Traceabiity and genetic improvement in Pirenaica Cattle

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INTRODUCTION

In recent years, new information systems have been developed to guarantee traceability of animal products and veterinary epidemiological surveillance. European Union has obliged to each member state to create a computerized database to record the identity of all animals, all holdings and animal movements. In Spain, the traceability SIMOGAN – Sistema Nacional de Identificación y Movimiento de Ganado Bovino- was set up (BOE, 1999).

The Pirenaica beef cattle is an extensive population from Northern Spain that consist of about 20,000 individuals. The phenotypic information recorded by the SIMOGAN database consist of Carcass Weight (CCW), Carcass Conformation (CON), Fat Cover (FC), and Meat Colour (COL). From a different point of view, since 1988, a selection program has been applied based on a Weaning Weight (WW) index (Altarriba et al., 1996; Varona et al., 1997).

The objective of this study was to explore the possibilities of implementing new selection criteria for the Pirenaica Breed, given the information provided by the SIMOGAN database.

MATERIAL AND METHODS

Data

The individuals included in the analysis were purebred Pirenaica animals slaughtered between 1999 and 2007 in 12 slaughterhouses located in the Basque Country and Navarre (Spain). A summary of the data is presented in Table 1.

Model of Analysis

Data were analyzed using a multivariate animal model. The model of analysis for CCW, CON, FC and COL was:

$$y_{ijklm} = S_i + YS_j + H_k + SH_l + b{*}AGE_m + u_m + e_{ijklm}$$

where *S* was the Sex – 2 levels- , *YS* was the year-season -35 levels, 3 months per level -, *H* was the herd -579 levels- , *SH* was the slaughterhouse effect -12 levels- and *b* was the covariate on age at slaughter (AGE).

The model of analysis for WW was:

$$y_{ijkl} = S_i + YS_j + H_k + b{*}AR_l + u_l + e_{ijkl}$$

where *AR* was the Age of Recording. For WW, the *YS* effect included up to 73 levels.

A Bayesian multivariate analysis was performed for the five traits jointly with a pedigree of 55, 747 animals.

Table 1. Mean, standard deviation (SD) and coefficient of variation (CV) of the studied traits.

Trait	CCW	CON	FAT	COL	WW
N	20,010	15,808	13,739	3,477	15,561
Mean	297.7	3.604	2.161	2.257	264.8
SD	55.2	0.465	0.515	0.337	58.9
CV	18.5	12.9	23.8	14.9	22.2

Comparison of Selection Criteria

After (co) variance component estimation, we evaluated the potential consequences of the inclusion of CCW on the Selection Criteria. We defined three alternative selection criteria.

1.) **CCW-ST**: Single Trait genetic evaluation on CCW without individual information for the candidates of selection.

2.) **WW-ST**: Single Trait genetic evaluation on WW with individual information.

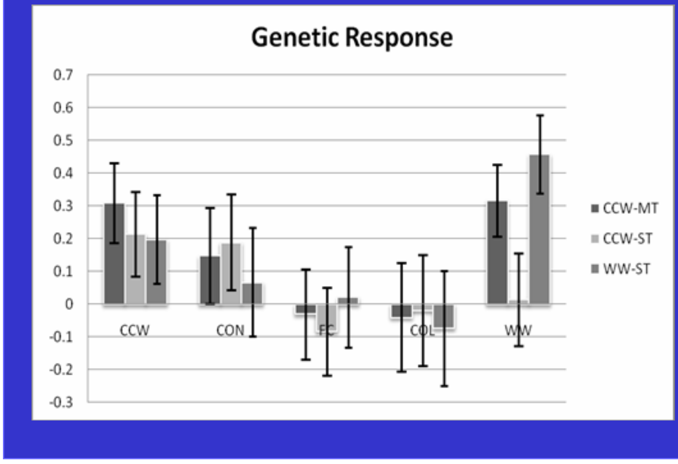
3.) **CCW-MT**: Multiple Trait genetic evaluation on WW and CCW, with and without individual records for the candidates of selection, respectively.

RESULTS

Table 2. Estimates of posterior mean (and standard deviation) for heritabilities (diagonal), genetic correlations (upper triangle) and residual correlations (lower triangle). Estimates with posterior intervals not including zero are in bold.

Trait	CCW	CON	FC	COL	WW
CCW	**0.34 (0.03)**	**0.30 (0.04)**	-0.05 (0.08)	**0.22 (0.05)**	**0.54 (0.03)**
CON	**0.34 (0.02)**	**0.28 (0.03)**	**-0.35 (0.04)**	0.00 (0.15)	-0.04 (0.06)
FC	**0.14 (0.02)**	**-0.08 (0.02)**	**0.19 (0.02)**	0.03 (0.10)	**0.23 (0.08)**
COL	0.06 (0.04)	**0.11 (0.03)**	-0.00 (0.03)	**0.23 (0.04)**	0.04 (0.10)
WW	**0.47 (0.03)**	**0.13 (0.03)**	0.02 (0.03)	0.08 (0.03)	**0.38 (0.02)**

Figure 1. Direct and Correlated Genetic Response (in phenotypic standard deviations) from sire and dam subpopulations for three alternative selection criteria (CCW-MT, CCW-ST and WW-ST)



CONCLUSION: There is enough genetic variability for selection in CCW, CON, FC, COL and WW. With respect to the current selection criteria (WW-ST), the percentage of increase for expected genetic response in CCW was 9% using only the data provided by the SIMOGAN database and 56 % with the combined use of the data from the breeders association (WW) and the traceability database (CCW).