

Democratization of Genomic Tools to Improve Autochthonous Sheep Breeds Productivity in Developing Countries

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Abstract

While the gap is widening between developed and developing countries in the field of classical animal genetics and breeding, genomic tools are becoming the method of choice in developed countries. The objectives of this study were to: 1) demonstrate by a real case how the lack of suitable breeding strategies can be a major threat to autochthonous sheep breeds improvement and 2) show how genomic tools could be an efficient alternative tool to reverse the decrease of native breed productivity. A total of 54,476 fat tail Barabrine lambs from 77 flocks recorded during the period 2010-2014 were used in this study. Lamb growth traits were evaluated based on an additive linear model including flock ownership type (state or private), flock- season within flock ownership type, age of dam at lambing and lamb's sex-type of birth. An approximate estimation of lamb weights at weaning by 2030 was made. Main results showed that average weights of Barbarine lambs at birth, 30 d., 70 d. and 90 days of age were 4.22 ± 0.37 Kg, 8.11 ± 1.88 kg; 13.53 ± 3.04 kg and 16.05 ± 3.50 kg, respectively. Average daily gains between 10 -30 d., 30-70 d. and 30-90 d., were $129.92g/d \pm 50.91$; $135.49g/d \pm 43.54$ and $132.17g/d \pm 40.52$ g/d, respectively. These performances were lower than results reported in previous studies for the same breed since the sixties until 2000 indicating the negative effect due to a lack of reliable strategies to genetically manage the breed. If the situation continues without change, estimated lamb weaning weight will decrease by 200 g/year to be 13kg by 2030 (R²=0.85). The paper presented different uses and conditions to allow genomic tools to reverse the decreasing trend if they become democratized, their cost is lowered and the technology is transferred to low input production systems.

Keywords: Tunisian Barbarine Sheep Breed; Genetic Variability; Population Structure

Introduction

Animal Genetic Resources (AnGR) are at the same time a wealth and a heritage of humankind. Developed countries were successful on improving productivity of their animals through science, technology, farmers organizations, and, free market. On the other hand, developing countries failed to establish suitable breeding strategies for their local breeds and relied more on imported exotics leading to indiscriminate crossbreeding and a loss of well-adapted genotypes. The majority of livestock owners in developing countries are small size flock/herd holders (MOA, 2015) [1]. They lack recording and appropriate sustainable breeding schemes. Farmers rely very often on either the within flock/herd phenotypically chosen sires leading to inbreeding or on upgrading with exotics leading to the loss of the integrity of local breeds. The Barbarine sheep breed in Tunisia is a fat tail breed and the most important one in number representing 2/3 of a total sheep population of 3.9 million females. The objectives of this study were to: 1) demonstrate how sheep growth performances decreased due to the absence of coherent breeding strategies and 2) show how the use of genomic tools can reverse this decrease.

Material and Methods

Growth data recorded on 54,476 lambs from 77 flocks during 4 years (2010-2014) were used in this study. Growth records included: farm name, flock number, lamb ID, dam ID, date of birth, lamb's sex-type of birth and weights and weight gains from birth to weaning at 90 days of age. These weights are: Weight at Birth (W0), weight at 30 days of age (W30), weight at 70 days of age (W70), weight at 90 days of age (W90), weight gain between 10 and 30 days of age (ADG 10-30), Weight gain between 30 and 70 days of age (ADG 30-70) and Weight gain between 30 and 90 days of age: ADG 70-90. Flocks are raised in the semi-arid central Tunisia. All flocks are raised on natural grazing which is a low input production system in the country depending on the rhythm of annual rainfalls. The original growth data was edited and only growth values within the average of the trait plus and minus 2 standard deviations were kept for statistical analysis. The linear model (1) was used to identify main sources of variation of all identified growth traits

$$Y_{iiklm} = \mu + SEC_i + FS_{ii} + Agm_k + SMN_l + e_{iiklm}$$
(1)

where: Y_{ijklm} represents the weights and the weight gains; μ is the overall mean; SEC₁ is the ith owner of the flock (i = 1..6); FS_{ij} is the jth effect of flock-season within the ith sector; Agm_k is the kth effect of age of the dam (k = 1, .. 9); SMN₁ is the effect of the lth sex - birth type of lamb (l = 1..4) and e_{iiklm} is the Residual error.

A regression linear model (2) was used to estimate future lamb weights at 90 days of age by year based on available weights recorded since the sixties.

$$Y_i = b_0 + b_1 Ai + ei$$
 (2)

Where Y_i is lamb weight at 90 d of age in the ith year; b_0 and b_1 are regression coefficients; Ai is the ith year of weighing lambs at 90 d. and e is the residual error.

Results and Discussion

Average Growth Traits of the Barbarine Breed

Average weights and weight gains of a Barbarine lamb raised under Tunisia low input grazing conditions were: 4.22 ± 0.37 Kg, 8.11 ± 1.88 kg; 13.53 ± 3.04 kg and 16.05 ± 3.50 kg at birth, 30 d., 70 d. and 90 d., respectively. Average weight gains were:

129.92g/d ±50.91; 135.49g/d ±43.54and 132.17g/d ±40.52 g/d, between 10-30, 30-70 and 30-90 days, respectively (Table 1).

Trait	Lambs	Average	Standard Deviation
W ₀ (kg)	30 166	4.22	0.37
W ₃₀ (kg)	30 166	8.11	1.88
W ₇₀ (kg)	30 166	13.53	3.04
W ₉₀ (kg)	30 166	16.05	3.50
$ADG_{10-30}(g/d)$	30 028	129.92	50.91
$ADG_{30-70} (g/d)$	30 028	135.49	43.54
$ADG_{30.90}(g/d)$	30 028	132.17	40.52

Legend: W_0 : Weight at Birth; W_{30} : weight at 30 days of age; W_{70} : weight at 70 days of age; W90: weight at 90 days of age; ADG_{10:30}: weight gain between 10 and 30 days of age; ADG_{30:70}: weight gain between 30 and 70 days of age; ADG_{30:90}: weight gain between 30 and 90 days of age **Table 1:** Means and Variation of Barbarine lambs growth traits

These performances are relatively low if compared to those reported on the same breed since the sixties. Lamb growth performances of the breed during the 1963-2014 period are shown in Table 2.

WB (kg)	W ₃₀ (kg)	W ₉₀ (kg)	ADG ₁₀₋₃₀ (g/d)	ADG ₃₀₋₉₀ (g/d)	Period	Author
3.5	10	21.8	236 ¹ 257 ²	185 ¹ 178 ²	(1963- 1969)	Tchamitchan et Sarson, [2]
3.5 (0.5)	9.6 (1.5)	19 (3.7)	200 (45)	156 (32)	(1971- 1979)	Sarson, 1972; Bedhiaf et al., 2001. [3,4]
3.5	10	20	207	166	(1963- 1979)	Ben Hamouda, 1985 [5]
3.4 (0.6)	9.1 (2.2)	17.8 (4.5)	183 (65)	146 (48)	(1968- 1988)	Khaldi et al., 1987 [6]
3.4 (0.7)	9.06 (2.4)	17.75 (4.9)	187.1 (72.7)	153 (53.5)	(1968- 1997)	Djemali et al., 1994 [7]
4,22	8,11	16,05	129,92	132,17	(2011-2014)	This study

Table 2: Growth performance of Barbarine lambs during 1963-2014 period

It appears clearly that lamb weights at weaning (90 d.) dropped gradually from 22 Kg (1960) to only 16 Kg (2014). The linear regression (Model 2) used under these conditions showed that if the situation does not change the weight of lambs at 90 d. will continue to decline by 200g / year to be 13.37 Kg in 2030 ($R^2 = 0.89$).

Genomics and Shortcuts

Many applications of Genomics could be identified under low input production systems. Saving DNA samples from threatened local breeds is one alternative to capture real variability before the disappearance of some valuable local breeds. Genetic variation

is the difference in DNA sequences between individuals within a population. Variation occurs in germ cells i.e. sperm and egg, and also in somatic (all other) cells. Only variation that arises in germ cells can be inherited from one individual to another and so affect population dynamics, and ultimately evolution (European Bioinformatics Institute). The second alternative can be the identification, using DNA's, of non-inbred males within flocks and reduce, consequently, the inbreeding effects. The third and the potential one should be to set up genomic evaluation based on a reference population with phenotypic data. This method, if DNA's sequencing becomes a cheap operation, will allow farmers in low input production systems to pick the most adapted animals with a descent production for reproduction.

Conclusion

Local animal breeds are a wealth and a heritage of humankind. Indiscriminate crossbreeding and the absence of reliable breeding strategies threaten the majority of native breeds in developing countries, like the Barbarine sheep breed. The lack of suitable breeding strategies including farmers' organization should be a priority that could be enhanced and consolidated if genomics is democratized.

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