



HAL
open science

Genetic parameters of litter size in Creole goat and their implication for a breeding programme including adaptation traits

Mélanie Gunia, Nathalie Mandonnet, Gisèle Alexandre, Michel Naves,
Florence Phocas

► To cite this version:

Mélanie Gunia, Nathalie Mandonnet, Gisèle Alexandre, Michel Naves, Florence Phocas. Genetic parameters of litter size in Creole goat and their implication for a breeding programme including adaptation traits. *Advances in Animal Biosciences*, 2010, 1 (2), pp.402-403. 10.1017/S2040470010000300 . hal-01193769

HAL Id: hal-01193769

<https://hal.science/hal-01193769v1>

Submitted on 29 May 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Selection Index

The selection index will include traits measured during performance recording. These traits can be the same as in the objective or correlated to them. They will be adapted from the French sheep performance recording. Pre-weaning growth and reproduction parameters such as fertility and litter size will be recorded. In addition to these traits, post-weaning growth and faecal egg count (FEC) will also be recorded. FEC gives an indication of the level of parasitism of the animals.

Genetic parameter estimation

The genetic parameters were estimated to calculate the weighting of the traits in the index (Gunia *et al.*, 2010b). The experimental Creole goat flock at INRA Gardel provided enough data for the calculation of the genetic parameters. More than 20 years of data about growth and reproduction traits were available.

Organisation of the breeding programme

The mating scheme will be designed. A sample of interested farmers (owning 300 does in total) will select the Creole goat. They will sell improved reproducers to a "user" group of farmers. These users will rear Creole goats and sell them for meat purpose, either in totally pure breed systems, or by using Creole does as a maternal line for crossbreeding. The different organisations of the programme will be studied with extension services to choose the most adapted solution.

Conclusion

As it happened for other indigenous breeds, the value of the Creole goat was long underestimated (Gauly *et al.*, 2010). Technical, economical, and genetic factors were taken into account in this programme to allow a more efficient selection of the Creole goat. The disease resistance characteristic of Creole goat was emphasised along with growth and reproduction traits. All participants (farmers, research, extension services) were integrated in this project.

Acknowledgements

The authors thank Ranjit Manicom and Marie-Hélène Madassamy (Carbicoop), Régis Alexandre (Chambre d'Agriculture) and Rémy Arquet (INRA Gardel).

References

- Gauly M, Besbes B and Pinard-van der Laan MH *et al.* 2010. Animal Genetic Resources (in press).
Gunia M, Mandonnet N, Arquet R, de la Chevrotière C, Naves M, Mahieu M and Alexandre G 2010a. Animal (in press).
Gunia M, Phocas F, de la Chevrotière C, Bambou JC and Mandonnet N 2010b. In Proc 9th WCGALP. Leipzig, Germany.
Mandonnet N, Menendez-Buxadera A, Arquet R, Mahieu M, Bachand M and Aumont G 2006. Animal Science 82, 283–287.
Mandonnet N, Naves M, Gunia M, Arquet R and Alexandre G 2010. 10th International Conference on Goats. IGA. Recife, Brazil.

doi:10.1017/S2040470010000300

Genetic parameters of litter size in Creole goats and their implication for a breeding programme including adaptation traits

M. Gunia¹, N. Mandonnet^{1†}, G. Alexandre¹, M. Naves¹ and F. Phocas²

¹INRA UR143, Unité de Recherches Zootechniques, 97170 Petit-Bourg, F.W.I.; ²INRA Génétique Animale et Biologie Intégrative, 78352 Jouy en Josas, France

Introduction

The Creole goat of Guadeloupe is a small-sized breed reared for meat. This breed, well adapted to its environment, has strong reproductive qualities (Alexandre *et al.*, 1997). The prolificacy of this breed is high, around 2.1. Farmers want to maintain this prolificacy, but without increasing it. Studies were needed to determine how to analyse this trait.

† E-mail: Nathalie.Mandonnet@antilles.inra.fr

Material and methods

The performances were collected in the Creole goat flock of INRA-Gardel in Guadeloupe from the past 30 years. Climate is tropical humid with a marked dry season. Goats grazed all year round. Only does were supplemented during lactation. The reproduction rhythm was of 3 kidding in 2 years. The first kidding happened at 16 months. The litter size (LS) at birth was recorded at each kidding. Data were available for 1962 does born from 273 sires and 903 dams.

Litter size was considered as a character of the mother. Two different models were studied using ASREML software developed by Gilmour *et al.* (2006). Model 1 was a multitrait model. Litter size at parity 1, 2 and 3 were considered as three genetically different traits. They were written LS1, LS2 and LS3. Model 2 was a repeatability model. Litter size was considered to be the same trait over time and was written LSt. Random effects were additive direct and residual for both models. Model 2 also included a permanent environmental effect related to the repeated records of does over parities. A combined effect of cohort-sex was found to be significant in both models. Parity of the doe was added as a fixed effect for model 2.

Results

LS1, LS2 and LS3 were 1.7, 2.0 and 2.1 kids respectively with a standard-deviation of 0.6. LSt was 2.1kids \pm 0.7.

For model 1, the same genetic variance of 0.04 was found for LS1, LS2, and LS3. Heritabilities and correlations were reported in Table 1. The heritabilities were moderate and very similar for the three parities, with a small decrease at the third parity. The phenotypic correlations were low, whereas the genetic correlations were very high. The genetic parameters for model 2 (table 2) were close to those found in model 1. Heritability was the same and the genetic variance was similar. Repeatability was moderate.

Heritabilities for LS1 were similar to those found by Bagnicka *et al.* (2007) for Polish and Norwegian goats, where heritabilities were 0.14 and 0.18 at first kidding for each breed respectively. For LS2 heritabilities were also on the same range. LS was within the range of heritabilities reported by Shrestha and Fahmy (2007) for different goat breeds.

Preliminary studies showed that the genetic correlation between litter size and faecal egg counts was positive (and thus unfavorable). The faecal egg counts are a practicable and valuable way to evaluate the genetic resistance to gastrointestinal parasites (Woolaston and Piper, 1996).

Table 1 Litter size at parity 1, 2 and 3 estimated with multitrait model (Model 1). Heritability (with its standard-error) on the diagonal, phenotypic correlation above and genetic correlation below the diagonal

	LS1	LS2	LS3
LS1	0.12 \pm 0.01	0.18	0.16
LS2	0.95	0.12 \pm 0.01	0.15
LS3	0.98	0.97	0.10 \pm 0.01

Table 2 Estimated genetic parameters for litter size considered as one character with repeatability model (Model 2)

	σ_a^2	σ_{pe}^2	σ_e^2	σ_p^2	h_a^2	c^2	R
LSt	0.05	0.02	0.36	0.43	0.12 \pm 0.02	0.05 \pm 0.01	0.16

σ_a^2 = direct additive genetic variance; σ_{pe}^2 = permanent environmental variance; σ_e^2 = residual variance; σ_p^2 = phenotypic variance; h_a^2 = direct heritability; c^2 = permanent environmental effect; R = repeatability \pm standard error.

Conclusion

Litter size can be considered as the same trait over time, at least for parities 1, 2 and 3. The genetic correlations between LS1, LS2 and LS3 were close to unity. All records had equal genetic variance. If these results were confirmed for the next parities, we could consider repeatability model as a better model to estimate litter size. Increasing litter size would lead to an increase of faecal egg count. When the litter size increased, the infection level and sensitivity to the gastrointestinal parasite increased too. It would also lead to a higher pre-weaning mortality. Targeting a stabilisation of the variability of the litter size seems to be the most sustainable solution for a selection programme.

References

- Alexandre G, Aumont G, Fleury J, Mainaud JC and Kandassamy T 1997. INRA Productions Animales 10, 7–20.
 Bagnicka E, Wallin E, Lukaszewicz M and Adnoy T 2007. Small Ruminant Research 68, 256–262.
 Gilmour AR, Gogel BJ, Cullis BR and Thompson R 2006. ASReml User Guide Release 2.0. VSN International Ltd, UK.
 Shrestha JNB and Fahmy MH 2007. Small Ruminant Research 67, 113–125.
 Woolaston RR and Piper LR 1996. Animal Science 62, 451–460.