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Comparison between Ecuadoran Genotypes of Cavy Litters (*Cavia porcellus*) and Cavies Bred in Peru

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ABSTRACT

Background: The threat of extinction posed on different unprotected genotypes from the Andean Ranges of Ecuador is calling for new studies and preservation measures to keep the biological diversity of the area, which has enormous perspectives for human nutrition. The aim of this paper was to compare the sizes and weights up to the weaning stage of native Ecuadoran cavy litters in Azuay province, with the Peruvian-bred line.

Methods: The study took place on Irquis experimental farm, belonging to the Faculty of Agricultural Sciences, University of Cuenca, Ecuador. The database was based on the records of breeding animals screened among farmers from Azuay and Cañar, and it included their phenotypic traits.

Results: No significant differences were observed in the month of parturition, or the number of parturitions, or the genotype regarding the size of the litter at weaning. The data from Azuay and Peru were similar in terms of litter size at birth (3.1 and 3.2, respectively). However, it was higher regarding litter weight at birth and weaning (432 and 837 g, compared to the 313 and 570 g from Azuay, but no different from Cañar).

Conclusions: The native genotypes from Azuay and Cañar were inferior to the Peruvian genotype, in terms of birth weight and weaning weight. Azuay was no different from Peru, according to litter size at birth or weaning. The potential observed in this genotype should be further developed.

Key words: *Peruvian cavies, birth, weaning*

INTRODUCTION

For several decades, the study of cavies as a meat producing species has been led by Peruvian researchers, and their success in the genetic breeding of various lines, like Andean and Peru, have been reported by Chauca (1997), Xicohtencatl-Sánchez, Barrera, Orozco, Torres, and Monsiváis (2013). In the central coast of Peru, reports of the same Peruvian lines have been made by Nayarit, México, and Rodríguez, Gutiérrez, Palomino, and Hidalgo (2015). However, studies on multiple genotypes from the Andean mountain range of Ecuador have lacked proper attention.

The danger of extinction of different, non-studied, and unprotected genotypes from the Andean ranges of Ecuador has forced researchers to study and suggest preservation measures to maintain the region's biological wealth. This area has enormous perspectives in terms of nutrition globally.

The aim of this paper was to compare the sizes and weights up to the weaning stage of native Ecuadoran cavy litters in Azuay and Cañar provinces, and the genetically bred Peru line.

MATERIALS AND METHODS

This study was conducted on Irquis experimental farm, in Irquis, property of the Faculty of Agricultural Sciences, University of Cuenca, in Victoria Portete parish, Cuenca Canton, Azuay province, km 23 via Giron, 2 664 m above sea level, with temperature values between 7 and 12 °C.

The database was based on the records of local breeding animals screened among farmers from Azuay and Cañar, and it included the phenotypic traits for native animals of Ecuador described in the literature (Avilés, 2016). The animals underwent a period of adaptation and quarantine before the introduction of the experimental shed, and various clusters were arranged depending on their origin. The animals were matched according to the size of the cage, 1:5 male and females, respectively, making up to 15 matching cages with the same structure.

Feeding was mixed, and food supply was based on the live weight, using weekly calculations of a forage mix made of graminaceae and leguminosae *Lolium perene* and *Trifolium repens*, including 15.8% dry matter, plus a supplement based on commercial feed containing 20.2% protein, 87.5% dry matter, plus water supplied *ad libitum*.

Upon adaptation, animals of the same genotypes were matched (5 males per 25 females). Female fertility was determined by observation and palpation. During the first three weeks, 4 females had died: 1 Azuay, 2 Cañar, and 1 Peru lines.

Litter identification with their respective mothers was done on a daily basis at feeding. The data were recorded in the corresponding field charts, which included the date, and the number and weight of newborn animals along with the code in the mother's ring. Weaning took place at 15 days. The dependent variables were, SLB (size of litters at birth); SLW (size of litters at weaning); WLB (weight of litters at birth), and WLW (weight of litters at weaning).

A linear mixed-effect model analysis of variance was used through R software, version 3.4.4 (2018), which included the fixed effects: genotypes (Azuay, Cañar, and Peru), number of parturitions (1 and 2), month of parturition (1, ..., 12), and breeder (1, ..., 63), as random effect. The Tukey's test was used as well. A total of 151 parturitions were included.

RESULTS AND DISCUSSION

Significant differences were only observed in the effect of genotypes (Table 1). The remaining effects showed no significant effects. The high variabilities observed were also influential; hence, the determination coefficients found for the model were acceptable for this field study.

Table 1. Results of weight variance analysis of different traits

Variation source	lg	SLB	SLW	WLB	WLW
genotype	2	0.003	0.076	0.000	0.000
mother	62	0.221	0.684	0.686	0.723
No. of parturition	1	0.350	0.161	0.222	0.269
month	11	0.352	0.493	0.182	0.129
error	72	-	-	-	-
r^2		0.58	0.50	0.59	0.60
vc		0.39	0.44	0.47	0.49

The genotypes differed significantly in terms of litter size and litter weight at birth and weaning, respectively, though no significant differences were observed at birth. Rodríguez *et al.* (2015) did find significance in the season-parturition number interaction for weight of litters at weaning. They also found significance for the season in the same variables used in the current study. A steady and constant management by the personnel, similar features of the cages, and stable and satisfactory nutrition throughout the experimental period explained why months did not influence on the variables.

Concerning the number of parturitions in Peru, Rodríguez, Palomino, Hidalgo, and Gutiérrez (2013) found significant influences of this factor on the weight of litters, and at weaning. Later, the same authors (Rodríguez *et al.*, 2015) found significant differences for the live born, and the weight of litters at birth and weaning, but they coincided with this work in that the size of litters at weaning was not influenced by this factor.

The size of litters at birth (SLB) showed that genotypes Azuay and Peru did not show any statistically significant differences ($P<0.05$) between themselves, but both differed from Cañar cavies, which was approximately 0.7 animals in the litter (Table 2). The maximum size found showed high variety (7 animals for Peru and 5 for Cañar and Azuay). Xicohtencatl-Sánchez *et al.* (2013) reported a large Peru litter at birth (3.46) in the same genotype. Chauca (1997) and Rodríguez *et al.* (2015) reported 2.95 and 2.92, respectively, except for cavies Peru and the ones used in this study.

Table 2. Size and weight of litters at birth and weaning of the three genotypes

Traits	Genotypes						SIG.
	Azuay		Cañar		Peru		
	Mean	SE	Mean	SE	Mean	SE	
SLB	3.1	0.15^{b}	2.4	0.17^{a}	3.2	0.18^{b}	*
SLW	2.7	0.14^{a}	2.3	0.16a	2.8	0.18^{a}	NS
WLB	313.5	19.61^{a}	246.5	22.01a	432.0	24.36^{b}	*
WLW	570.8	38.47^{a}	457.0	43.18^{a}	837.0	47.79^{b}	**

NS: Not significant

Means with unequal letters on the same row differ significantly: *P<0.05 ** P<0.01.

The size of litters at weaning (SLW) was the only non-significant variable. Chauca (1997), Barrera (2010), and Rodríguez *et al.* (2015) found means of 2.18, 2.10, and 2.34 animals, lower than the results of this investigation. However, the studies of Xicohtencatl-Sánchez, Barrera, Orozco, Torres and Monsiváis (2013), and Osorio (2016) resulted in 0.2 animals, slightly higher than Cañar cavies.

The means and low variabilities from genotypes Azuay and Peru were considered acceptable. Although mortality was greater during lactation (14 days), it was not very high, the mean was almost 3 cavies, with better average weights than the Cañar animals. Genotype Cañar showed the lowest mortality.

Regarding weight of litters at birth (WLB) (Table 2), there was a clear difference between Peru and the native genotypes, since no differences were observed in the latter among themselves. Osorio (2016) found 340 g, similar to Azuay cavies, but less than the genetically bred Peruvian types used in this research, which were similar to the findings of Rodríguez *et al.* (2015), about 431 g.

The evidence has shown that improvements of Peruvian lines, with 668 g (Chauca, 1997), 692 g (Rodríguez *et al.*, 2015), and 634 g (Osorio, 2016), represented high litter weights at weaning. The native Azuar and Cañar cavies, which were not selected, had lower weights. This research found that the genetically bred Peru line cavies were superior to previous studies done of the same line. They were even higher than the Azuar and Cañar cavies. Management and feeding conditions played a key role in the improvements of the genetically bred and Azuay cavies, which came close to 600 g.

CONCLUSIONS

The native genotypes Azuay and Cañar were inferior to the Peru genotype in terms of birth weight and weaning weight. Azuay was no different from Peru, according to litter size at birth or weaning. The potential observed in this genotype should be further developed.

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AUTHOR CONTRIBUTION

Author participation included the following: Conception and design of research: CJRJ, GEGV; data analysis and interpretation: CJRJ, JRC, JTP, PNE, JQG, GEGV; manuscript redaction: CJRJ, JTP, GEGV.

CONFLICT OF INTERESTS: None