

Fischer, T.M., Gilmour, A. R., & van derWerf, J. H. (2004). Computing approximate standard errors for genetic parameters derived from random regression models fitted by average information REML. *Genetic Selection and Evolution*, 36(3), 363–369.

Gengler, N., Tijani, A., & Wiggans, G. R. (2000). Use of Sequential Estimation of Regressions and Effects on Regressions to Solve Large Multitrait Test-Day Models. *Journal of Dairy Science*, 83(2), 369.e1–369.e18.

Gilmour A. R., Gogel, B. J., Cullis, B. R., & Thompson, R. (2009). *ASReml user guide release 3.0*. VSN International Ltd., Hemel.

Grunert, K. G. (2006). Future trends and consumer lifestyles with regard to meat consumption. *Meat Science*, 74(1), 149–160.

Hazel, L. N. (1943). The Genetic Basis for Constructing Selection Indexes. *Genetics*, 28(6), 476–90.

Hickey, J. M., Keane, M. G., Kenny, D. A, Cromie, A R., & Veerkamp, R. F. (2007). Genetic parameters for EUROP carcass traits within different groups of cattle in Ireland. *Journal of Animal Science*, 85(2), 314–21.

- Hornibrook, S.A., A. Fearne. (2001). The knowledge domain of chain and network science. *Journal of Chain and Network Science*, 1(2), 77–85.
- Huisman, A. E., Veerkamp, R. F., & Van Arendonk, J. A. M. (2002). Genetic parameters for various random regression models to describe the weight data of pigs. *Journal of Animal Science*, 80(3), 575–582.
- Jamrozik, J., Jansen, G., Schaeffer, L. R., & Liu, Z. (1998). Analysis of persistency of lactation calculated from a random regression test day model. *Interbull Bulletin*, 17, 64–69.
- Jones, H.E., White, I.M.S., & Brotherstone, S. (1999). Genetic evaluation of Holstein Friesian sires for daughter condition-score changes using a random regression model. *Journal of Animal Science*. 68(3),467-475
- Keane, M. ., & Allen, P. (1998). Effects of production system intensity on performance, carcass composition and meat quality of beef cattle. *Livestock Production Science*, 56(3), 203–214.
- Kirkpatrick, M., & Heckman, N. (1989). *Mathematical Wology*. 27(4), 429–450.
- Koivula, M., Nousiainen, J. I., Nousiainen, J., & Mäntysaari, E. A. (2007). Use of herd solutions from a random regression test-day model for diagnostic dairy herd management. *Journal of Dairy Science*, 90(5), 2563–2568.
- Laloë, D., Fouilloux, M., & Guerrier, J. (2007). Field Genetic Evaluation of Beef Cattle in France : From Birth to Slaughterhouse. *Interbull Bulletin*, 36, 19–24.
- Mayeres, P., Stoll, J., Bormann, J., Reents, R., & Gengler, N. (2004). Prediction of daily milk, fat, and protein production by a random regression test-day model. *Journal of Dairy Science*, 87(6), 1925-1933.
- Meyer, K., & Kirkpatrick, M. (2005). Uphill, down dale: quantitative genetics of curvaceous traits. *Philosophical Transactions of the Royal Society of London. Series B, Biological Sciences*, 360(1459), 1443–55.
- Moore, K.L., Draper, J., Glasgow, A., Kerr, I., Mead, S., Roberts, S., Wilkinson, S., & Coffey, M. (2014). Using video image analysis (VIA) to assess abattoir carcass yields and produce genomic breeding values (GEBV) for genetic improvement of beef carcass traits. *British Cattle Breeders Club. Digest* 69.

Mrode, R. A, Swanson, G. J. T., & Paget, M. F. (2003). Implementation of the test day model for production traits in the UK. *Interbull Bulletin*, 31, 193–196.

Olori, V. E., Hill, W. G., McGuirk, B. J., & Brotherstone, S. (1999). Estimating variance components for test day milk records by restricted maximum likelihood with a random regression animal model. *Livestock Production Science*, 61(1), 53–63.

Pabiou, T., Fikse, W. F., Näsholm, a, Cromie, A. R., Drennan, M. J., Keane, M. G., & Berry, D. P. (2009). Genetic parameters for carcass cut weight in Irish beef cattle. *Journal of Animal Science*, 87(12), 3865–76.

Pabiou, T., Fikse, W. F., Amer, P. R., Cromie, A. R., Näsholm, A., & Berry, D. P. (2011). Genetic variation in wholesale carcass cuts predicted from digital images in cattle. *Animal*, 5(11), 1720–7.

Reverter, A., Johnston, D. J., Graser, H. U., Wolcott, M. L., Upton, W. H., & Graser, H. (2000). Genetic analyses of live-animal ultrasound and abattoir carcass traits in Australian Angus and Hereford cattle. *Journal of Animal Science*, 78(7), 1786–1795.

Van Der Werf, J. H. J., & De Boer, W. (1989). Influence of Nonadditive Effects on Estimation of Genetic Parameters in Dairy Cattle. *Journal of Dairy Science*, 72(10), 2606–2614.

Van Groningen, C., Devitt, C. J. B., Wilton, J. W., & Cranfield, J. A. L. (2006). Economic evaluations of beef bulls in an integrated supply chain. *Journal of Animal Science*, 84(12), 3219–3227.

Wilton, J. W., & Goddard, M. E. (1996). Selection for Carcass and Feedlot Traits Considering Alternative Slaughter End Points and Optimized Management. *Journal of Animal Science*, 74(1), 37–45.

Windig, J. J., Calus, M. P. L., & Veerkamp, R. F. (2005). Influence of herd environment on health and fertility and their relationship with milk production. *Journal of Dairy Science*, 88(1), 335–347.

Figure 1. Ratio of finishing herd-year variance to total phenotypic variance in (a) heifers, (b) steers and (c) young bulls, for carcass weight (—), conformation score (—) and fat score(•••); standard errors ranged from 0.02 to 0.10 for carcass weight, 0.01 to 0.10 for conformation score and 0.2 to 0.11 for fat score.

Figure 2. Eigen functions associated with the first (—), second (—) and third (•••) eigenvalues of finishing herd-year variance in steers for (a) carcass weight, (b) conformation score and (c) fat score.

Figure 3. Finishing herd-year correlations between the earliest and all subsequent ages at slaughter in (a) heifers, (b) steers and (c) young bulls, for carcass weight (—), conformation score (—) and fat score (•••); standard errors ranged from 0.00 to 0.07 for carcass weight, 0.00 to 0.11 for conformation score and 0.00 to 0.18 for fat score.

Figure 4. Finishing herd-year correlations between carcass weight and conformation score (—), conformation score and fat score (—), and carcass weight and fat score (•••) across ages at slaughter for (a) heifers, (b) steers and (c) young bulls; standard errors ranged from 0.01 to 0.06 between carcass weight and conformation score, 0.02 to 0.23 between conformation score and fat score, and 0.02 to 0.10 between carcass weight and fat score.

Figure 5. Overall fixed finishing herd curves (—) for young bulls slaughtered in one year and three individual finishing herd curves, A (—), B (•••) and C (— • — •), in the same year for (a) carcass weight, (b) conformation score and (c) fat score.

Figure 6. Average (—) and individual finishing herd-year curves for carcass weight at 540 days of age at slaughter (a) and 840 days of age at slaughter (b); conformation score at 540 days of age at slaughter (c) and 840 days of age at slaughter (d); fat score at 540 days of age at slaughter (e) and 840 days of age at slaughter(f), in two finishing herds, A (•••) and B (—), of steers slaughtered between 2003 and 2012.

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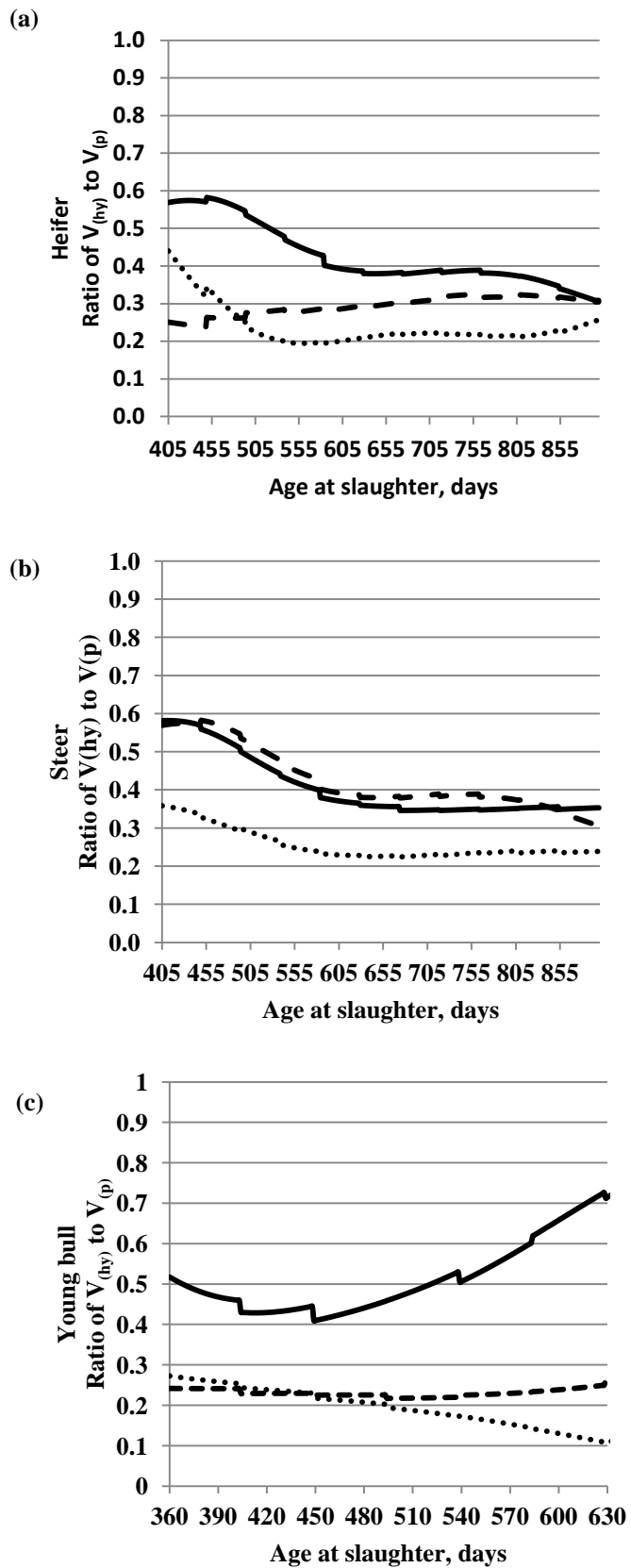
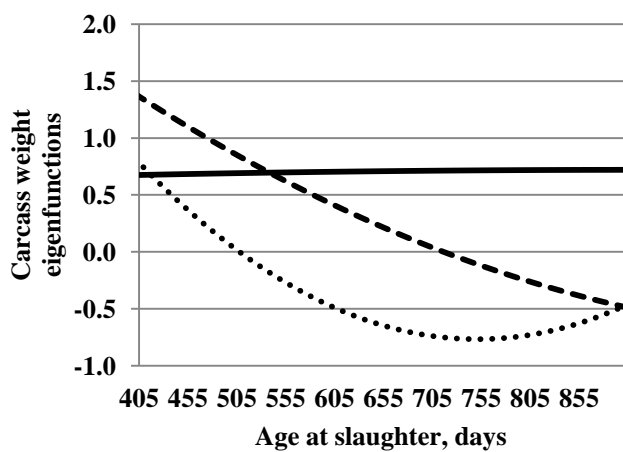
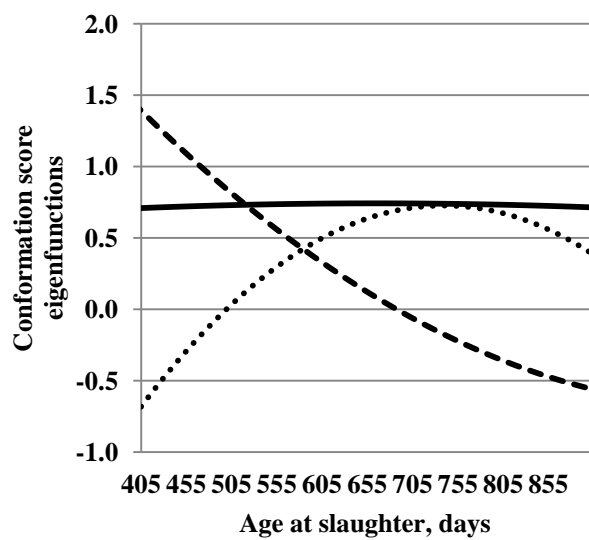


Figure 1.

(a)



(b)



(c)

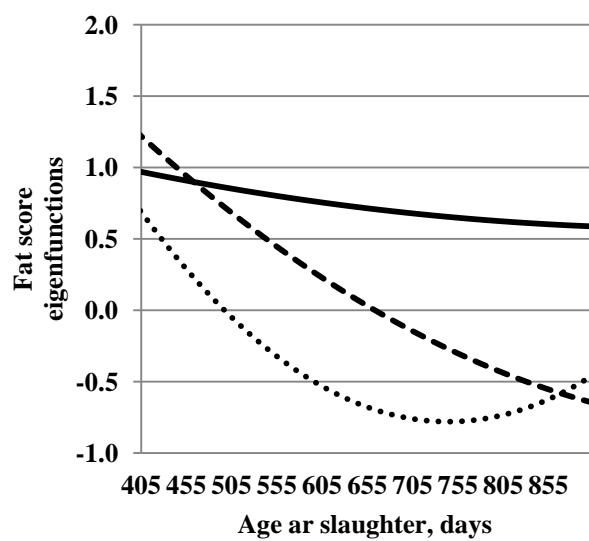


Figure 2.

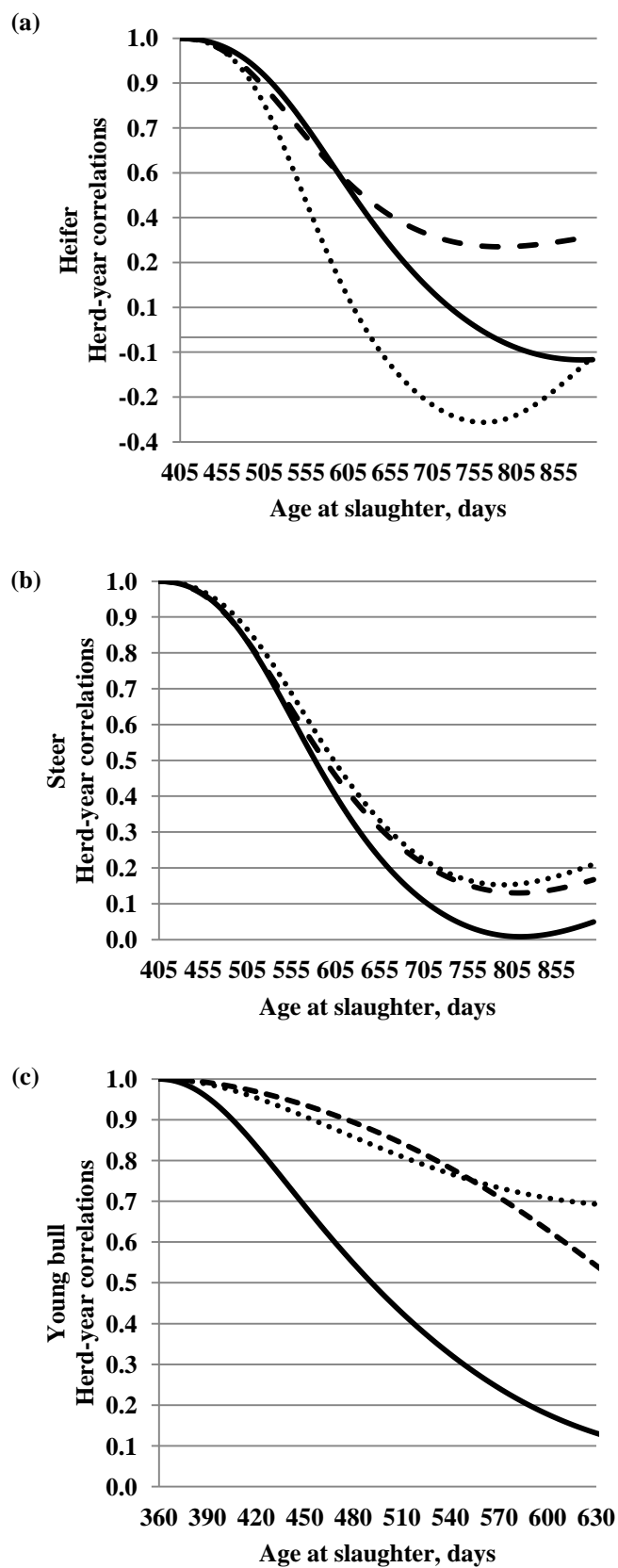


Figure 3.

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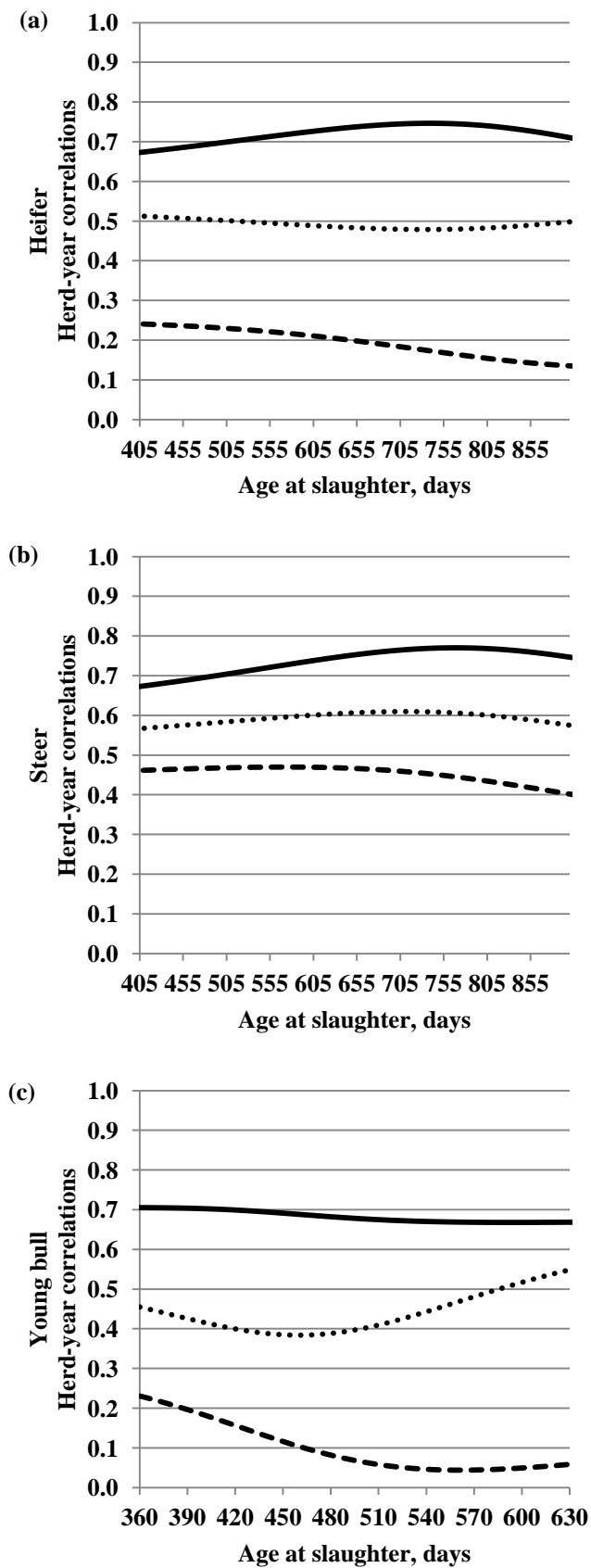


Figure 4.

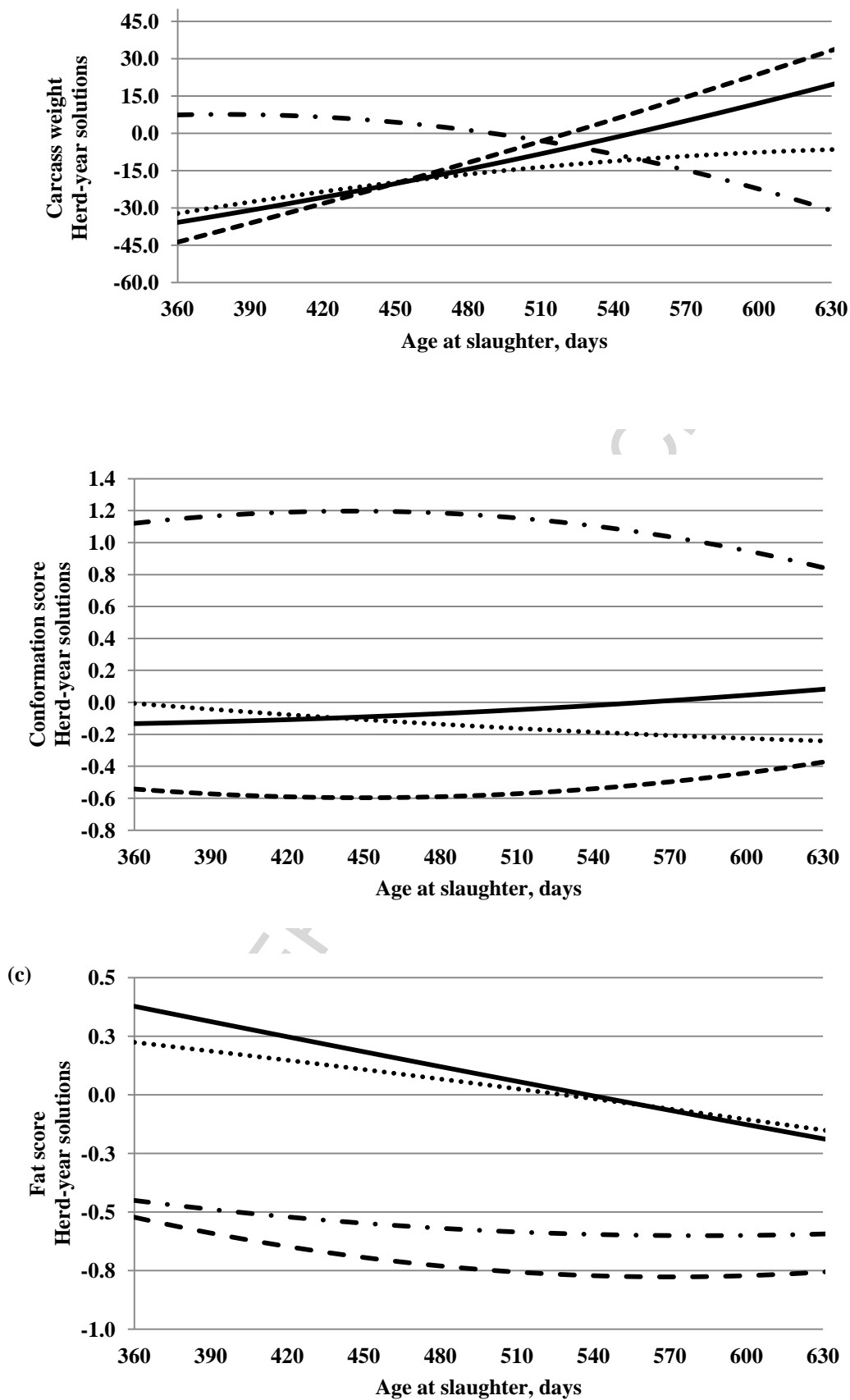
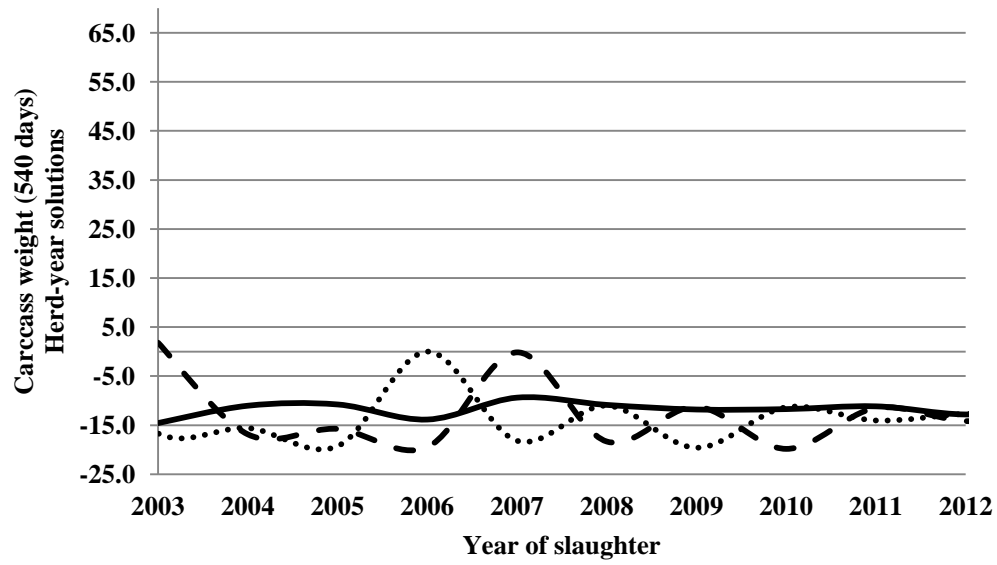


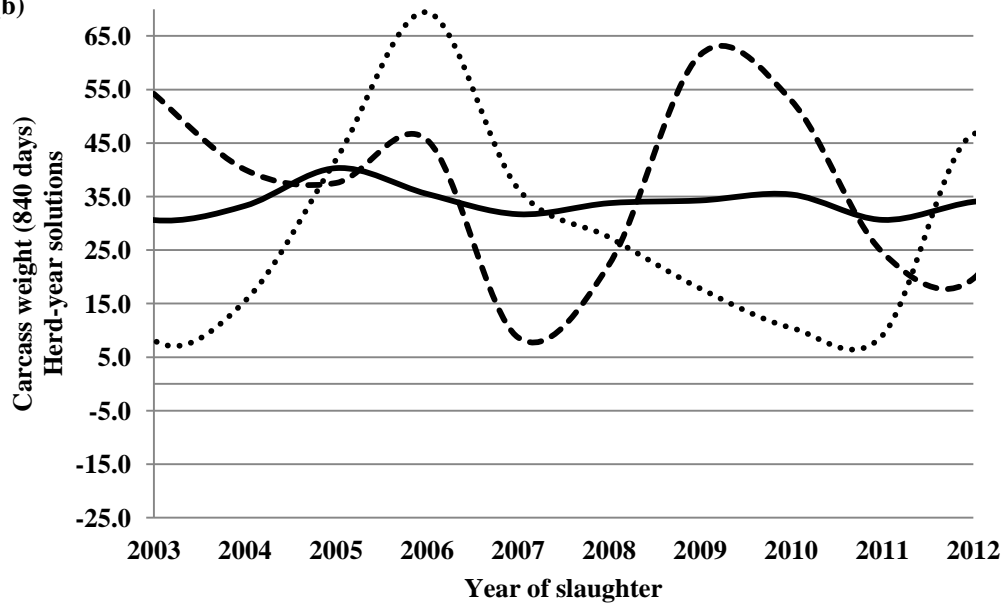
Figure 5.

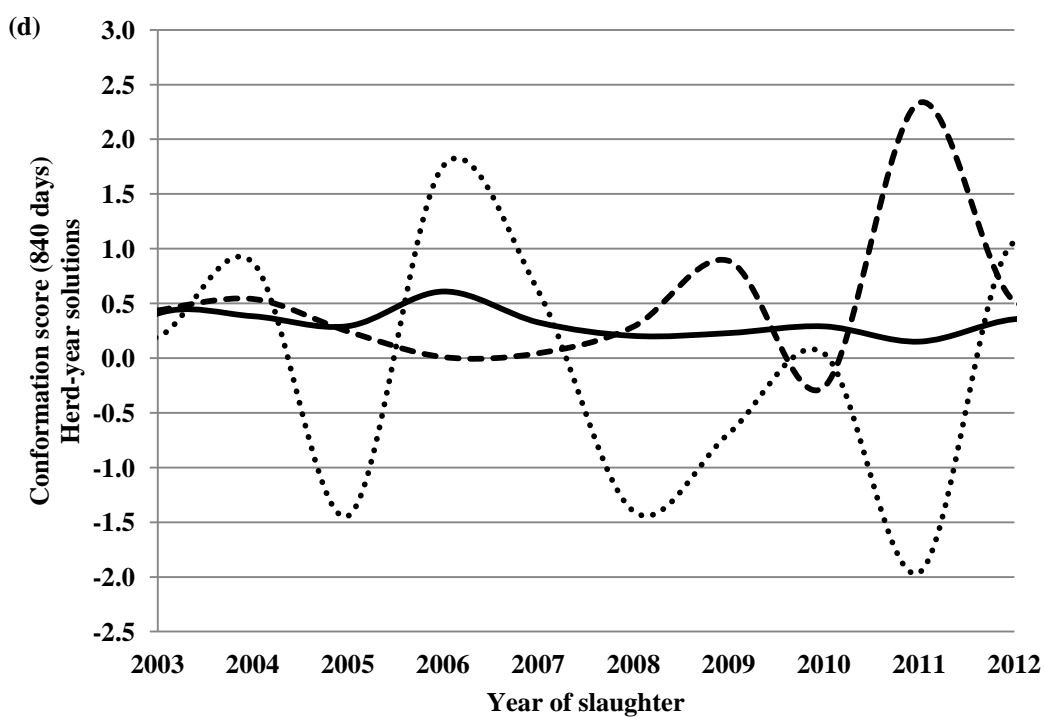
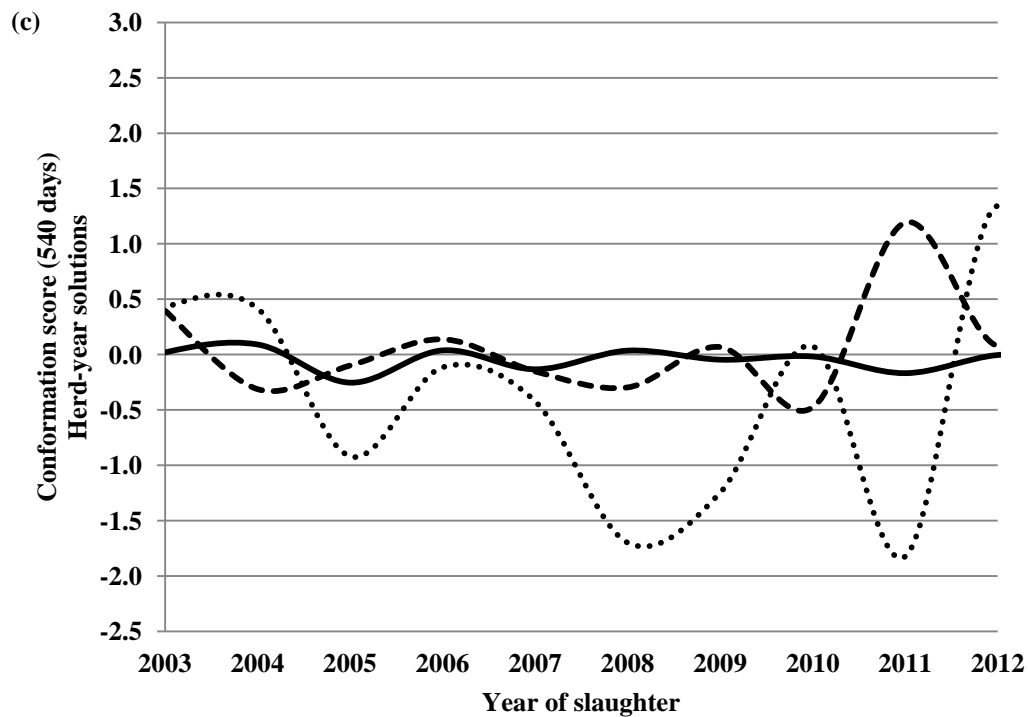
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(a)



(b)





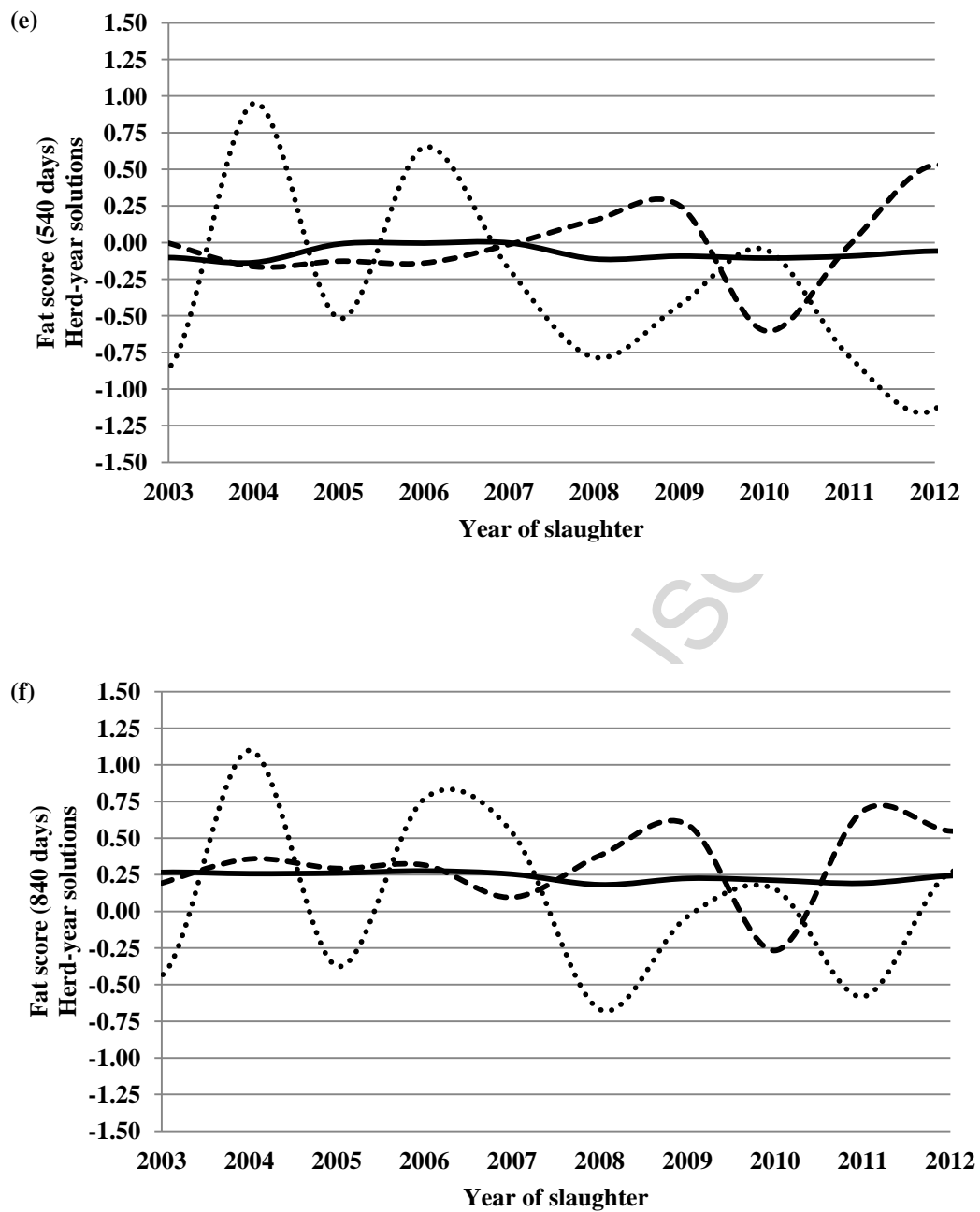


Figure 6.

Table 1. Numbers of heifer, steer, and young bull records per residual variance class representing age at slaughter.

Class (days)	Heifers	Steers	Young Bulls
360-405	133	386	3,680
406-450	574	1,228	7,459
451-495	1,245	1,874	8,632
496-540	2,441	3,416	1,843
541-585	4,616	6,569	793
586-630	7,193	9,409	328
631-675	7,491	11,923	166
676-720	6,900	12,477	70
721-765	5,405	10,506	N/A
766-810	4,288	8,676	N/A
811-855	3,386	6,850	N/A
856-900	2,443	5,526	N/A

N/A= not applicable

Table 2. Mean, standard deviation (sd), coefficient of variation (CV%), average ratio of finishing herd-year of slaughter to phenotypic variance ($V_{(hy)}/V_{(p)}$) estimates (\pm SE), and average heritability (h^2) estimates (\pm SE) for each gender by carcass trait.

Gender	Trait	Mean	s.d	CV%	$V_{(hy)}/V_{(p)}$	h^2
Heifers n=46,115	Carcass weight (kg)	292.72	35.53	12.14	0.43 \pm (0.02)	0.30 \pm (0.02)
	Conformation ¹	7.32	1.51	20.63	0.29 \pm (0.03)	0.34 \pm (0.02)
	Fat ²	10.26	1.55	15.11	0.24 \pm (0.02)	0.39 \pm (0.03)
	Age at slaughter (d)	676.23	105.47	15.59		
Steers n=78,790	Carcass weight (kg)	334.06	41.49	12.42	0.41 \pm (0.02)	0.34 \pm (0.02)
	Conformation ¹	7.44	1.48	19.84	0.43 \pm (0.02)	0.38 \pm (0.02)
	Fat ²	9.84	1.49	15.02	0.26 \pm (0.02)	0.38 \pm (0.02)
	Age at slaughter (d)	690.69	108.65	23.82		
Young bulls n=22,971	Carcass weight (kg)	354.27	52.18	14.72	0.51 \pm (0.03)	0.19 \pm (0.03)
	Conformation ¹	9.31	2.16	23.20	0.23 \pm (0.03)	0.38 \pm (0.03)
	Fat ²	8.18	2.02	24.69	0.20 \pm (0.03)	0.35 \pm (0.03)
	Age at slaughter (d)	454.77	51.35	11.29		

¹Scored on a 15 point scale 1 (worst) to 15 (best).

²Scored on a 15 point scale 1 (leanest) to 15 (fattest).

n = number of animals.

Table 3. Eigenvalues and their proportions for the herd-year of slaughter variance covariance matrices for carcass traits in each gender.

Gender	Trait	Eigenvalue%		
		First	second	third
Heifers	Carcass weight	57.80	37.15	5.05
	Conformation	72.32	21.85	5.83
	Fat	48.63	38.25	13.12
Steers	Carcass weight	57.53	34.82	7.55
	Conformation	64.56	29.40	6.04
	Fat	62.58	30.06	7.36
Young bulls	Carcass weight	82.67	14.73	2.60
	Conformation	85.00	14.50	0.50
	Fat	93.30	5.88	0.82