

## GENETIC PARAMETERS ESTIMATES FOR WEIGHT GAINS OF SANTA INÊS SHEEP USING TWO-TRAIT MODEL

Joiane A. da Porciúncula<sup>\*1</sup>, Anderson A. C. Alves<sup>1</sup>, Ciro T. M. Júnior<sup>1</sup>, Diego R. de Sousa<sup>2</sup>, Michelle S. da Silva<sup>3</sup>, Raimundo N. B. Lôbo<sup>4</sup>

<sup>\*</sup>Undergraduate student; Universidade Estadual Vale do Acaraú (UVA); Av. da Universidade, 850; Campus Betânia; 62040-370 – Sobral - CE; <sup>1</sup>UVA, Sobral - CE; <sup>2</sup>PPG em Zootecnia UVA/Embrapa Goats and Sheep, Sobral - CE; <sup>3</sup>PPG em Produção Animal, Mossoró - RN;

<sup>4</sup>Embrapa Goats and Sheep, Sobral - CE

<sup>\*</sup>joyane\_araujo@hotmail.com

The growth speed evaluation in meat animals it is fundamental to check the efficiency of production. This growth speed can be evaluated by taking into account weight gain in life stages of animals. These gains, expressed in kg/day or g/day reflect the animals' productive performance, being of great importance in genetic improvement programmes for selection and genetic evaluation of animals. The genetic parameters provide important information and are necessary to predict direct and correlated answers, assisting in the choice of more appropriate selection methods. Modern sheep slaughter seeks to maximize the efficiency of exploration through the selection of precocious animals, both in relation to their age for slaughtering and the reaching of reproductive age. The aim of this study was to estimate Santa Inês sheep's genetic parameters for weight gains from birth to weaning (WG1), from weaning to slaughter (WG2) and from weaning to the age of one year (WG3). The data used in this study come from a flock which belongs to the company Gaasa Alimentos LTDA, located in Inhumás (a town in the Brazilian state of Goiás), and they are part of the Programme of Genetic Improvement of Goats and Sheep (GENECOC), managed by the company Embrapa Goats and Sheep. The parentage matrix used consisted of 13,440 animals. Because they are slaughtered before turning one year old, the ones with information for WG2 do not present information for WG3. Two two-trait analyses were carried out, one of which contained WG1 and WG2 and the other with WG1 and WG3, avoiding endangering the samples if it was carried out analysis of WG2 with WG3. This kind of situation usually brings about difficulties of convergence for this method. The analyses were carried out by the Derivative-Free Restricted Maximum Likelihood method (DFREML), using the MTDFREML software. Both the additive direct genetic random effect and the fixed one relating to a contemporary group (animals born in the same season and year, with the same type of birth and sex, as well as subjected to the same handling) were taken into account for the all traits. The additive maternal genetic random effect as well as the permanent maternal environment, the fixed for class of maternal age in parturition, and the age at weaning covariate (mean of  $55.69 \pm 9.56$  days) were used for WG1. The age at weaning (mean of  $141.80 \pm 42.27$  days) covariate was also used in the models for WG2 and WG3, while the age at slaughter covariate was used in the model for WG2. The means for WG1 ( $n = 7,330$ ), WG2 ( $n = 2,168$ ) and WG3 ( $n = 963$ ) were respectively  $0.211 \pm 0.053$  kg/day,  $0.221 \pm 0.070$  kg/day and  $0.094 \pm 0.018$  kg/day. The direct heritabilities for the traits WG1, WG2 and WG3 were 0.08, 0.06 and 0.22, respectively, and the maternal heritabilities for WG1 was 0.07. The genetic correlations, direct and maternal ( $m =$  maternal), were: WG1 x WG2 (0.29); WG1 x WG3 (0.65); WG2 x WG1m (0.29); WG1 x WG1m (-0.50); e WG3 x WG1m (-0.13). The estimative values are within the expected for a commercial population subjected to selection.

**Keywords:** animal model, genetic correlations, heritability

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