

# MULTIPLE TRAIT GENETIC ANALYSIS OF GROWTH IN THE PIRENAICA BEEF CATTLE BREED

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**ABSTRACT:** One of the main objectives of selection for beef cattle is weight at slaughter. Live weights along growth are currently used as selection criteria under the hypothesis of a positive genetic correlation with weight at slaughter. In this study we have used data for weight at 120 (W120) and 210 (W210) days and at slaughter (WS) and the gain of weight between them ( $\Delta 120-210$  and  $\Delta 210-WS$ ) in the Pirenaica Beef Cattle Breed to increase our knowledge about the genetic and environmental relationships between different phases of growth. The posterior mean (and standard deviation) estimates of heritability were 0.343 (0.016), 0.347 (0.019), 0.349 (0.022), 0.292 (0.030), and 0.334 (0.058) for W120, W210, WS,  $\Delta 120-210$  and  $\Delta 210-WS$ , respectively. Further, genetic correlations were high and positive between weights at different ages (W120 and W210), but more moderate when related with weight at slaughter (WS). These results question the efficiency on the current scheme of selection. Genetic and residual correlations among gains of weight and immediately posterior weights ( $\Delta 120-210$  and W210 and  $\Delta 210-WS$  and WS) were positive and very high. However, genetic correlations between gains of weight and previous weights were low or null and residual correlations between them were negative (-0.30). The presence of these negative residual correlations suggests the existence of compensatory growth that is not considered in regular strategies of genetic evaluation.

**Keywords:** Beef Cattle, Growth, Genetic correlation, Residual Correlation.

## INTRODUCTION

One of the most relevant traits in beef cattle production is weight at slaughter (Golden et al, 1998; MacNeil, 2003; Bouquet et al., 2010). Unfortunately, phenotypic records cannot be available for candidates of selection. As a consequence, a widely used criterion of selection is the weight of individuals along different growth stages. This approach invokes the hypothesis of a positive genetic correlation with weight at slaughter (Meyer et al., 1993; Bennett et al., 1996; Altarriba et al., 2009, Bouquet et al., 2010). In particular, the breeding scheme developed by the Pirenaica breeders association (CONASPI - Confederación Nacional de Asociaciones de Vacuno Pirenaica) uses records between 110 and 310 days of age as predictors for weight at slaughter (Altarriba et al., 1996; Varona et al., 1997). However, the structure of those genetic correlations should be studied more deeply. As a consequence, the aim of this study is to estimate genetic and residual correlations between weight at different stages and gain of weight between those stages.

## MATERIAL AND METHODS

### Data

The dataset analyzed in this study included 25,894 records from individuals between 80 and 160 days of age that were attributed to weight at 120 days (W120), 18,283 between 170 and 250 days of age assigned to weight at 210 days (W210), and 23,204 of weight at slaughter (250-480 days of age), obtained by the division of the cold carcass weight by the average dressing percentage of the population. Live weights were provided by CONASPI, whereas slaughter records were registered into the SIMOGAN database (System of Identification and Registration the Movements of the Bovines). Moreover, we also calculated the gain of weight between 120 and 210 days of age ( $\Delta$ 120-210) and between 210 days and slaughter ( $\Delta$ 210-WSL) for those individuals where both records were available. Table 1 summarizes the main statistics for the analyzed traits. In addition, we used a pedigree of 94,931 individuals also provided by CONASPI.

**Table 1.** Means and phenotypic standard deviations for the analyzed trait.

Traits	N° Data	Mean	Standard Deviation
W120	25,894	163.23	40.09
W210	18,283	265.25	56.34
WS	23,204	481.46	91.04
$\Delta$ 120-210	8,815	119.34	41.28
$\Delta$ 210-WS	3,350	206.68	81.60

W120 is weight at 120 days of age, W210 is weight at 210 days of age, WS is weight at slaughter,  $\Delta$ 120-210 is gain of weight between 120 and 210 days of age,  $\Delta$ 210-WS is gain of weight between 210 and slaughter.

### Statistical Model

The above described data were analyzed using bivariate animal models which were taken in pairs. The following model was used to analyze W120, W210, and  $\Delta$ 120-210:

$$y_{ijklm} = N_i + S_j + R_l + b \cdot AGE_m + u_m + e_{ijklm}$$

Where  $N$  was season of birth -4 levels-,  $S$  was sex -2 levels-,  $R$  was herd -348 levels for W120, 386 levels for W210, and 231 levels for  $\Delta$ 120-210-,  $b$  was a covariate on age of recording in W120, W210, and days between the two records in  $\Delta$ 120-210 respectively,  $u$  was the additive genetic effect and  $e$  was residual effect.

The following model was used to analyze WS y  $\Delta$ 210-WS:

$$y_{ijklm} = N_i + S_j + M_k + R_l + b \cdot AGE_m + u_m + e_{ijklm}$$

Where  $N$  the season of birth -4 levels-,  $S$  was sex -2 levels-,  $M$  was slaughterhouse -14 levels-,  $R$  was the herd -623 levels for WS and 177 levels for  $\Delta 210$ -WS-,  $b$  was a covariate on age at slaughter for WS and days between the both weights for  $\Delta 210$ -WS respectively,  $u$  was the additive genetic effect and  $e$  was residual effect.

The analysis was performed using Bayesian inference with a Gibbs sampler algorithm (Gelfand and Smith, 1990) using the software program TM (Legarra et al., 2008). Bounded uniform distributions were assumed for systematic effects, variance components and covariates, and multivariate Gaussian distributions for additive genetic effects and residuals. The analysis was performed with a single long chain of 225,000 iterations after discarding the first 25,000.

## RESULTS AND DISCUSSION

The posterior mean and standard deviations for heritabilities, genetic and residual correlations for the five traits are presented in Table 2.

**Table 2.** Posterior Mean (and Standard Deviation) estimates of heritabilities (diagonal), genetic correlations (upper triangle) and for residual correlations (lower triangle)

Trait	W120	W210	WS	$\Delta 120-210$	$\Delta 210-WS$
W120	0.343 (0.016)	0.715 (0.027)	0.381 (0.050)	0.178 (0.064)	-0.014 (0.047)
W210	0.670 (0.010)	0.347 (0.019)	0.475 (0.047)	0.773 (0.026)	-0.020 (0.116)
WS	0.449 (0.023)	0.511 (0.026)	0.349 (0.022)	0.356 (0.082)	0.633 (0.062)
$\Delta 120-210$	-0.038 (0.023)	0.763 (0.009)	0.263 (0.039)	0.292 (0.030)	-0.013 (0.127)
$\Delta 210-WS$	0.047 (0.048)	-0.304 (0.044)	0.745 (0.024)	-0.321 (0.049)	0.334 (0.058)

W120 is weight at 120 days of age, W210 is weight at 210 days of age, WS is weight at slaughter,  $\Delta 120-210$  is gain of weight between 120 and 210 days of age,  $\Delta 210-WS$  is gain of weight between 210 and weight at slaughter.

These results confirmed heritability estimates over 0.30 for every trait, in agreement with previous estimates from the literature obtained in the same (Varona et al., 1997; Altarriba et al., 2009) or different populations (Bennett et al., 1996; Rios Utrera and Van Vleck, 2004; A. Bouquet et al., 2010). Moreover, a high and positive genetic correlation was observed between W120 and W210. However, the estimates between weights along growth and WS were positive but more moderate (0.38 between W120 and WS and 0.48 between W210 and WS). These results question

the efficiency on a scheme of selection based exclusively in records obtained in different phases of growth and reinforce the importance of the use of weight at slaughter provided by SIMOGAN database, as proposed previously in Altarriba et al. (2009).

Genetic and residual correlations among gain of weight and immediately posterior weights ( $\Delta 120-210$  and  $W210$  and  $\Delta 210-WS$  and  $WS$ ) were always positive and very high. On the contrary, genetic correlations between gain of weights and previous weights were low or null (0.18 between  $W120$  and  $\Delta 120-210$ , -0.01 between  $W120$  and  $\Delta 210-WS$  and -0.02 between  $W210$  and  $\Delta 210-WS$ ). These results suggest that the genetic determinism of previous phases of weight have very low predictive ability for the posterior behavior of growth.

Furthermore, it is remarkable that residual correlations between  $W210$  and  $\Delta 210-WS$  and  $\Delta 120-210$  and  $\Delta 210-WS$  were negative and around -0.30. The presence of these negative residual correlations may indicate the existence of compensatory growth in the Pirenaica beef cattle population, which also depreciates the value for the usual strategies of genetic evaluation.

In future, we will explore the relationship between traits using recursive models (Gianola and Sorensen, 2005; Varona et al., 2007), in special with their non-linear version (Lopez de Maturana et al., 2009; Ibañez-Escriche et al., 2010) with the aim of obtaining predictions of the additive genetic value that considers the effect compensatory growth.

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