Direct And Maternal Genetic Parameters For Birth And Weaning Weight Traits In The “Creole Sheep Of Chiapas”

Reyes López-Ordaz*, Iván Olivera-Vega*, José M. Berruecos*, Marisela Peralta-Lailson [1], Raúl Ulloa-Arvizu*, *Carlos G. Vásquez**

Introduction

A large population of Creole sheep mainly in the Highlands of Chiapas originated from the Spanish breeds Churra, Lacha and Manchega introduced in the XVII century has remained geographically isolated and closed to other breeds. These Creole sheep has socio-cultural and economic importance in the region (Perezgrovas 2009).However there is not information available of genetic parameters for growth traits to be use in a breeding programs.

Several authors have recently assessed genetic parameters of the direct, maternal and permanent environment for growth traits in different breeds (Rashidi et al., 2008, Ajoy et al., 2008). Genetic and phenotypic studies have shown that correlations between the direct genetic and maternal effects have unfavorable relationships. (Co)variances and genetic parameters for growth traits in the “Creole sheep of Chiapas” have not been estimated; therefore the objective of this research was to assess genetic parameters at birth and weaning weight in Creole sheep.

Material and methods

This study was carried out at the Center for Research and Technology Transfer of the Autonomous University of Chiapas (CUITT, UNACH), located in “Los altos de Chiapas” (Highlands); 1780 m above sea level and 16°32'24 N and 92°28'19" W; annual mean temperature 13°C and annual rainfall 1059.2 mm. All animals grazed for 6 to 8 hours on pastures covered with kikuyu grass (*Pennisetum clandestinum*), penned at afternoon and night, additional nutritional supplement was provided based on whole ground corn (cob and stubble) and soybean meal, including mineral and salts. Sanitary management focuses on control *Fasciola hepatica*, *Moniezia expansa*, gastroenteric worms, *Oestrus ovis* and coccidiosis. Ewe were exposed to rams in single-sire pens once a year for a 60 days period, lambing begin in November to the end of December from 1991 to 2006, weaning was at 3 month of age. Records of birth (BW) and weaning (WW) weights of 1326 progeny were used for the analysis; pedigree represents 53 sires and 523 ewes.

Statistical analyses. A single-trait individual model was performed in a full model for fixed effects for the two traits; litter size (single, twin), parity of dam (1,2,3,4), birth year (1991-2006), sex of lamb (male or female) and dam biotype (white, brown or black); days for

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[1] Universidad Autónoma de Chiapas, México

*Facultad de medicina Veterinaria y Zootecnia, Universidad Nacional Autónoma de México 04510, México DF. carlosgv@unam.mx

weaning was included as a covariate for weaning weight (mean 89 days). The double interactions were not significant ($P> 0.05$) (JMP5, 2002) therefore, were removed from the final model. (co)variance components were estimated through the REML, ASREML (version 1.10) Guilmour et al., 2001. Six Univariate animal models were fitted to estimate the genetic parameters for each trait by ignoring or including various combinations of maternal genetic and permanent environmental effects as (1) $\mathbf{Y}=\mathbf{Xb}+\mathbf{Z_1a}+\mathbf{e}$; (2) $\mathbf{Y}=\mathbf{Xb}+\mathbf{Z_1a}+\mathbf{Wap}+\mathbf{e}$; (3) $\mathbf{Y}=\mathbf{Xb}+\mathbf{Z_1a}+\mathbf{Z_2m}+\mathbf{e}$ and cov(am)=0; (4) $\mathbf{Y}=\mathbf{Xb}+\mathbf{Z_1a}+\mathbf{Z_2m}+\mathbf{e}$ and cov(am)=$A\sigma_{am}$; (5) $\mathbf{Y}=\mathbf{Xb}+\mathbf{Z_1a}+\mathbf{Z_2m}+\mathbf{Wap}+\mathbf{e}$ and cov(am)=0; (6) $\mathbf{Y}=\mathbf{Xb}+\mathbf{Z_1a}+\mathbf{Z_2m}+\mathbf{Wap}+\mathbf{e}$ and cov(am)=$A\sigma_{am.}$ where: **Y** is the vector of records for birth (BW) and weaning (WW) weights; **b** is the vector of fixed effects from the final model; **a** is the vector of additive genetic effect of the lamb; **m** is the additive-maternal genetic vector; **ap** is the maternal permanent environment vector; **X**, **Z**, **W** are the incidence matrices that relate this effects to **Y** and **e** is the vector of random residual effects. Chi square test was performed for the Likelihood Ratio values (-2logL), in order to choose the appropriate model for each trait (Meyer, 1992). Genetic and phenotypic correlations were estimated trough a bivariate analysis.

Results and discussion

Least Square means for BW and WW was 2.48 ± 0.52 kg and 8.96±2.54 kg respectively. Males were 5% heavier than females for BW and WW ($P<0.01$); single-born lambs were 41.53% heavier at birth compared with those from multiple deliveries ($P<0.01$), the difference in favor of single-born animals decreased with age, being13.90% at WW; the lowest lamb weight were in primiparous ewes, being the greatest weight in sheep from the third and on for both traits ($P<0.001$). All three biotypes showed similar performance ($P>0.05$) for the studied traits; similar results for fixed effects has being observed in other breeds Rashidi et al., 2008. Genetic parameters for BW and WW under the six models used in this study are in Table 1.

Table 1. Direct additive heritability (h^2_a), maternal heritability (h^2_m), correlation additive-maternal (r_{am}) and ratio of permanent environment variance (c^2) for birth weight (BW), weaning weight (WW) for Chiapas Creole sheep.

Trait	Model	h_a^2±S.E	h_m^2±S.E	r_{am}	c^2±S.E	-2logL
BW	1	0.37±0.06				405.13[a]
	2	0.17±0.06			0.20±0.03	422.90[b]
	3	0.09±0.05	0.23±0.04			425.67[b]
	4	0.08±0.05	0.20±0.04	-0.38±0.08		425.93[b]
	5	0.10±0.05	0.15±0.06		0.07±0.05	424.00[bc]
	6	0.15±0.09	0.24±0.09	-0.58±0.09	0.11±0.08	427.19[bd]
WW	1	0.22±0.07				-1195.58[a]
	2	0.08±0.06			0.12±0.04	-1190.42[b]
	3	0.08±0.06	0.11±0.04			-1191.16[b]
	4	0.15±0.09	0.17±0.07	-0.51±0.29		-1190.58[b]
	5	0.07±0.06	0.04±0.05		0.08±0.06	-1190.10[b]
	6	0.14±0.09	0.09±0.08	-0.61±0.34	0.08±0.06	-1189.61[b]

S.E=standard error, [a,b,c,d] Values with different letters among models are statistically different ($p<0.05$) Likelihood Ratio (-2logL) Model 1: direct additive effect, Model 2: direct and additive maternal effect, model 3: additive direct effect and maternal permanent environment effect.

Birth Weight Additive direct heritability (h^2_a), depended on the model used, in this study the ranges are between 0.08 to 0.37, similar to Gizaw et al., 2007 and Bosso et al., 2007. h^2_a decreased when the effect of permanent maternal environment was included to 0.17, similar to published by Mandal et al. (2006). The inclusion of the maternal genetic effect and the proportion of maternal permanent environmental in the model affect negatively to h^2_a, h^2_m and c^2 0.10, 0.15 and 0.07, respectively. The h^2_a was similar to the results by Mandal et al. (2006). The h^2_m calculated with Model 6 was similar to the one mentioned by Maxa et al., 2007. The c^2 value is within the range mentioned in literature (0.01 to 0.20), Mandal et al., 2006. According to Neser et al. (2001), the influence of the permanent environment variance (c^2) on BW is due to the effect of uterus and multiple births; furthermore, the c^2 exclusion from the model leads to overestimation of h^2_m values, particularly for birth weight.

The correlation between direct and maternal genetic effects for growth traits were low to medium and consistently negative, suggesting a possible antagonism between additive genes of the lamb and the mother genes that contribute to the maternal effect. For BW it was similar to what is reported by Ligda et al. (2000).

Weaning Weight The additive direct heritability (h^2_a) was between 0.07 to 0.22, similar result was reported by Safari et al., 2005 in dual purpose breeds (0.02 to 0.19). When maternal effect is added, h^2_a decreased by 36%, while the h^2_m was 0.08.

The Chi square test shown model 6 as the appropriated model for estimation, additive and maternal heritability show low values: h^2_a 0.14±0.09 and h^2_m 0.09±0.08. On the other hand, c^2 value was 0.08, which is within the range reported in literature (Safari et al., 2005).

Correlation between maternal and direct genetic effects was -0.51 to -0.61 for weaning weight, lower than the one reported by Maria et al. (1993) and El Fadili et al. (2000). Hagger (1998) concluded that the high correlation between the direct additive and maternal effects (in negative values) may be caused by the absence of the of herd-sire or year-sire effects in the model as mentioned by Lewis and Beatson. (1999), they also mention that it may be caused by the exclusion of other effects in the model (number of sire per herd), or by the lack of adjustment of any residual covariance (such as lamb growth and ewe milk production). Similar results have being reported (Al-Shorepy et al., 2002), concluding that direct heritability is overestimated by ignoring the maternal effect. The genetic and phenotypic correlations (0.34 ± 0.03; 0.81 ± 0.13 for BW with WW), are similar to those reported by Safari et al., 2005; Gizaw et al., 2007. Heritabilities, phenotypic and genetic correlations for BW and WW, estimated from a bivariate model, was very similar to the previous ones 0.38±0.07; 0.19±0.06 for BW and WW respectively, being the genetic and phenotypic correlation 0.81±0.13 and 0.34±0.03 respectively.

Conclusion

Results in this research indicate that birth weight and weaning weight in Chiapas creoles sheep were low and perhaps are the smallest sheep in Mexico. These weights are affected by some environmental factors. Assessed values for direct and maternal heritability and permanent environmental effects for birth weight and weaning weight for this herd are within ranges in literature. The variance components, according to the proposed models, were affected in its accuracy due to data structure and size.

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