Multivariate analysis of founder specific inbreeding depression effects in Pirenaica Beef Cattle

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Introduction

Inbreeding is defined as the probability of identity by descent at an autosomal locus caused by mating of related individuals (Wright, 1922; Malecot, 1948). The consequences of inbreeding have been usually associated with changes in mean and variance of quantitative traits (Charlesworth and Charlesworth, 1987).

Recently, some studies have proposed to model inbreeding depression through partial inbreeding coefficients associated with founder individuals (Lacy et al., 1996). This approach allows to attribute the effects of inbreeding depression to specific founders (Lacy et al., 1996) and its assumptions has been confirmed in several traits in pigs (Rodrigañez et al, 1998; Casellas et al, 2009a), sheep (Casellas et al., 2009b), dairy (Gulisika et al., 2006) and beef cattle (Carolino and Gama, 2008).

The inbreeding depression specific effects can be also model by using parametric distributions (Casellas et al., 2008) facilitating their generalization to a multivariate scope. The aim of this study is to define a multivariate model to analysis specific inbreeding coefficients and to present the results of their application to 6 traits of the Pirenaica beef cattle.

Material

For this study, we have used data for birth weight (BW), weight at 120 days (W120) and 210 days (W210), provided by CONASPI (Confederación Nacional de Asociaciones de Vacuno Pirenaico), and cold carcass weight (CW), conformation (CONF) and Fat Cover (FC), from the SIMOGAN (Sistema Nacional de Identificación y Movimiento de Ganado Bovino). A summary of the raw data used in this analysis is presented in Table 1.

Table 1. Number of individual (N), mean and standard deviation (SD) for BW, W120, W210, CW, CONF and FC.

	BW (Kg.)	W120 (Kg.)	W210 (Kg.)	CW (Kg.)	CONF	FC
N	52559	26188	15559	20011	15809	13740
Mean	41.66	163.5	264.8	297.7	3.67	2.16
SD	5.01	45.76	58.87	55.21	0.46	0.51

Methods

Partial and total inbreeding coefficients were calculated with the ENDOG program (Gutierrez et al., 2003), that uses the algorithms described by Meuwissen et al. (1992) y Lacy et al. (1996). Total inbreeding for the ith individual (F_i) was split following:

$$F_i = \sum_{j=1}^{f} F_{ij}$$

Where F_{ij} is the probability of identity by descent attributed to the jth founder on the ith individual. Moreover, f is the number of founders. For this study, we select the 150 founders highly represented on the total population.

The statistical model of analysis was:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \sum_{i=1}^{f} \mathbf{F}_i c_i + \mathbf{F}_R c_R + \mathbf{e}$$

Where **y** is the vector of phenotypic data (BW, W120, W210, CW, CONF and FC), **b** is the vector of systematic effects (season, year, sex, herd and a covariate with age of recording), **u** is the vector of breeding values and **e** is the vector of residuals. $\mathbf{F}_i$ is vector of partial inbreeding coefficients for the ith individual and $\mathbf{F}_R$ is the residual inbreeding coefficient:

$$\mathbf{F}_R = \mathbf{F} - \sum_{i=1}^{150} \mathbf{F}_i$$

Moreover, c_i is the inbreeding depression coefficient associated with the ith founder and c_r is the inbreeding depression coefficient associated with the residual inbreeding, and **X** and **Z** are the incidence matrices. A bayesian analysis was implemented by using the Gibbs sampler. The following prior distributions were assumed for **u**, e and $\mathbf{f}_i$.

$$\mathbf{u} \sim N(0, \mathbf{A} \otimes \mathbf{G})$$

$$\mathbf{c} \sim N(m, \mathbf{I} \otimes \mathbf{D})$$

$$\mathbf{e} \sim N(0, \mathbf{I} \otimes \mathbf{R})$$

Where **G**, **D** and **R** and the (co) variance matrices between breeding values, founder inbreeding depression coefficients and residuals, respectively. Moreover, m is the mean of the inbreeding depression coefficients. Prior distributions for **G**, **D**, **R**, **m** and **b** were assumed uniform. The analysis was performed with 225,000 iterations after discarding the first 25,000.

Results and Discussion

Posterior mean and standard deviation for the variance components and the additive genetic and inbreeding depression coefficients are presented in Table 2 and 3. The results of heritatibilities and additive genetic correlations are in the range of expected values in the literature (Rios-Utrera and Van Vleck, 2004; Altarriba et al., 2009).

Correlations between inbreeding depressions were in general of the same direction than the additive genetic correlations, although in some cases, the posterior distributions for the additive genetic and inbreeding depression correlations do not overlap (ie. BW and W120). These results indicate that the genetic regulation of both correlations are not regulated by the same genes or at least they act in a different way.

Table 2. Additive (σ^2_a), founder inbreeding depression (σ^2_d) and residual (σ^2_e) variances and average inbreeding depression (m) for BW, W120, W210, CW, CONF and FC.

	BW	W120	W210	CW	CONF	FC
σ^2_a	7.19 (0.21)	338.87 (14.70)	686.07 (38.26)	445.88 (30.84)	0.044 (0.004)	0.028 (0.003)
σ^2_d *	1.69 (0.64)	111.78 (44.64)	414.04 (200.03)	125.57 (52.43)	0.016 (0.010)	0.010 (0.007)
σ^2_e	14.05 (0.16)	629.60 (11.24)	1283.91 (30.44)	839.36 (23.43)	0.112 (0.003)	0.127 (0.003)
m*	-0.31 (0.15)	-2.67 (1.27)	-4.91 (2.43)	-6.24 (1.53)	0.008 (0.018)	-0.028 (0.016)

* The estimates were calculated for F=0.10

Table 3. Additive genetic (upper diagonal) and inbreeding depression (below diagonal) correlations between BW, W120, W210, CW, CONF and FC.

	BW	W120	W210	CW	CONF	FC
BW	-	0.30 (0.02)	0.26 (0.03)	0.51 (0.03)	0.11 (0.05)	-0.06 (0.06)
W120	0.46 (0.23)	-	0.80 (0.02)	0.43 (0.04)	-0.10 (0.05)	0.09 (0.06)
W210	0.64 (0.20)	0.74 (0.16)	-	0.54 (0.04)	-0.09 (0.06)	0.20 (0.06)
CW	0.32 (0.34)	0.18 (0.31)	0.22 (0.33)	-	0.40 (0.05)	-0.12 (0.07)
CONF	0.09 (0.35)	0.02 (0.35)	0.27 (0.35)	0.35 (0.31)	-	-0.24 (0.07)
FC	0.07 (0.42)	0.05 (0.39)	0.04 (0.40)	0.18 (0.39)	-0.35 (0.39)	-

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