

## GENETIC PARAMETERS ESTIMATES FOR GROWTH TRAITS OF GOATS FROM THE ARGAN GROVE OF AGADIR IN MOROCCO

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### Abstract

The main objectives of this study were to estimate the heritability and genetic advance for growth traits in the Argan grove of Agadir in Morocco goat. Traits included, birth weight (BW), 10 days weight (W10), 30 days weight (W30) and at 70 days weight (W70), average daily gain from birth to 30 days (ADG1) and average daily gain from 30 days to 70 days (ADG2). The measurements concern 81 parent-offspring pair distributed in two generations G1 (maternal parent) and G2 (offspring). Genetic parameters are estimated using the parent-offspring regression method after adjusting data for significant non genetic factors. In G2, the birth weights (BW), 10 days (W10), 30 days (W30) and at 70 days (W70) are respectively  $1.75 \pm 0.23$  kg,  $2.42 \pm 0.24$  kg,  $3.57 \pm 0.27$  kg and  $5.54 \pm 0.46$  kg. The average daily gains (ADG1: 0-30 d) and (ADG2: 30-70 d) are  $62.38 \pm 5.38$  g and  $50.34 \pm 10.62$  g respectively. The heritability and genetic advance estimates of different growth traits under study were found moderate in magnitude. Genetic correlations between body weight traits ranged from 0.18 to 0.77, whereas phenotypic correlations ranged from 0.13 to 0.52. these estimates suggest that there is no genetic contradiction between these traits and their assigned genes which were responsible for phenotypic expression. The exploitation of this variability could be used for the selection of better performing goats kids adapted to local breeding conditions.

**Key words:** arganeraie (argan forest), genetics parameters, goats, growth traits.

### INTRODUCTION

Goat farming is a key sector of agriculture and its versatile function, is of socio-economic importance and plays a dynamic role in the development of economic activity in rural areas. Goat herds account for just over 1 billion goats worldwide, of which about 420 million head (40.9%) are raised in Africa. Morocco's goat herd currently accounts for 5.23 million head (FAO, 2017) is composed mainly of hardy local breeds which are characterized by a good adaptation to local climatic conditions and it is mostly concentrated in difficult and mountainous areas (Benlekhal & Tazi, 1996). Several authors have pointed out the important role of this adaptation of these local breeds to the difficult farming conditions and for the production in harch environments (Hoffmann, 2013; Alexandre & Mandonnet, 2005). Knowing the growth dynamics of young animals may be used as one of the indicators to evaluate the level of adaptation under conditions of a given production system (Kume & Hajno, 2010).

The livestock system is extensive, traditional and oriented exclusively for the production of meat. The goat herd is heterogeneous and composed mainly of local breeds, with the dominance of the Atlas (Black) and Barcha breeds which represent approximately 80% of all goats (El Kheyyat & El Madidi, 2020). The main objective of this study is the analysis were to estimate the heritability and genetic advance for growth traits in the Argan grove of Agadir in Morocco goat.

### MATERIALS AND METHODS

The study was conducted in Amskroud commune in the province of Agadir (Figure 1) with 35 goat farmers randomly selected in 9 villages. Goat farming is extensive, and its diet is based on silvopastoral resources (forest resources), either through direct grazing or lopping, all year round, except for the duration of the grazing period. of "Agdal" for the argan tree, between July and September. During this period the animals exploit the areas occupied by *Juniperus phoenicea* [Arar] and other fodder

shrubs. During the winter, the animals graze on the neighboring paths. The argan tree is a predominant pastoral resource, the goats take in both pulp and leaves, on the ground, or during aerial grazing. The history of the goat in the argan tree is part of a long process of continuous presence in the family activities of the local populations of South-West Morocco and the goat is the only species able to take advantage of the agropastoral resources of the argan tree (Lacombe & Casabianca, 2015).

For the monitoring of the animals of each farm, the goats were identified by ear tags with a number specific to each animal.

Live weight at birth (0), 30 and 70 days of kidding and parity of doe were recorded.

Birth date, birth weight, gemellarity and sex of kid were recorded within 24 h of the new birth.

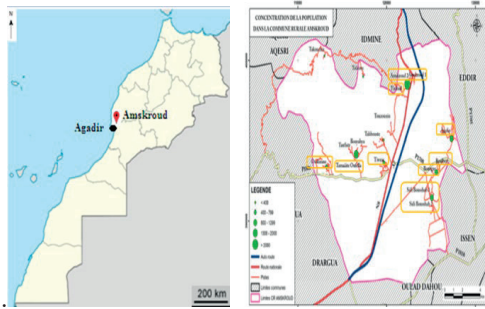


Figure 1. Map showing location of the study area (left) and location of villages sampled (right)

Kids were weighed using Brecknell 235 10S Hanging Scale having 50 kg capacity and 200 g division within 24 h after birth. The data used in present study were collected between 2018 and 2019 from a total of 81 kids (33 males and 48 females), the progeny 81 dams. The birth weights (BW), 10 days (W10), 30 days (W30) and at 70 days (W70) were recorded. Based on the weight records of individual kids, the average daily gains ADG1 (from birth to 30 days), ADG2 (from 30 to 70 days) were calculated assuming linear growth rate between the appropriate weights under the existing management conditions by recruited enumerators.

Genetic parameters are estimated using the parent-offspring regression method after adjusting data for significant non genetic factors. The major non-genetic factors included

for the adjustment are age of dam, birth season, sex and type of birth.

The heritability for any measurable characteristic and production performance indicate the ability of both the parents to transmit superior productivity to their offspring. Heritability in the narrow sense is the ratio of the additive genetic variance ( $\sigma_A^2$ ) to total phenotypic variance ( $\sigma_P^2$ ), which is given

by:  $h^2 = \sigma_A^2 / \sigma_P^2$ . Heritability can be calculated in a number of ways. One method uses phenotypic measures for some trait in parents and their offspring. The slope of the line relating the performance of offspring to that of their parents or midparent average gives a measure of heritability in the narrow sense

The covariance parents offspring:

$Cov(P, O) = 1/2 \sigma_A^2$  and the regression coefficient of the value of the offspring (y) as a function of the value of the parent (x) is written:

$$b_{PO} = \frac{(1/2)\sigma_A^2}{\sigma_P^2} = \frac{\sigma_A^2}{2\sigma_P^2}$$

The genetic advance was calculated by:

$GA = i h^2 \sigma_P$  where  $I = 1.76$  at 10 % of selection intensity (standardized selection differential),  $h^2$  is heritability in the narrow sense and  $\sigma_P$  is the phenotypic standard deviation.

The relative genetic advance (GA as % of the mean):  $RGA = (\sqrt{GA}) / m \times 100$ , where:

$GA$  = genetic advance and  $m$  = mean of the population.

Phenotypic correlations ( $r_p$ ) were estimated based on variances and covariances estimates calculated from half sib family variances, parent-offspring covariances. To estimate the phenotypic correlation between two characters we compute what might be called the cross-covariance obtained from the product of the value of trait X in parents and value of trait Y in offspring or vice versa.

$$r_p = \frac{Cov_{P(XY)}}{\sqrt{V_{P(X)}V_{P(Y)}}$$

where:

$COV_{P(XY)}$  is the phenotypic covariance of X and Y traits and  $V_{P(X)}$  and  $V_{P(Y)}$  are the phenotypic variance value of the traits X and Y.

Genetic correlations ( $r_G$ ) were estimated by regressing average offspring values of trait X on average parent values of trait Y, and vice versa, in accordance with the methods described in (Lynch & Walsh, 1998). Prior to these analyses, all traits were corrected for significant effects of age, sex, year and ringer (see above).

The calculation of  $r_G$  involves dividing the covariances between different traits X and Y ( $Cov_{XY}$ ) in parents and offspring with the square-root product of the covariances between the same traits ( $Cov_{XX}$  and  $Cov_{YY}$ , respectively). Since there are two possible products of  $Cov_{XY}$  there are also two estimates of  $r_G$  ( $r_{G1}$  and  $r_{G2}$ ). The data used for estimating  $r_{G1}$  and  $r_{G2}$  were balanced in the sense that there were no missing values for trait X and Y in neither parents nor offspring. Thus, the calculation of  $r_{G1}$  and  $r_{G2}$  for trait X and Y are based on the same individual samples. To estimate the standard error of  $r_G$ , we applied the procedures described in (Robertson, 1959; Falconer & Mackay, 1996).

The cross covariance is half the genetic covariance of the two characters that is  $\frac{1}{2} COV_{A(XY)}$ . In addition, the covariance of offspring and parents for each of the trait are also needed separately for the estimation of genetic correlation and the genetic correlation is given by

$$r_G = \frac{(1/2)Cov_{A(XY)}}{\sqrt{(1/2)V_{A(X)}(1/2)V_{A(Y)}}} = \frac{Cov_{A(XY)}}{\sqrt{V_{A(X)}V_{A(Y)}}}$$

where:

$COV_{A(XY)}$  is the genetic covariance of the additive deviations between X and Y traits and  $V_{A(X)}$  and  $V_{A(Y)}$  are the additive genetic variance value of the traits X and Y.

All statistical analyzes were performed using SAS version 9.3 software (SAS, 2010).

## RESULTS AND DISCUSSIONS

In G1 (maternal parent), the weight at birth, weights at 10 days, weights at 30 days and weights at 70 days varied between 1.17 to 2.68, 1.40 to 3.76, 2.30 to 5.26 and 3 to 9.12 kg, respectively. The average daily gains, ADG 1 (0-30) and ADG 2 (30-70) varied between 10.3 to 101 and 10.5 to 110.8 g respectively (Table 1).

Table 1. Descriptive statistics for the measured characters (growth traits) in G1

Parameters	n	Mean	Min	Max	SD	CV (%)
BW (Kg)	81	1.91	1.17	2.68	0.35	18.20
W10 (Kg)	76	2.47	1.40	3.76	0.53	21.32
W30(Kg)	72	3.71	2.30	5.26	0.73	19.82
W70(Kg)	69	5.60	3.00	9.12	1.38	24.64
ADG1 (g)	72	62.28	18.3	101.0	8.95	30.42
ADG2 (g)	69	47.79	10.5	110.8	14.6	51.5

ADG: Average Daily Gains, BW: birth weight, W30: weight at 30 days, Min: Minimum, Max: Maximum, SD: Standard deviation, CV: Coefficient of variation. ADG 1: (0-30 days) and ADG 2: (30-70 days).

For weights at typical age, the coefficient of variation (CV) estimates ranged from 18.20% to 24.64 % whereas for the average daily gain, we observed that the coefficient of variation are higher and are equal to 30.42 and 51.50 % for ADG 1 (0-30) and ADG 2 (30-70) respectively. In G2 (offspring), the average values recorded for birth weights, weights at 10 days, weights at 30 days and weights at 70 days was  $1.75 \pm 0.23$  kg,  $2.42 \pm 0.24$ ,  $3.57 \pm 0.27$  and  $5.54 \pm 0.46$  kg, respectively. The average daily gains, ADG 1 (0-30) and ADG 2 (30-70) was  $62.38 \pm 5.34$  and  $50.8 \pm 10.8$  g respectively (Table 2).

Table 2. Descriptive statistics for the measured characters (growth traits) in G2

Parameters	Mean	Min	Max	SD	CV (%)
BW (Kg)	1.75	1.19	2.25	0.23	12.95
W10 (Kg)	2.42	1.98	2.91	0.24	10.11
W30(Kg)	3.57	2.94	4.12	0.27	7.55
W70(Kg)	5.54	4.13	6.75	0.46	8.30
ADG1 (g)	62.38	44.5	79.31	5.34	8.56
ADG2 (g)	50.34	16.1	78.21	10.6	21.09

For weights, the coefficient of variation (CV) estimates ranged from 7.55% to 12.95% whereas for the average daily gain, the coefficient of variation is equal to 8.56 and 21.1% for ADG 1 (0-30) and ADG 2 (30-70) respectively.

Heritability in the narrow sense refers to the part of the genetic variance in the phenotypic variance of a trait and it is a statistical datum allowing an estimation by genetic factors in the expression of the character (Nyquist, 1991; Falconer & Mackay, 1996). The estimation of heritability is a first step in establishing a genetic evaluation for a given trait and the knowledge of this parameter is particularly important for the objective of selection. The  $h^2$  estimates ranged from 0.20 to 0.34 for weights and ranged from 0.20 to 0.28 for The average daily gains. The estimated values for the genetic gain for the different weights ranged from 190 to 490 g while the values recorded for the daily gain are equal to 6.61 g for ADG 1 and 12.12 g for ADG 2 (Table 3).

Table 3. Heritability and genetic advance estimates for the growth traits

	$b_{op}$	$h^2$	GA (g)	RGA %
<b>BW</b>	0.1549	0.31	190	124.85
<b>W10</b>	0.1718	0.34	320	106.26
<b>W30</b>	0.1714	0.34	440	90.54
<b>W70</b>	0.1001	0.20	490	50.50
<b>ADG 1</b>	0.0981	0.20	6.67	13.63
<b>ADG 2</b>	0.1396	0.28	12.12	14.16

$b_{PO}$ : regression slope,  $h^2$ : heritability in the narrow sense, GA: genetic advance and RGA : relative genetic advance.

Table 4. Estimates of phenotypic (P) and genetic correlation (G) among the growth traits analyzed

	<b>W10</b>	<b>W30</b>	<b>W70</b>	<b>ADG 1</b>	<b>ADG 2</b>
<b>WB</b>	P 0.398 G 0.745	P 0.320 G 0.507	P 0.227 G 0.394	P 0.521 G 0.775	P 0.187 G 0.367
<b>W10</b>	- -	P 0.392 G 0.444	P 0.129 G 0.179	P 0.394 G 0.557	P 0.226 G 0.431
<b>W30</b>		- -	P 0.212 G 0.274	P 0.341 G 0.411	P 0.421 G 0.677
<b>W70</b>			- -	P 0.192 G 0.365	P 0.514 G 0.767
<b>ADG 1</b>				- -	P 0.412 G 0.524

P: phenotypic correlation, G: genetic correlation

These results indicated that the genetic component played a relatively important role in the expression of these traits and its significant genetic progress could be obtained by selection based on phenotypic performance. In this study, low birth weights were recorded for kids. Similar results have been observed in other

local breeds (Zahraddeen, 2008; Montaldo et al., 2010; Mabrouk et al., 2010). This low weight is considered as an indicator of adaptation to harsh environments (Najari et al., 2007).

The values of the phenotypic and genetic correlations are presented in Table 4. The estimates of genetic and phenotypic correlations were moderate to high and showed no genetic antagonisms among the growth traits analyzed. The estimated phenotypic correlations were positive and were between 0.129 (W10-W70) and 0.521 (WB-ADG1). Genetic correlations varied from 0.179 and 0.775. The highest genetic correlation was recorded between BW and ADG1 and the lowest was found between W10 and W70.

The positive genetic correlations between the traits studied suggest that the genetic factors that influence these traits play an important role in the correlation between traits and vary in the same directions and suggest that there is no genetic contradiction between these traits and their assigned genes which were responsible for phenotypic expression, therefore selection for one of these traits will bring a positive response to selection for others. Similar to our estimates, moderate to high and positive genetic correlations have been reported by several authors in various breeds of goats (Al-Shorepy et al., 2002; Baneh et al., 2012; Rashidi et al., 2008).

Goat meat production is an important source of income for farmers in this region. This production is based exclusively on local breeds because of their adaptation to climatic conditions unfavorable to intensive farming. The improvement of the production requires an evaluation of the variability of the characters related to the growth of the animals and the selection of the best performing individual kids. Moderate heritability values were observed for growth traits analysed. Similar results have been reported by several authors (Rout et al., 2018; Anggraeni et al., 2020; Mohammed et al., 2018). These moderate values of genetic parameters for the growth traits gives hope for the possibility to improving the traits by selecting the best performing individuals in selection programs.

## CONCLUSIONS

Genetics parameters for growth traits were moderate to high and genetics correlations between measured traits are positive. Consequently the genetic selection for local goats are possible to improve meat production. The improvement of technical farming conditions and the selection of more efficient individuals for growth traits are essential for improving productivity in this region.

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