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Genetic parameters for body weight, reproduction, and parasite resistance traits in the Creole goat¹

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ABSTRACT: We estimated the genetic parameters for BW, reproduction, and parasite resistance traits to implement a breeding program for the Creole goat. The traits were preweaning BW at 70 d of age (BW70d), BW at 11 mo of age (BW11), fecal egg count at 11 mo of age (FEC11) for all animals, packed cell volumes of lactating does (PCV), and their fertility (FER) and litter size (LS). We analyzed about 30 yr of data, which included 18,450 records on 11,970 animals from the INRA experimental flock in Guadeloupe (French West Indies). Heritability estimates were low for reproduction traits (0.11 ± 0.02 for LS and FER) to moderate for production traits (0.32 ± 0.03 for BW11; $0.20 \pm$

0.03 and 0.08 ± 0.02 for the direct and maternal heritability estimates of BW70d, respectively). Heritability estimates for gastrointestinal nematode resistance traits were situated in an intermediate range (0.13 ± 0.05 for PCV and 0.18 ± 0.04 for FEC11). Genetic correlations between FER, PCV, BW11, and the maternal effect of BW70d were altogether positive, whereas LS and FEC11 were almost uncorrelated phenotypically and genetically. These correlations are very favorable for setting up a breeding program, making it possible to improve BW, reproduction, and parasite resistance traits simultaneously.

Key words: body weight, fertility, genetic parameter, goat, litter size, parasite resistance

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INTRODUCTION

Goats in the tropics provide a broad range of benefits to farmers (e.g., food, income, insurance, savings). Diversity of goat breeds ensures food security and adaptability to different environments. Characterization of these breeds is required for better management and conservation of the species as well as for the implementation of breeding programs (FAO, 2007).

Recently, a farmer association, extension services, and the Research Institute in Guadeloupe have collaborated to implement a breeding program for Creole goat. This local breed has evolved under natural selection since the introduction of goats on the island during the early colonization of the 17th century. Nowadays,

this breed is used for meat production, mostly in low- to medium-input farming systems. As shown by a survey (Gunia et al., 2010), growth and conformation are highly desired traits by farmers to improve the level of production of the breed, as are also the maternal abilities of females, especially for farmers using the Creole breed as a maternal line for crossbreeding with bucks of the Boer phenotype.

The importance of disease resistance has been underestimated by farmers, although different studies emphasize the negative consequences of gastrointestinal nematodes (**GIN**) on health and productivity of goats (Aumont et al., 1997; Mandonnet et al., 2005).

The INRA experimental flock provided enough reliable records to analyze the genetic parameters of the traits of interest. Therefore, this study aimed at estimating genetic parameters for BW, reproduction, and parasite resistance traits to optimize the selection index to implement in the future breeding scheme for Creole goats.

MATERIALS AND METHODS

The care and use of animals were performed according to the Certificate of Authorization to Experiment

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Flock Management

From 1980 to 2010, data were collected at the experimental flock of INRA-Gardel in Guadeloupe, a tropical island in the Caribbean. The climate is oceanic-tropical, characterized by 2 annual climatic seasons: a wet and hot season (June to November with 80 to 188 mm of rainfall/mo and a temperature of 23 to 31°C at INRA-Gardel) and a dry and fresh season (December to May with 47 to 115 mm of rainfall/mo and a temperature of 21 to 30°C). Most of the droughts and hurricanes did not significantly affect production, except for the Hugo hurricane in September 1989, which caused 50% mortality.

The average population of the flock was approximately 250 does. Does were divided into 2 flocks and were exposed to males during 1 mo for 3 kiddings in 2 yr in February, June, and October. Small groups of about 15 does were joined to a single buck. The number of kids reared per doe was artificially limited to a maximum of 2 kids, with excess kids being almost immediately sent to an artificial rearing unit. About 26% of litter size records were greater than 2. Kids were weaned at 84 ± 11 d of age on average. At 11 mo of age, about 25% of females and 7% of males were kept in the herd for kid production. They replaced the dead and culled animals. The animals in excess were sold.

Goats grazed on *Digitaria decumbens* pastures managed in a rotation system. In addition, does were fed commercial pellets during the last month of pregnancy and all the suckling period. Kids were also fed pellets from 5 wk of age until 2 wk after weaning. The quantity given and composition of the pellets varied over the 30 yr of data collection.

Animals were naturally infected by GIN when grazing on pasture. The main nematode species were *Haemonchus contortus*, *Trichostrongylus colubriformis*, and *Esophagostomum columbianum*. After weaning, kids were drenched every 2 mo with an anthelmintic to control gastrointestinal parasites. Does were drenched 3 times during a reproductive period: at the end of the pregnancy, after kidding, and before weaning. The main products used were benzimidazole from 1980 to 1985, ivermectin from 1986 to 1990, netobimin in 1991 and 1992, levamisole and ivermectin from 1993 to 2002 (except in 1999), netobimin and levamisole in 2003 and 2004, and cydectin since 2005. Changes in products were made because of resistance in the worm population. In 1998, resistance to levamisole in the worm population led to a 50% productivity loss. In 1999, goats had to be kept inside for 6 mo and treated fortnightly with netobimin and cydectin while pastures were decontaminated. Then the resistant strain of *Trichostrongylus colubriformis* was replaced with a susceptible strain (Chevalier, 2001). Since 2002, targeted drenching of does according to the Famacha method has been progressively imple-

mented to slow down resistance to anthelmintic in the worm population (Mahieu et al., 2007).

Data Recording and Traits Analyzed

We chose 6 traits to assess reproduction, parasite resistance, and BW performance. Reproduction traits included fertility (**FER**) and litter size (**LS**) of does. Fertility was the reproductive success of each female joined (it was either 0 for no kidding or 1 for kidding); LS was the number of offspring born per doe kidding (it varied from 1 to 7) and was considered in the analysis as a trait of the dam and not of the kid.

Packed cell volume of lactating does 6 wk after kidding (**PCV**) and fecal egg count at 11 mo of age (**FEC11**) were used to assess resistance to GIN. The PCV is a measurement of the proportion of red cells in the blood used to diagnose anemia caused by hematophagous parasites. It is more often considered as a measurement of resilience, especially in infection coming predominantly from *H. contortus* (Baker et al., 2001). For convenience, we will discuss both PCV and FEC11 as measurements of resistance. These 2 measurements were taken at 2 key moments: the periparturient increase in parasites for does and the fattening period for kids. Blood samples were taken on lactating does and analyzed using the capillary microhematocrit method to determine PCV. Fecal samples were taken on 11-mo-old kids after using an enema and analyzed with a modified McMaster method (Aumont et al., 1997) to count the number of eggs of gastrointestinal parasites found in animal feces (**FEC**).

Body weight traits included a preweaning BW adjusted at 70 d of age (**BW70d**) and a postweaning BW adjusted at 11 mo of age (**BW11**). Farmers prefer heavier goats at 11 mo, the mating or selling age, so BW11 is a highly desirable trait, whereas BW70d is used as a proxy for weaning weight ($84 \text{ d} \pm 11$). Animals were weighed every 10 d before weaning period and every 25 d thereafter. Both BW measurements were calculated by linear interpolation (Naves et al., 2001), except for BW11 when there were no records after 11 mo of age. In that case, BW11 was calculated by superior linear extrapolation when the difference between 11 mo and the last age at BW measurement was inferior to 30 d. Because many animals were sold around 11 mo of age, superior extrapolation increased the number of data available for BW11.

The setup of the data included the 6 traits (FER, LS, PCV, FEC11, BW11, BW70d) measured on the same animal when available. Thus, males and females sold at 11 mo only had records for FEC11, BW11, and BW70d.

Statistical Analyses

Summary statistics and numbers of data for each trait are presented in Table 1. The total data set in-

cluded measurements on 11,973 animals. Some traits were measured since the creation of the flock, when others were measured only during a fixed period of time. Measurements on both BW70d and BW11 occurred on 5,222 animals. Joint measurements on BW70d, BW11, and FEC11 occurred on 2,074 animals. Only 121 of them were also measured for FER, although 4,679 other females had FER records. Because the FEC11 variable was not normally distributed, a logarithm transformation $\log(\text{FEC11}+15)$ was performed before analysis.

Variances were estimated using the REML procedure fitting an animal model with ASReml software (Gilmour et al., 2006). Preliminary analysis of single-trait models and bivariate models were run to check the consistency of phenotypic and genetic parameters across traits and models (results not shown). The final model included all 6 traits described previously: LS and FER (reproduction traits), PCV and FEC11 (parasite resistance traits), as well as BW11 and BW70d (BW traits).

Fixed effects were tested with an ANOVA by using the Proc GLM (SAS Inst. Inc., Cary, NC). They are presented in Table 2. Only the significant effects were kept. The kidding cohort of the does was the group of does kidding at the same period. They were 3 kidding periods per year for 30 yr of experiment, which gave a total of 90 modalities. Using kidding cohort allowed us to take into account the year and season of kidding. The parity-of-the-does-at-kidding effect had 10 modalities. The 9 first modalities were the number of parities of the does. The 10th modality grouped all does with more than 9 kiddings. The age-at-mating-of-the-does effect had 8 modalities. The 7 first modalities were the age of the does expressed in years. The eighth modality grouped all does aged 8 yr or more. These 3 effects concerned only does, and their significance was only tested on the 3 doe traits (FER, LS, and PCV). The birth-cohort effect was the equivalent of the kidding cohort for birth. The cohort gathers all kids born at the same period. This effect also had 90 modalities. The birth cohort \times sex of the animal had 180 modalities and was a combined effect of the birth cohort (90 modalities) and the sex of the animal (2 modalities). The effect of the combination of the LS at birth, after 15 d, and artificial milking had 4 modalities. This effect grouped animals according to their LS at birth, after 15 d, and took into account if they were placed in artificial rearing unit. The effect of groups of parity of the dam had 3 modalities: the first grouped the parities 1 and 2, the second the parities 3 to 5, and the third the parities greater than 5.

All traits were analyzed using a linear model. Litter size and FER have a discrete distribution, which imply that a threshold model (Gianola and Foulley, 1983) should theoretically be preferred. However, assumption of a continuous distribution for these traits is justified for genetic evaluation and for estimates of genetic correlations with continuous traits (Kadarmideen et al., 2003). Threshold and linear models showed very little differences in genetic parameters for FER (Weller and

Ron, 1992; Boichard and Manfredi, 1994) and LS (Matos et al., 1997; Olesen et al., 1994).

Therefore, for each trait y_i ($i = 1$ to 6 for FER, LS, PCV, FEC11, BW11, and BW70d, respectively), a linear mixed model fitted with repeated measurements was accounted for in the case of doe traits (LS, FER, PCV) or maternal environmental effect for the kid trait BW70d. A multivariate normal distribution was assumed for all random effects. The likelihood ratio test was used to determine the significance of variance components. The multivariate animal model was

$$\begin{aligned} \begin{bmatrix} y_1 \\ y_2 \\ y_3 \\ y_4 \\ y_5 \\ y_6 \end{bmatrix} &= \begin{bmatrix} X_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & X_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & X_3 & 0 & 0 & 0 \\ 0 & 0 & 0 & X_4 & 0 & 0 \\ 0 & 0 & 0 & 0 & X_5 & 0 \\ 0 & 0 & 0 & 0 & 0 & X_6 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \\ b_3 \\ b_4 \\ b_5 \\ b_6 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & Z_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & Z_3 & 0 & 0 & 0 \\ 0 & 0 & 0 & Z_4 & 0 & 0 \\ 0 & 0 & 0 & 0 & Z_5 & 0 \\ 0 & 0 & 0 & 0 & 0 & Z_6 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \\ a_3 \\ a_4 \\ a_5 \\ a_6 \end{bmatrix} \\ &+ \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & S_6 \end{bmatrix} \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ m_6 \end{bmatrix} + \begin{bmatrix} W_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & W_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & W_3 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} c_1 \\ c_2 \\ c_3 \\ 0 \\ 0 \\ 0 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \\ e_3 \\ e_4 \\ e_5 \\ e_6 \end{bmatrix}, \end{aligned}$$

where y_i is the vector of observations available for each animal, b_i is the vector of fixed effects, a_i is the vector of random additive genetic direct effects, m_i is the vector of random maternal genetic effects, c_i is the vector of random permanent environmental effects either of the dam for kid trait, or of the individual doe for doe traits, and e_i is the vector of random residual effects. The X_i , Z_i , S_i , and W_i are the corresponding incidence matrices connecting y_i to the effects in the model.

The variance-covariance structure of the model was as follows:

$$\text{Var} \begin{bmatrix} a_1 \\ a_2 \\ a_3 \\ a_4 \\ a_5 \\ a_6 \\ m_6 \end{bmatrix} = \begin{bmatrix} A\sigma^2 a_1 & A\sigma a_{12} & A\sigma a_{13} & A\sigma a_{14} & A\sigma a_{15} & A\sigma a_{16} & A\sigma a_{m_6} \\ A\sigma a_{21} & A\sigma^2 a_2 & A\sigma a_{23} & A\sigma a_{24} & A\sigma a_{25} & A\sigma a_{26} & A\sigma a_{m_6} \\ A\sigma a_{31} & A\sigma a_{32} & A\sigma^2 a_3 & A\sigma a_{34} & A\sigma a_{35} & A\sigma a_{36} & A\sigma a_{m_6} \\ A\sigma a_{41} & A\sigma a_{42} & A\sigma a_{43} & A\sigma^2 a_4 & A\sigma a_{45} & A\sigma a_{46} & A\sigma a_{m_6} \\ A\sigma a_{51} & A\sigma a_{52} & A\sigma a_{53} & A\sigma a_{54} & A\sigma^2 a_5 & A\sigma a_{56} & A\sigma a_{m_6} \\ A\sigma a_{61} & A\sigma a_{62} & A\sigma a_{63} & A\sigma a_{64} & A\sigma a_{65} & A\sigma^2 a_6 & A\sigma a_{m_6} \\ A\sigma a_{m_6} & A\sigma a_{m_6} & A\sigma a_{m_6} & A\sigma a_{m_6} & A\sigma a_{m_6} & A\sigma a_{m_6} & A\sigma^2 m_6 \end{bmatrix}$$

$$\text{Var} \begin{bmatrix} c_1 \\ c_2 \\ c_3 \\ c_6 \end{bmatrix} = \begin{bmatrix} I\sigma^2 c_1 & I\sigma c_{12} & I\sigma c_{13} & I\sigma c_{16} \\ I\sigma c_{21} & I\sigma^2 c_2 & I\sigma c_{23} & I\sigma c_{26} \\ I\sigma c_{31} & I\sigma c_{32} & I\sigma^2 c_3 & I\sigma c_{36} \\ I\sigma c_{61} & I\sigma c_{62} & I\sigma c_{63} & I\sigma^2 c_6 \end{bmatrix}$$

$$\text{Var} \begin{bmatrix} e_1 \\ e_2 \\ e_3 \\ e_4 \\ e_5 \\ e_6 \end{bmatrix} = \begin{bmatrix} I\sigma^2 e_1 & I\sigma e_{12} & I\sigma e_{13} & I\sigma e_{14} & I\sigma e_{15} & I\sigma e_{16} \\ I\sigma e_{21} & I\sigma^2 e_2 & I\sigma e_{23} & I\sigma e_{24} & I\sigma e_{25} & I\sigma e_{26} \\ I\sigma e_{31} & I\sigma e_{32} & I\sigma^2 e_3 & I\sigma e_{34} & I\sigma e_{35} & I\sigma e_{36} \\ I\sigma e_{41} & I\sigma e_{42} & I\sigma e_{43} & I\sigma^2 e_4 & I\sigma e_{45} & I\sigma e_{46} \\ I\sigma e_{51} & I\sigma e_{52} & I\sigma e_{53} & I\sigma e_{54} & I\sigma^2 e_5 & I\sigma e_{56} \\ I\sigma e_{61} & I\sigma e_{62} & I\sigma e_{63} & I\sigma e_{64} & I\sigma e_{65} & I\sigma^2 e_6 \end{bmatrix},$$

Table 1. Summary of data including means and SD, number of records, as well as number of animals, sires, and dams for reproduction, parasite resistance, and BW traits in Creole goats¹

Trait (unit)	Means \pm SD	Year of record	No. of			
			Records	Animals	Sires	Dams
Reproduction trait						
LS, kids	2.14 \pm 0.73	1980 to 2010	7,851	1,987	265	857
FER, %	0.83 \pm 0.38	1997 to 2010	4,800	1,539	206	640
Parasite resistance trait						
PCV, %	24.13 \pm 4.97	1998 to 2004	852	688	130	389
FEC11, log(eggs/g + 15)	6.35 \pm 1.43	1995 to 2006	2,446	2,446	124	727
BW trait						
BW11, kg	17.91 \pm 4.13	1992 to 2005	5,631	5,631	158	948
BW70d, kg	7.40 \pm 1.79	1980 to 2010	10,943	10,943	302	1,669
Total			18,450	11,973	317	1,741

¹LS = litter size; FER = fertility; PCV = packed cell volume; FEC11 = fecal egg counts at 11 mo; BW11 = BW at 11 mo; BW70d = BW at 70 d.

where \mathbf{A} is the numerator relationship matrix across animals, \mathbf{I} is the identity matrix, $\sigma^2 a_i$ and σa_{ij} are the additive genetic variance and covariance for the direct effects, $\sigma^2 m_i$ is the maternal genetic variance, σam_{ij} is the covariance between direct and maternal additive effects, $\sigma^2 c_i$ and σc_{ij} are the variance and covariance for the permanent environmental effects, $\sigma^2 e_i$ and σe_{ij} are the variance and covariance for the residual effects.

RESULTS AND DISCUSSION

Basic Statistics on Raw Traits

Basic statistics are presented in Table 1. Creole breed has a large LS with 2.14 kids per doe. Other goat breeds have a similar prolificacy: the Criolla in Argentina with 2.20 kids (Rabasa et al., 2001), the Egyptian Zaribi with 2.15 kids (Shaath and Maki-Tanila, 2009), and the Common African goat breed in Rwanda with 2.17 kids (Mourad, 1994). Highly specialized dairy goats are reported to have less prolificacy: Alpine average 1.25 kids per parturition, Nubians average 1.38 kids (Dickson-Urdaneta et al., 2000), and Polish dairy goats average 1.75 kids (Bagnicka et al., 2007).

Fertility (kidding success) in the Creole breed was greater than the pregnancy rate of 0.56 in the common African goat after AI (Mourad, 1994), but was consistent with FER in Merino sheep of 0.80 (Safari et al., 2007).

In the Creole breed, the nontransformed mean of FEC11 was 1,262 eggs per gram ($\pm 1,898$). Means after the logarithm transformation are reported in Table 1. The wide range of variation of the nontransformed mean of FEC as well as the different transformations performed on FEC in other studies make comparison difficult. However, Morris et al. (1997) found a similar average FEC in the Saanen goat in New Zealand (1,136 eggs/g). The geometric mean of FEC for the Small East African goat (1,380 eggs/g) was also in accordance with our estimate (Baker et al., 2001). The PCV of Galla and Small East African goat breeds were slightly greater than those of the Creole breed (24.1) with 25 and 25.6 at 14 mo of age (Baker et al., 2001).

The BW at 11 mo for Creole goat (17.9) was more than twice the BW at 360 d in the West African Dwarf goat (8.04 kg; Bosso et al., 2007). It was also slightly greater than BW at 12 mo of the Small East African goat (14.3 kg) and very close to the BW at 12 mo of the

Table 2. Significance (P -values) of fixed effect for reproduction, parasite resistance, and BW traits in Creole goats¹

Fixed effect	No. of modalities	LS	FER	PCV	FEC11	BW11	BW70d
Kidding cohort of the does	90	$P < 0.001$	$P < 0.001$	$P < 0.001$	—	—	—
Parity of the does at kidding	10	$P < 0.001$	—	$P < 0.01$	—	—	—
Age at mating of the does	8	NS ²	$P < 0.001$	NS	—	—	—
Birth cohort	90	$P < 0.001$	$P < 0.001$	NS	—	—	—
Birth cohort \times sex of the animal	180	—	—	—	$P < 0.001$	$P < 0.001$	$P < 0.001$
Combination of the litter size at birth, after 15 d and artificial milking	4	NS	NS	NS	NS	$P < 0.001$	$P < 0.001$
Groups of parity of the dam	3	NS	NS	NS	NS	$P < 0.001$	$P < 0.001$

¹Reproduction traits: LS = litter size, FER = fertility; parasite resistance traits: PCV = packed cell volume, FEC11 = fecal egg counts at 11 mo; BW traits: BW11 = BW at 11 mo, BW70d = BW at 70 d.

²NS = not significant.

Galla goat (17.0 kg). On the opposite, Creole goat BW was only one-half the yearling BW in the Boer goat (36.9 kg; Schoeman et al., 1997). The BW70d of the Creole breed (7.4 kg) was lighter than BW at 60 d in the Sicilian Girgentana goat (8.5 kg in males; Portolano et al., 2002) but within the range of estimates of 2-month-old Galla (8.0 kg) and Small East African goat breeds (6.3 kg; Baker et al., 2001).

Heritability Estimates and Environmental Permanent Effects

Table 3 presents estimates of phenotypic, permanent environmental, and residual variances and estimates of direct and maternal heritabilities. Heritability estimates are low for reproduction traits (about 10%) to moderate for production traits (about 30%). Heritability estimates of parasite resistance traits are situated in an intermediate range, around 15%. Repeatability estimates were moderate for LS, FER, PCV, and BW70d. Permanent environmental variances were small but significant for reproduction traits and pre-weaning BW. However, its ratio over phenotypic variance was greater than the heritability for PCV. The estimates of direct, maternal heritability, and permanent environmental variance of the reproduction and BW traits of our study were remarkably consistent with the weighted mean of estimates in sheep from the Safari et al. (2005) literature review.

The heritability estimate of LS in the Creole breed (0.11) was also in good agreement with the estimates reported by Bagnicka et al. (2007) for Polish and Norwegian goat breeds in second kidding (0.11 and 0.13, respectively) as well as with the estimate of 0.12 reported by (Zhang et al., 2009) in the Boer goat. The heritability estimate for FER (0.11) was slightly greater than the estimate of 0.06 in the Common African goat (Mourad, 1994).

The heritability estimate of BW11 (0.32) was similar to the estimates of 0.30 for BW at 360 d in West African Dwarf goat (Bosso et al., 2007). The heritability estimate of BW11 was in general agreement with the range of estimates (0.13 to 0.60) for BW at 12 mo

reported in the Shrestha and Fahmy (2007) review for goats. The direct and maternal heritabilities of BW70d (0.20 and 0.08, respectively) were slightly greater than the estimates reported by Schoeman et al. (1997) for weaning weight in Boer goat (0.18 and 0.05, respectively). The direct heritability in the Creole goat was also greater than the estimate for Galla and Small East African goats at 3 mo (0.16), but the maternal heritability was smaller than the estimate of 0.14 for these breeds (Baker et al., 2001). All these results suggest a relative stability of heritability estimates for growth and reproductive traits in most domestic goat and sheep breeds.

Heritability estimates of FEC11 and PCV were similar to the estimates of previous study in the Creole goat (Mandonnet et al., 2006). These 2 traits were measured at key moments. The increase in maternal nematode infection during the periparturient period is a major source of pasture larval contamination in ruminants, leading to an increase of mortality and BW loss in suckling kids (Mandonnet et al., 2005). Parasitism in fattening kids decreases farmer profit for the same reasons (mortality and BW loss). Moreover, genetic variability was the greatest 6 wk after kidding in does and 11 mo after birth in kids (Mandonnet et al., 2001, 2006). Heritability of PCV (0.13) was in good agreement with the only estimate of 0.15 in dry ewes (Vanimisetti et al., 2004). Heritability estimate of FEC in our study (0.18) was slightly greater than the estimate of 0.13 for Barbari goat with a similar model (Mandal and Sharma, 2008) and situated in between the estimate of 0.24 at 10 mo and 0.13 at 12 mo for Galla and Small East African goat breeds (Baker et al., 2001). However, our estimate was much less than the weighted mean of heritability estimates in sheep (0.27) in the literature review of Safari et al. (2005). As observed by Mandonnet et al. (2006), heritability of FEC in goats is about one-half that of sheep. Mechanisms of resistance in goats could indeed differ from those in sheep. Goats are predominantly browsers, whereas sheep are grazers. The selection pressure for parasite resistance was therefore less strong on goats (Mirkena et al., 2010), leading to less complex resistance mechanisms in goats (Bambou et al., 2009).

Table 3. Genetic parameters for reproduction, parasite resistance, and BW traits in Creole goats^{1,2}

Trait	σ_a^2	σ_m^2	σ_c^2	σ_e^2	σ_p^2	h_a^2	h_m^2	c_c^2	Repeatability
LS	0.05		0.02	0.38	0.45	0.11 ± 0.02		0.05 ± 0.02	0.16
FER	0.02		0.01	0.11	0.14	0.11 ± 0.02		0.08 ± 0.02	0.19
PCV	2.56		3.00	14.47	20.03	0.13 ± 0.05		0.15 ± 0.07	0.28
FEC11	0.14			0.64	0.78	0.18 ± 0.04			
BW11	3.59			7.66	11.25	0.32 ± 0.03			
BW70d	0.48	0.20	0.10	1.53	2.39	0.20 ± 0.03	0.08 ± 0.02	0.04 ± 0.01	0.24

¹ σ_a^2 = direct additive genetic variance; σ_m^2 = maternal additive genetic variance; σ_c^2 = permanent environmental variance of the individual doe for doe traits or of the dam for BW70d; σ_e^2 = residual variance; σ_p^2 = phenotypic variance; h_a^2 = direct heritability; h_m^2 = maternal heritability; c_c^2 = permanent environmental effect either of the individual doe for doe traits or of the dam for BW70d; ± SE.

²Reproduction traits: LS = litter size, FER = fertility; parasite resistance traits: PCV = packed cell volume, FEC11 = fecal egg counts at 11 mo; BW traits: BW11 = BW at 11 mo, BW70d = BW at 70 d.

Table 4. Genetic correlations (above diagonal) and phenotypic correlations (below diagonal) with their SE for reproduction, parasite resistance, and BW traits in Creole goats¹

Item	LS	FER	PCV	FEC11	BW11	aBW70d	mBW70d
LS		0.25 ± 0.15	-0.10 ± 0.22	0.05 ± 0.15	0.23 ± 0.09	0.13 ± 0.11	-0.18 ± 0.11
FER	0.10 ± 0.02		0.45 ± 0.24	0.01 ± 0.17	0.65 ± 0.09	0.13 ± 0.13	0.90 ± 0.10
PCV	-0.13 ± 0.03	-0.24 ± 0.04		-0.21 ± 0.22	0.29 ± 0.15	0.25 ± 0.19	0.37 ± 0.20
FEC11	0.04 ± 0.08	-0.01 ± 0.07	-0.07 ± 0.11		0.10 ± 0.12	0.08 ± 0.14	0.04 ± 0.16
BW11	0.22 ± 0.03	0.18 ± 0.04	-0.10 ± 0.05	-0.12 ± 0.02		0.76 ± 0.05	0.82 ± 0.06
BW70d	0.16 ± 0.03	0.13 ± 0.03	0.03 ± 0.05	0.01 ± 0.02	0.61 ± 0.01		0.30 ± 0.12

¹Reproduction traits: LS = litter size, FER = fertility; parasite resistance traits: PCV = packed cell volume, FEC11 = fecal egg counts at 11 mo; BW traits: BW11 = BW at 11 mo; aBW70d = direct effect of BW at 70 d; mBW70d = maternal effect of BW at 70 d.

Correlations Within Reproduction, Parasite Resistance, and BW Groups of Traits

Table 4 presents genetic and phenotypic correlations across the 6 traits.

Reproduction Traits. The phenotypic correlation between FER and LS was very low. The LS was considered a missing value when FER was equal to 0. Such assumptions had already been made and had given satisfactory results (Urioste et al., 2007). However, the low phenotypic correlation observed could be due to a bias in the estimate of environmental covariance between the 2 traits because LS had a value only when the binary trait FER was equal to 1 (success of kidding). Nevertheless, it should not affect the genetic correlation that accounts through the relationship matrix across animals of females with FER equal to 0. Even if the measured FER is a discrete trait, the EBV are continuous (Kadarmideen et al., 2003). The genetic correlation was favorable, but very moderate and not significantly different from zero. This correlation (0.25) was similar to the estimate of 0.22 in African Common goats in Rwanda (Mourad, 1994) and in Merino sheep (Safari et al., 2007) but much less than the weighted mean of 0.44 given in the literature review of Safari et al. (2005).

Parasite Resistance Traits. In our study, the genetic correlation between FEC11 measured on all kids and PCV of does 6 wk after kidding was moderately negative (-0.21), but not significantly different from 0, as was the phenotypic correlation. Considering this result, it seems that FEC11 of kids and PCV of does are 2 different traits. More records are needed to get a more accurate estimation of these correlations by reducing the large SE of their first estimates due to the small proportion of does that had both FEC11 and PCV records (only 11% of the does whose PCV was recorded also had FEC11 records). In the literature, genetic correlations between FEC and PCV measured at the same age during the postweaning period were moderately to highly negative in Galla, Small East African, and Creole goat breeds (Baker et al., 2001; Mandonnet et al., 2001). This correlation in Creole does 6 wk after kidding was also highly negative (-0.79; Mandonnet et al., 2006). These authors also found high positive genetic correlations between measurements of PCV at different ages on one hand and between measurements

of FEC at different ages on the other. Mandonnet et al. (2006) estimated a reasonably high genetic correlation (0.76) between FEC measured at 11 mo in does and FEC measured 6 wk after their first kidding.

BW Traits. The different components (phenotypic, direct, and maternal genetic effects) of BW were strongly correlated to one another across time periods. The genetic correlation between BW70d and BW11 in Creole breed (0.76) was greater than the genetic correlation of 0.54 between BW at 60 and 210 d in Common African and crossbred breeds (Mourad, 1994) and similar to the genetic correlation of 0.73 in West African Dwarf goat between birth and yearling weight (Bosso et al., 2007). Nevertheless, it was slightly less than the weighted means of literature estimates of 0.85 reported by Safari et al. (2005) in sheep. The estimate of the correlation between direct and maternal genetic effects for BW70d was moderately favorable (0.30). The maternal genetic effect of BW70d can be related to the milking ability of the dam, which is due to the associate effects of her milk production and her mothering ability (Mandal et al., 2006). Therefore, the milking ability and the preweaning growth in the Creole breed evolved genetically together in a favorable direction. Our estimate is consistent with the estimates of 0.33 for Rambouillet and 0.34 for Columbia sheep (Hanford et al., 2002, 2005) and with the weighted mean of estimates of 0.34 in the literature review of Safari et al. (2005) in sheep. In their literature review in goats, Shrestha and Fahmy (2007) observed that the genetic correlation estimates between direct and maternal effects for BW were low to moderate and varied from negative to positive, without any indication of significance.

Correlations Between BW and Reproduction Traits

BW and FER. The phenotypic correlation between BW11 and FER was moderate. The genetic correlation between BW11 and FER (0.65) was on the same range as the estimate of Fogarty et al. (1994) of 0.63 in Hyfer sheep. At 11 mo, age at first mating in the INRA-Gardel flock, the heavier females had better reproductive success. Mellado et al. (2005) observed that kidding rate was greater in does with greater fat

reserves. The heaviest BW of fertile goats could therefore be associated with greater fat reserves.

The phenotypic correlation between BW70d and FER was low. The genetic correlation between the direct effect of BW70d and FER (0.13) was not significantly different from zero. Our estimates differ from the negative genetic correlation between BW at 90 d and FER of -0.31 found by al-Shorepy and Notter (1996) in a composite breed of sheep.

The genetic correlation between the maternal effect of BW70d and FER is highly favorable (0.90). Because the maternal genetic effect on the preweaning BW is closely linked to the genetic potential for milking ability of the Creole goat, milking ability and FER can therefore be assumed to be positively correlated. This result is in opposition with what has been observed in dairy sheep such as the Lacaune breed, with a negative genetic correlation of -0.23 between milk yield and FER (David et al., 2008), and in dairy cattle with a correlation of -0.16 (Kadarmideen et al., 2003). However, our results are in accordance with the observations in beef cattle where milk production of primiparous cows had been recorded in stations (Phocas and Sapa, 2004). Depending on the orientation of selection in a breed (milk or meat) the energy allocation would differ, hampering FER in specialized milk breeds of ruminants.

BW and LS. The phenotypic and genetic correlations between BW11 and LS were moderate. The genetic correlation (0.23) was in the range of the weighted mean of literature estimates of 0.17 given by Safari et al. (2005). As observed by Constantinou (1989) and Mellado et al. (2005), heavier does at mating had a greater LS. This association may be attributed to a greater ovulation rate.

The phenotypic correlation between BW70d and LS was moderate. Nevertheless, LS was not significantly genetically correlated with the direct or maternal effects of BW70d. In many sheep breeds, whose prolificacy is low, these correlations are moderate to high (Hanford et al., 2002, 2003, 2005). However, in the highly prolific Polypay sheep, the genetic correlation between LS and the direct effect of weaning weight was less (0.24) compared with other sheep breeds; the genetic correlation between LS and the maternal effect of weaning weight was also low and negative (Hanford et al., 2006). In Polypay sheep as well as in Creole goat, mothers were not allowed to rear more than 2 newborns of the litter. Artificially removing kids in excess of 2 prevents the full expression of the maternal genetic effect on BW70d. This limitation could explain the very low genetic correlation observed between LS and milking ability.

Correlations Between Parasite Resistance Traits and Reproduction

FEC and Reproduction Traits. There is no significant genetic or phenotypic correlation between

FEC11 and reproduction traits. Improving reproduction in does will not influence FEC11. This result is in accordance with Vanimisetti et al. (2004), who found that EBV for FER and prolificacy in ewes were not related to parasite resistance in lambs.

PCV and FER. The phenotypic correlation between PCV and FER was moderate and negative, whereas the genetic correlation was greater and positive. The low precision of the genetic correlation estimates could lead to this difference in trends between genetic and phenotypic correlations (Koots and Gibson, 1996).

PCV and LS. The phenotypic and genetic correlations between PCV and LS were small and negative, but not significantly different from zero. Greater number of kids would be more demanding for the mother, decreasing her capacity to cope with parasites. This effect of increased number of kids on the health of does has already been observed in sheep (Donaldson et al., 1998). However, further records are needed to increase the accuracy of our estimation and confirm this observation.

Correlations Between Parasite Resistance Traits and BW

FEC and BW. The phenotypic correlation between FEC11 and BW11 was small and negative, whereas the genetic correlation was not significantly different from zero. These results are consistent with the observation of Baker et al. (2001) in Galla and Small East African goat breeds. Previous study on Creole goats also showed no significant genetic correlations between BW and FEC for kids between weaning and 10 mo of age, with the same range of SE (Mandonnet et al., 2001). In their literature review in sheep, Safari et al. (2005) observed a low and negative genetic weighted means of correlation estimates of -0.24 , meaning that an increased BW leads to a reduction in the number of GIN eggs excreted. Improving BW11 of Creole kids will probably not influence FEC11, but further studies are needed to increase the accuracy of these early estimates.

PCV and BW. The phenotypic correlation between PCV and BW70d was not significantly different from zero. The genetic correlations between PCV and the direct and maternal effects of BW70d were positive and moderate. This trend suggests that resilient mothers tend to have a better ability to contribute positively to their kid growth.

The phenotypic correlation between PCV and BW11 was small and negative (-0.10). On the other hand, the genetic correlation was moderate and positive (0.29). The difference in trends between phenotypic and genetic covariances may be due to the low precision of the genetic correlation estimates. Baker et al. (2001) found positive phenotypic and genetic correlations between BW and PCV between weaning and 14 mo of age for

Galla and Small East African goat breeds, with an average of 0.33 for the phenotypic correlation and 0.58 for the genetic correlation.

The positive genetic correlation between PCV and BW11 would mean that heavier goats at mating are more resilient to GIN. Valderrábano et al. (2006) observed that fat mass stored by ewes in early pregnancy was associated with the expression of immunity against GIN infection around parturition. Thus, the heavier goats could be the ones with the greatest fat deposits.

Consequences for the Implementation of a Breeding Scheme

Our study provides estimates of genetic correlation for different groups of traits in goats that were not previously found in the scientific literature. The heritability estimates for reproduction and BW in Creole goats were very consistent with the estimates in sheep, and it could be interesting to verify these results in other studies in goats. Standard errors of our estimates of genetic correlations were relatively high, ranging from 0.10 to 0.25. Further recording will be needed to increase their accuracy, especially for PCV.

Genetic correlations, together with heritability and other parameter estimates provide the basis for designing a breeding program in Creole breed aimed at improving several traits. Four traits (FER, PCV, BW11, and maternal effect of BW70d) evolve favorably together, whereas LS and FEC11 appear to be almost unlinked to the other traits. The positive genetic correlations between FER, parasite resistance, BW at first mating, and milking ability of does are very favorable for an easy and efficient implementation of a breeding scheme in Creole goats. However, increase of BW will have to be monitored, to see if it leads to a greater increase of fat over lean content in the meat, because consumer preference for the quality of the meat has to be taken into account. Litter size was not strongly correlated with any of the other traits studied. Maintaining the already high prolificacy of the Creole goat while improving other traits will therefore be possible. The FEC11 could also be improved without negatively affecting the other traits.

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