

Application Of The Grouped Data Model To The Study Of Conformation And Fat Cover Scores In Beef Cattle

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Introduction

Meat and carcass quality traits are becoming more important in beef cattle production (Eriksson et al. (2003)). Some of them, such as conformation and fat cover scores, obtain their records from subjective grading that usually involve classification under a categorical and arbitrary predefined scale. Theoretically, the discrete nature of the performance should be taken into account for the genetic evaluation by using a threshold model (Gianola and Foulley (1983)). As the scale of grading may be different according to different technicians, Varona et al. (2009) compared different threshold models by the deviance information criteria, and the slaughterhouse specific ordered category threshold model was selected as the most plausible. However, threshold models are not the only ones that can take into account the discrete nature of a trait. Prentice and Gloeckler (1978) presented an approach for the analysis of discrete measures of failure time called the grouped data model (GDM), but it can be applied to any other variable measured discretely. Ducrocq (1999) reparameterized and extended GDM to include random effects for its use in animal breeding. The aim of this paper is to use the grouped data model for the estimation of genetic parameters of conformation and fat cover scores in beef cattle and to compare the estimated parameters with the ones obtained using a slaughterhouse specific ordered category threshold model.

Material and methods

Field data source. Data were recorded between 2005 and 2009 in 12 slaughterhouses located in Catalonia (Spain), and included data from 2539 beef carcasses participating in the Yield Recording Scheme of the Bruna dels Pirineus breed. The traits contributed by DAR database to this study were: cold carcass weight (CW), conformation (CON) according to the (S)EUROP scale (CEE no 2930/81, 1981) and fat cover score (FC). The categorical scale of CON was converted to a numeric scale from 2 (O) to 5 (E) because S and P scores were not observed. Similarly, FC could take scores between 1 and 5, but scores over 4 were not observed. A summary of the descriptive statistics of the phenotypic traits is presented in Table 1. The data were completed with pedigree records provided by the Bruna dels Pirineus Breeders Association (FEBRUPI). The pedigree file contained 5153 animals, 332 being sires

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Grouped data model for a discrete variable (GDM). Assuming that Y is a discrete variable that can take values $k=1, 2, \dots, n$ (e.g. CON or FC), the probability that the discrete variable Y takes a value k can be calculated as:

$$P\{Y = k\} = P\{Y \geq k\} - P\{Y > k\} = \frac{P\{Y = k\}}{P\{Y \geq k\}} P\{Y \geq k\},$$

with $P\{Y \geq 1\} = 1$. In GDM, these conditional probabilities are modelled as (Ducrocq, 1999):

$$\frac{P\{Y = k\}}{P\{Y \geq k\}} = 1 - \exp\{-\exp(\xi_k)\},$$

with $\xi_k = \mu_k + \mathbf{X}\boldsymbol{\beta} + \mathbf{X}_{sh,k}\boldsymbol{\beta}_{sh,k} + \mathbf{Z}_1\mathbf{h} + \mathbf{Z}_2\mathbf{u}$. The variables included as proportional in $\boldsymbol{\beta}$ were sex (males and females), parity (1st to 4th or over), age at slaughter (9 months to 14 months), season at slaughter (winter, spring, summer and autumn) and year of slaughter (2005 to 2009). The slaughterhouse effect (12 levels) was assumed to be Y -dependent, i.e. different effects $\boldsymbol{\beta}_{sh,k}$ were estimated for each value k of CON and FC, in order to give more flexibility to the model. The herd effects \mathbf{h} and the direct breeding values \mathbf{u} were included as random variables with incidence matrices \mathbf{Z}_1 , and \mathbf{Z}_2 . Herd effects (73 levels) were assumed to be normal $f(\mathbf{h}) \sim N(0, \mathbf{I}\sigma_h^2)$, where σ_h^2 is the herd variance. For direct breeding values, the distribution was $f(\mathbf{u}) \sim N(0, \mathbf{A}\sigma_u^2)$, where \mathbf{A} is the numerator relationship matrix and σ_u^2 is the genetic variance. The Survival Kit package (Ducrocq (1999)) was used for the GDM analysis. Given the estimates of the variance components, the effective heritability was computed as in Yazdi et al. (2002).

The Bayesian slaughterhouse specific ordered category threshold model (SHTHM). The variable response, i.e. CON or FC was modelled as a discrete variable Y conditional in the underlying variable I as in Varona et al. (2009), with $t_{sh,1}$, $t_{sh,2}$ and $t_{sh,3}$ being thresholds that define the four categories of response and had a different position depending on the slaughterhouse. Thresholds $t_{12,2}$ and $t_{12,3}$ were assumed to be known, i.e. fixed to 0 and 2.0 for CON and for FC, providing a simpler sampling scheme than the one defined by fixing the residual variance of the categorical trait. The underlying variable I had the following distribution:

$$\mathbf{I} \sim N(\mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_1\mathbf{h} + \mathbf{Z}_2\mathbf{u}, \mathbf{I}\sigma_e^2),$$

where the effects were defined as in the previous GDM. Each analysis consisted of a single chain of 125,000 iterations, with the 1st 25,000 samples discarded. All iterations in the analysis were used to compute posterior means and standard deviations so that all the available information from the output of the Gibbs sampler could be considered.

Results and discussion

Descriptive statistics. Results not presented in tables show that the average carcass of the Bruna dels Pirineus breed under commercial conditions weights around 279 kg at 12.5 months of age (377 d), with an average conformation score of 3.43 and a slight fat cover average (2.48). Male calves were slaughtered one month later than females (387 d vs. 360 d)

with a higher cold carcass weight (305 kg vs. 231 kg) and conformation (3.61 vs. 3.35) but a slightly lower fat cover (2.47 vs. 2.54). These averages were calculated from the frequencies for all data, but huge differences in CON and FC frequencies were detected stratifying by slaughterhouse (Table 1). There were two slaughterhouses with over 80% of carcasses qualified as R for CON, whereas in the other slaughterhouses most of the carcasses were qualified as U (Table 1). These differences among slaughterhouses were even greater for FC scores, and can be explained in part because some slaughterhouses preferred to sacrifice light young animals with less than one year of age whereas other slaughterhouses preferred heavier and older animals, but also because CON and FC were scored by a different technician in each slaughterhouse.

Table 1: Frequency (percent) of carcass conformation (CON) and fat cover (FC) scores stratifying by slaughterhouse.

Slaughterhouse	n	CON				n	FC			
		O	R	U	E		1	2	3	4
1	182	1.1	34.6	64.3	0.0	164	0.0	0.0	100	0.0
2	158	1.9	36.1	47.4	14.6	149	6.0	55.0	38.9	0.0
3	320	1.3	38.1	59.4	1.2	318	1.3	24.8	73.9	0.0
4	166	0.6	33.1	56.6	9.6	161	0.0	0.0	100	0.0
5	95	0.0	50.5	49.5	0.0	95	0.0	4.2	95.8	0.0
6	142	0.0	7.7	76.8	15.5	101	1.0	87.1	11.9	0.0
7	84	0.0	36.9	59.5	3.6	60	5.0	65.0	30.0	0.0
8	85	0.0	17.6	69.4	12.9	81	0.0	38.3	60.5	1.2
9	55	1.8	7.3	40.0	50.9	55	0.0	5.4	90.9	3.6
10	24	0.0	50.0	50.0	0.0	24	0.0	95.8	4.2	0.0
11	439	0.0	96.4	3.0	0.7	391	69.6	25.3	4.6	0.5
12	789	0.2	81.0	18.0	0.8	380	0.5	12.9	79.2	7.4
All data	2539	0.5	58.3	36.6	4.6	1979	14.7	25.1	58.5	1.7

Grouped data Model for carcass conformation and fat cover. Results from the likelihood ratio test (not presented in tables) show that the slaughterhouse had the biggest effect on CON and FC ($P < 0.001$). This effect was significantly Y-dependent for both traits, and therefore a different regression coefficient β_k for each CON and FC value should be estimated. The sex effect was also significant for both traits ($P < 0.001$). Males showed significantly higher average CON than females (3.56 vs. 3.37), with these results being very similar to that of Altarriba et al. (2009). The situation was reversed for FC where males showed a lower fat cover than females (2.47 vs. 2.75), due to their lower precocity. Calves from multiparous dams had significantly ($P < 0.001$) higher CON than calves from primiparous dams (3.45 vs. 3.32), but the differences were not significant for FC. Moreover, for age at slaughter effect, an almost linear increasing relationship was observed for CON, going from 3.31 at 9 months of age to 3.49 at 14 months of age, whereas for FC no clear

tendency was detected. The environmental factors season and year at slaughter had not a substantial effect on CON and FC.

Variance components and heritability estimates. Results obtained by using GDM were similar to the ones obtained applying SHTHM (Table 2). GDM calculations, however were over 10 times faster than those of SHTHM. The percentage of total variance explained by the herd effect was 11.3% for CON and 12.4% for FC. The heritability estimates indicate that a relevant additive genetic variance exists for all traits, confirming the results obtained by other studies (Eriksson et al. (2003); Hickey et al. (2007); Altarriba et al. (2009)). The results presented here are within the range of the estimates found by these authors in different breeds.

Table 2: Estimated additive (σ_u^2), herd (σ_h^2) and error (σ_e^2) variances and heritabilities (h^2) for carcass conformation (CON) and fat cover (FC) with the grouped data model (GDM) and the slaughterhouse specific ordered category threshold model (SHTHM)

	CON		FC	
	GDM	SHTHM	GDM	SHTHM
Genetic variance	0.418	1.206	0.205	0.131
Herd variance	0.180	0.548	0.170	0.063
Residual variance	1.000	2.304	1.000	0.451
Heritability	0.325	0.300	0.168	0.205

Conclusion

The grouped data model can be a powerful tool to investigate and assess the conformation and fat cover scores in beef carcasses. The slaughterhouse effect explained the biggest percentage of total variance for both traits revealing the complexity of normalization of carcass evaluation. On the genetic side, the heritabilities found indicate that a relevant additive genetic variance exists for both traits. In this study, similar conclusions are obtained analyzing both traits with GDM and SHTHM. An appropriate procedure to test for model fitting, however, would provide a clear framework to compare both models.

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