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## Estimation of genetic parameters of type traits in Asturiana de los Valles beef cattle breed

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### Summary

Ten type traits and a final score were analysed in 5868 records of the Asturiana de los Valles beef cattle breed. Traits were grouped into two classes: (i) traits scoring skeletal and muscular development and (ii) traits scoring adjustment to the breed standard. Heritabilities were moderate to low, ranging from 0.04 to 0.26. Genetic correlations among traits were, in general, in the same direction as, but higher than, phenotypic correlations. The genetic variability shown, in general, for the analysed traits would justify the inclusion of morphological assessment in the Asturiana de los Valles beef cattle breed sire selection programme. Main characteristics of the current type classification system are criticized. The knowledge of (co)variances among type and economically important productive and reproductive traits is recommended before revision of the classification methodology.

### Zusammenfassung

*Schätzung genetischer Parameter für Exterieurmerkmale in der Asturiana de los Valles Fleischrinder-rasse*

5868 registrierte *Asturiana de los Valles* Tiere wurden bezüglich 10 Exterieurmerkmalen und eines Gesamtwertes auf der Basis einer gewichteten Berücksichtigung dieser Einzelmerkmale untersucht. Die Merkmale wurden in zwei Klassen unterteilt: (i) Merkmale, die Skelett- und Muskelentwicklung betreffen und (ii) rassespezifische Merkmale. Die Heritabilitäten lagen zwischen 0,04 und 0,26. Genetische Korrelationen zwischen den Merkmalen waren allgemein mit den phänotypischen Korrelationen gleichgerichtet, aber mit höheren Werten. Die aufgezeigte genetische Variabilität der untersuchten Merkmale würde deren Eingliederung in die morphologische Bewertung im Rahmen des *Asturiana de los Valles* Fleischrinder Selektionsprogrammes für Bullen rechtfertigen. Wichtige Charakteristika der gegenwärtigen Exterieurbeurteilung werden kritisiert. Es wird empfohlen erst (Ko-)varianzen zwischen Exterieur und ökonomisch wichtigen Produktions- und Reproduktionsmerkmalen zu ermitteln, bevor die Bewertungsmethodik überarbeitet wird.

### Introduction

Cattle breeders have long held the belief that type traits have an important influence on cattle performance. In beef cattle, type traits are expected to be useful for evaluating the animals as meat producers. However, type classification is difficult to carry out in beef cattle because of the normally extensive management conditions. In Spain, a simple type of assessment methodology has been standardized since the 1980s in most Spanish beef cattle breeds. This methodology is expected to describe the animal's conformation according to the breed standard as far as its skeletal and muscular development so as to evaluate the animal's productive aptitude.

The scientific literature has paid a great deal of attention to type traits in dairy cattle, not only as descriptive traits in their own right (THOMPSON et al. 1981; BROTHERSTONE et al. 1990), but also because of their influence on productive or longevity traits (MEYER et al.

1987; BROTHERSTONE 1994; VUKASINOVIC et al. 1997). However, there are no available references to genetic factors affecting type evaluation in beef cattle. The aim of this paper was to estimate the genetic parameters of type traits in the Asturiana de los Valles beef cattle breed in order to evaluate the usefulness of the current Spanish type classification system in sire selection programmes.

### Materials and methods

The analysed morphological classification system (CIMA 1986) included 10 different single traits for females (Table 1): breed characteristics (BC), size (S), head development (HD), forequarter quality (FQ), body depth (BD), back line (BL), rump (R), thigh development (TD), legs line (LL) and udder development (UD). These traits are expected to describe the animal's general appearance according to the breed's standard and functionality, as well as characterizing the animal's productive ability. A final score (FS) is built weighting these single traits.

BC scores the animal's accordance with the breed standard. This trait takes into account, within a given size, the coat colour variation and the general look of the animal. S scores the animal's skeletal development. HD is determined by the head size and, to a lesser extent, by the direction of the horns. FQ scores the skeletal and muscular development of the neck, chest and shoulders. BD scores the chest and belly depth. BL scores the adjustment of the lumbo-dorsal line to the horizontal, considered as the optimum. R is determined by the rump size and its muscular development. TD scores the degree of development of the muscular masses of the thigh. LL scores the adjustment to right angles of the fore and hind legs; legs showing a thin shin circumference are preferred. UD scores the udder size.

Traits can be scored from 1 to 9. If more than one trait is scored below 5 the assessed animal is not included in the Asturiana de los Valles Herdbook; consequently, only scores from 5 to 9 were available. In a similar way, as reported by VUKASINOVIC et al. (1997) in Brown Swiss cattle, traits are scored as a distance from the 'optimum' for each trait according to the sex and age of the assessed animal. Traits are scored numerically on a desirability scale from sufficient (5) to excellent (9).

The available data were comprised of type records of pedigree animals of the Asturiana de los Valles beef cattle breed obtained from 1993 to 1998 by four Asturiana de los Valles Breeders Association (ASEAVA) expert classifiers within the Principado de Asturias' Regional Cattle Improvement Program. Females must have calved at least once to be assessed. Distribution of available data is shown in Table 2. Assessments were performed regardless of the age or stage of lactation of the dam at classification. Most classified

Table 1. Type traits information for the analysed database

Trait	Abbreviation	Score		Mean	SD
		5	9		
Breed characteristics	BC	Sufficient	Excellent	7.43	0.93
Size	S	Small	Large	7.26	0.73
Head development	HD	Small	Well developed	7.41	0.68
Forequarter quality	FQ	Sufficient	Well developed	7.33	0.68
Body depth	BD	Shallow	Deep	7.53	0.61
Back line	BL	Odd	Regular	7.35	0.67
Rump	R	Narrow and angular	Wide and muscled	7.31	0.69
Thigh development	TD	Thin	Muscled	7.42	0.66
Legs line	LL	Odd	Regular	7.49	0.64
Udder development	UD	Small	Large	6.88	0.76
Final score	FS			73.34	4.44

Table 2. Distribution of available type assessment records

Source of variation	Number of records
Year of classification	
1993	585
1994	446
1995	1389
1996	1120
1997	1121
1998	1207
Season of classification	
First season	4223
Second season	1645
Classifier	
A	3596
B	719
C	1124
D	429
Age	
2 years old	1542
3 years old	995
4 years old	711
5–9 years old	2177
> 9 years old	443
Stage of lactation of dams	
Fewer than 5 months from calving	3579
Five or more months from calving	2289

animals were from 5 to 9 years old (34%) and 2 years old (32%). Thirty-nine per cent of the dams were classified 5 or more months after calving. Because of the important computational cost, unrelated animals and doubtful age or sex records were removed from the database. Records of herds with fewer than six assessed animals in the data set were deleted to optimize computing resources. Finally, the analysed database included 5868 records. Pedigree information included 2426 additional animals. In consequence, 8293 animals were involved in the estimation of genetic parameters.

Phenotypic correlation among traits was computed using SAS (1999). Additionally, principal component analysis was carried out to determine the number of independent traits that account for most of the phenotypic variation in type traits (VUKASINOVIC et al. 1997; ROUGHSEGE et al. 2000). This analysis was computed from the phenotypic correlation matrix among traits to ensure that all traits were treated as equally important, giving the same weight to the variables regardless their own variance. Only factors accounting for more variation than any individual type trait (eigenvalue  $\geq 1$ ) were retained. FS, as a linear function of the other traits, was not included in the principal component analysis.

Genetic parameters were estimated through a multivariate REML procedure applied to a mixed linear model including the animal additive genetic effect ( $u$ ) considered as a random variable ( $u \sim N(0, A\sigma^2u)$ ). As a result of previous analyses (GOYACHE et al. 2001a), the fitted model included the following as fixed effects: herd (424 levels), classifier-year-season (42 levels, considering two seasons, from January to June and from July to December), stage of lactation of the dam at classification (two levels: less than 5 months from calving, and 5 or more months from calving), and age of the dam at classification (five levels: less than 2 years old, 3 years, 4 years, from 5 to 9 years old and older than 9 years). All runs were carried out using the VCE programme (GROENEVELD and GARCIA CORTES 1998).

## Results and discussion

It is not possible to make the assumption that analysed type traits are all independent. The Spanish type traits assessment system is focussed to classify well-sized and muscled animals. However, traits involving the breed standard deserve greater attention. Eigenvalues and the proportion of the total aggregate phenotypic variance of type traits are shown in Table 3. Only two components showed eigenvalue  $\geq 1$ , accounting for 50% of the total variation of type traits; the first component accounting for 39% of the total variance. Eigenvectors showing the relative contribution of an individual type trait to the factors are listed in Table 4. The interpretation of factors is possible taking into account the sign and magnitude of the eigenvectors. Eigenvectors  $\geq |0.55|$  describe animals showing a good skeletal and muscular development (Factor 1) accounting for variation of S, FQ, BD, BL, R and TD, and differentiate animals by their adjustment to the breed standard (Factor 2) accounting for variation of BC, HD, LL and UD. VUKASINOVIC *et al.* (1997), using a similar methodology to that used in the present paper to assess 18 type traits in Brown Swiss cattle, retained five principal components showing an eigenvalue  $\geq 1$ , accounting for 57.9% of the total phenotypic variance. ROUGHSEGE *et al.* (2000), using 23 linear type traits in British Holstein cattle, retained seven principal components showing an eigenvalue  $\geq 1$ , accounting for 57.9% of the total phenotypic variance.

Phenotypic correlations and genetic parameters of type traits are shown in Table 5. FS is phenotypically correlated above 0.50 with all type traits except LL and UD. Phenotypic correlations between FQ, BD, BL, R and TD ranged from 0.39 to 0.50. The whole animal's body deserves a global appraisal from the experts. Correlations of S with BD, R and TD are near to 0.40. The other phenotypic correlations are below 0.36.

*Table 3.* Eigenvalues and proportion of the total phenotypic variance explained (in percentage) by principal component

Component	Eigenvalue	Proportion of total variance	Cumulative proportion
1	3.87	38.72	38.72
2	1.10	11.02	49.74
3	0.89	8.92	58.66
4	0.79	7.94	66.60
5	0.62	6.24	72.84
6	0.61	6.08	78.92
7	0.59	5.92	84.84
8	0.57	5.66	90.50
9	0.51	5.08	95.58
10	0.44	4.42	100.00

*Table 4.* Eigenvectors of the first two principal components

Trait	Factor 1	Factor 2
BC	0.31	0.56
S	0.58	0.23
HD	0.33	0.63
FQ	0.74	0.15
BD	0.75	0.12
BL	0.69	0.17
R	0.65	0.24
TD	0.74	0.18
LL	0.20	0.59
UD	- 0.03	0.75

Table 5. Heritabilities (in bold) genetic (above diagonal) and phenotypic correlations (below diagonal) of type traits. Standard errors of genetic parameters are in brackets

Trait	BC	S	HD	FQ	BD	BL	R	TD	LL	UD	FS
BC	<b>0.33</b> (0.02)	0.20 (0.02)	0.47 (0.04)	0.41 (0.04)	0.42 (0.03)	0.24 (0.05)	0.28 (0.05)	0.27 (0.05)	0.67 (0.07)	-0.48 (0.05)	0.62 (0.02)
S	0.28	<b>0.30</b> (0.04)	0.09 (0.05)	0.41 (0.03)	0.74 (0.04)	0.50 (0.04)	0.66 (0.04)	0.59 (0.04)	-0.04 (0.08)	0.18 (0.06)	0.75 (0.02)
HD	0.38	0.26	<b>0.25</b> (0.02)	0.50 (0.04)	0.48 (0.03)	0.41 (0.06)	0.66 (0.06)	0.51 (0.05)	0.66 (0.08)	-0.10 (0.06)	0.70 (0.08)
FQ	0.31	0.35	0.35	<b>0.21</b> (0.01)	0.64 (0.05)	0.94 (0.04)	0.74 (0.07)	0.88 (0.03)	0.81 (0.05)	-0.35 (0.05)	0.90 (0.06)
BD	0.26	0.40	0.30	0.48	<b>0.23</b> (0.02)	0.67 (0.06)	0.71 (0.06)	0.87 (0.03)	0.34 (0.10)	-0.27 (0.05)	0.88 (0.03)
BL	0.28	0.33	0.31	0.46	0.46	<b>0.11</b> (0.01)	0.83 (0.06)	0.84 (0.05)	0.60 (0.07)	-0.34 (0.07)	0.66 (0.16)
R	0.29	0.39	0.32	0.40	0.39	0.42	<b>0.07</b> (0.01)	0.74 (0.07)	0.45 (0.09)	-0.06 (0.10)	0.90 (0.07)
TD	0.30	0.40	0.31	0.50	0.52	0.43	0.46	<b>0.22</b> (0.01)	0.58 (0.07)	-0.20 (0.06)	0.84 (0.03)
LL	0.23	0.14	0.31	0.25	0.27	0.28	0.22	0.23	<b>0.06</b> (0.01)	-0.44 (0.13)	0.44 (0.11)
UD	0.21	0.24	0.24	0.10	0.13	0.13	0.18	0.18	0.21	<b>0.12</b> (0.02)	0.05 (0.06)
FS	0.60	0.65	0.55	0.63	0.67	0.67	0.71	0.74	0.43	0.43	<b>0.25</b> (0.02)

Heritabilities are moderate to low ranging from 0.06 (R) to 0.33 (BC). Heritability estimates for BL, R, LL and UD were lower or slightly higher than 0.10. The other type traits heritabilities ranged from 0.21 to 0.25, except for BC (0.33) and S (0.30). FS shows a heritability of 0.25, with genetic correlations higher than 0.60 with all type traits, except for LL and UD. UD does not genetically affect FS in practical terms. FS may be considered as a good index for an overall appraisal of the animals. Roughly speaking, genetic correlations among traits are in the same direction but generally higher than phenotypic correlations. Traits evaluating the animal's body (FQ, BD, BL, R and TD) are highly genetically correlated, ranging from 0.64 to 0.94. LL is genetically correlated above 0.40 with all other type traits except for the traits assessing the animal's skeletal development (S and BD). LL genetic correlation with UD is negative.

Heritabilities of the traits are, in general, in the same sense and lower than expected. In general, heritabilities of body traits are expected to be higher than those obtained for leg and udder traits (BROTHERSTONE et al. 1990). THOMPSON et al. (1981), using a linear type assessment methodology in Holstein cattle, reported heritabilities similar to but slightly higher than those obtained using a scoring system in relation to an ideal. The analysed traits score the deviation (positive or negative) from an 'optimum', measuring less phenotypic and genetic variation. Traits at the extremes of the biological (anatomical) observed variability could show the same low score, thus inducing a loss of biological relationships between traits (VUKASINOVIC et al. 1997). In addition, some traits included in the assessment system, such as HD, FQ and R, have a complex definition, comprising skeletal and muscular development. In consequence, these traits can be both difficult to explain and interpret.

Traits scoring the adjustment to the breed standard (BC, HD, LL and UD) show the highest and the lowest heritabilities (0.33 for BC and 0.06 for LL). BC is probably the result of the minor influence of a high number of breed characteristics on the expert's decision. BC is moderately genetically correlated with HD, while presenting the lowest found genetic correlation with UD (-0.48). BC seems to be a good index, taking account of all the characteristics defining the breed appearance, and shows moderate genetic correlations with the other traits. Usually, legs traits scored on a linear scale show low heritability, ranging from 0.10 to 0.20 (BROTHERSTONE et al. 1990; ROUGHSEGE et al. 2000) with positive and negative genetic correlations between them. LL is a subjective composite trait scoring legs direction (different fore and rear legs view) and feet quality. The genetic relations between these single traits could explain the low LL heritability.

Traits scoring skeletal development, S and BD, present moderate heritabilities (0.30 and 0.23, respectively) and high genetic correlation (0.74). However, traits scoring the animal's size on a linear scale show heritabilities from moderate to high. In British Holstein, BD show a heritability of 0.35 (BROTHERSTONE 1994; ROUGHSEGE et al. 2000). Other size scoring traits, such as stature, show heritabilities ranging from 0.40 to 0.50. S and BD are highly correlated with R. ALDERSON (1999) reported that rump dimensions are the last to reach the adult size. A wide rump at an early age could be a good indicator of the animal's adult size.

TD is the major trait for scoring the animal's muscular development, showing moderate heritability (0.22) and genetic correlations ranging from 0.51 to 0.88 with all traits except BC and UD. TD seems to show good genetic correlations with traits scoring animal's skeletal development. In British Holstein, the animal's beef shape shows a heritability of 0.26 and moderate to high genetic correlations with rump width (0.55) and chest width (0.82) (BROTHERSTONE 1994).

Despite the fact that in Holstein cattle, udder depth assessment, as a linear trait, usually shows moderate to high heritability (BROTHERSTONE et al. 1990; BROTHERSTONE 1994; ROUGHSEGE et al. 2000), in this analysis UD heritability is low. A possible explanation lies in the assessment recording used here. A high number of assessed females were in the final stage of lactation. At this time, the udder size is generally small, thus affecting the observed variability of the trait (GOYACHE et al. 2001a).

### Implications

Analysis of 10 type traits and a FS recorded using the current methodology applied in the major Spanish beef cattle breeds have been carried out. Traits can be grouped into two classes: (i) traits scoring skeletal and muscular development; and (ii) traits scoring adjustment to the breed standard. In general, the genetic variability found for the analysed traits would justify the inclusion of morphological assessment in the Asturiana de los Valles beef cattle breed sire selection programme.

However, the type classification system used here may be criticized. At first sight, the assessment methodology attaches great importance to breed standard. In the 1980s, when the morphological assessment system was implemented, many Spanish beef cattle breeds were endangered. Under these conditions, conservation of breed characteristics was a major goal for breeders. Moreover, the definition of some traits (FQ, R) is too broad, involving both skeletal and muscular development, insofar as they are difficult to understand on a biological basis. On the other hand, scoring type traits using subjective criteria from a desirability scale instead of a linear scale might result in an underestimation of the genetic variability affecting type classification and in a loss of biological relationships among traits (VUKASINOVIC et al. 1997). Taking all this into account, a re-consideration of the type classification system used in the Asturiana de los Valles beef cattle breed has been proposed (GOYACHE et al. 2001b), advocating the implementation of a linear type traits assessment system useful for evaluating the entire biological variability existing in the breed.

Nevertheless, the current type traits assessment system shows some advantageous characteristics. First, even though reasons which justify the significant weight of breed standard traits in the classification system are not so important at the moment, breed characteristics still show a large variability in Asturiana de los Valles, and the homogenization of breed appearance is a major goal for the breeders and ASEAVA. Secondly, the current classification system is easy to explain to breeders and is easily understood. Finally, assessments are easier to perform than in a linear classification system. ASEAVA's experts can classify an animal in 30–60 s, while a linear classification takes 3–4 min. This is an important advantage when classifying animals farmed under non-handled extensive conditions.

Before deciding on the implementation of a linear type assessment system in beef cattle, genetic (co)variances between the traits involved in the current classification system and economically important productive and reproductive traits must be ascertained. As genetic parameters of major productive and reproductive traits have been estimated in Asturiana de los Valles breed (GUTIERREZ et al. 1997; GOYACHE and GUTIERREZ 2001), this will provide an important focus for future research. Results from this paper may contribute to the knowledge of those type traits that show high genetic correlations with other type traits but which have low heritabilities or a doubtful interpretation. These traits could be dropped from the estimation of genetic correlations with productive or reproductive traits so as to avoid computational difficulties.

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