Chapter 2 Sustainable development of the dairy goat under the influence of heritability and genetic improvement

Capítulo 2 Desarrollo sostenible de la cabra lechera bajo la influencia de la heredabilidad y el mejoramiento genético

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Abstract

The objective of this chapter is to characterize the goat farming system for the production and marketing of milk through the comprehensive management of the national and international market, including an analysis of its main indicators of genetic improvement, to understand how they affect the permanence of goat farming in Mexico, particularly in the livestock subsector. In this sense, an updated bibliographic synthesis on the production and commercialization of goat's milk was conducted, in order to understand the commercial context in which companies compete with each other. This paper also provides information on the bases of heritability, the obtaining and use of genotypes associated with productive and reproductive traits in goat farming, and molecular technologies in goat genetic improvement. This information will serve as support to any person dedicated to, or related to, the sustainable production of dairy goats.

Dairy goat, Goat milk, Genetic improvement

Introduction

In Mexico, goat milk production represents an important resource for various social strata (Maldonado *et al*., 2018). A production of 163.59 million L of goat milk was reported for the year 2020 (Ministry of Agriculture and Rural Development, 2021), suggesting the common denominator of this sector is the scarce or non-existent technification in its production process (De Gea, 2006). Mexican goat production is mainly located in the northeastern and central-western regions (arid-semiarid zones), with limited production in their pastures, has shown a gradual increase in the national inventory, which reached 8.8 million goats in 2020 (Statistics Division of the Food and Agriculture Organization of the United Nations, 2020). In the planning and execution of genetic improvement programs for dairy goats, the increase in milk yield per animal should be the main objective for achieving sustained profit growth (Organization for Economic Cooperation and Development, 2020). In this sense, the correct application of a selection program would result in higher production income, lower feed costs, and greater permanence in the herd, thus leading to the sustainable development of the dairy goat production unit (Organization for Economic Cooperation and Development, 2020).

Based on the information provided in previous paragraphs, this paper reviews: i) International goat milk production; ii) domestic goat milk production; iii) dairy goat breeds; iv) generalities of heritability (h^2) in goat breeding; v) applications of heritability in goat herd selection and improvement; vi) molecular technologies in goat breeding; vii) uses and applications of molecular markers; and viii) marker-assisted selection -- information that will support anyone involved in, or related to, sustainable development in intensive dairy goat production.

References for acronyms and abbreviations

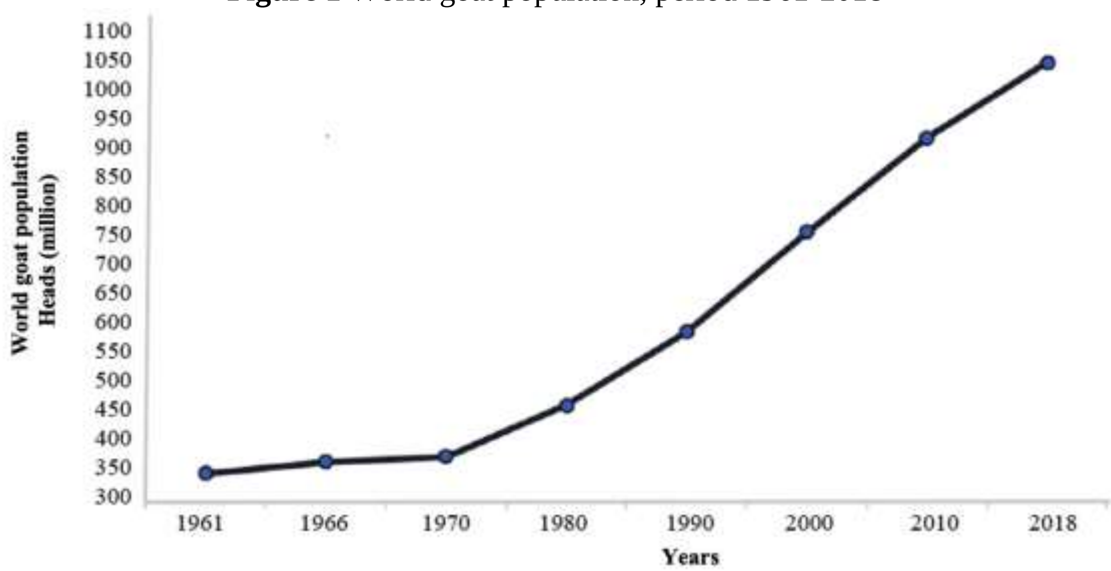
ADGA	American Dairy Goat Association
DNA	deoxyribonucleic acid
E_P	permanent environmental effects
E_T	temporary environmental effects
FAO	Food and Agriculture Organization of the United Nations
FAOSTAT	Statistics Division-Food and Agriculture Organization of the United Nations
G_A	additive genetic effects
GAS	genotyping assisted selection
G_D	dominance effects
G_E	epistatic effects
GWAS	genome-wide association study
h^2	heritability
IGA	International Goat Association
LM	Linked Markers
LPU	Livestock Production Units
MAS	marker-assisted selection
MST	Microbial Source Tracking
P	phenotype
PCR	polymerase chain reaction

SIAP Agri-Food and Fisheries Information and Statistics Service
SNP single nucleotide polymorphisms
USA United States

1. International goat milk production

The world population currently stands at 7.9 billion people and is expected to show a 30% increase over the next 30 years, reaching approximately 10.2 billion people by 2050 (Wesley and Peterson, 2017). This demographic increase will be accompanied by economic growth, which will result in an increased demand for goat dairy products (cheeses, in particular) (Kubicová *et al*., 2019). This increase in demand will be higher in developing countries, where growth is expected to be 103% (Kapaj and Deci, 2017). Faced with this trend, since 1982, the International Goat Association (IGA) has contributed to the expansion of knowledge, collaborative work policies, and the development of the goat sector in all corners of the world (International Goat Association, 2021). Within its platform, IGA notes that the domestication of goats (*Capra hircus*) occurred between 6,000 and 7,000 BC (Amills *et al*., 2017). Initially, most goats developed in Southwest Asia (Zheng *et al*., 2020), and by 2018, according to the database of the Food and Agriculture Organization of the United Nations (FAO), the world goat population reached 1.003 million head (Figure 1), equivalent to an increase of more than 30% since 2000 (Food and Agriculture Organization of the United Nations, 2020).

Figure 1 World goat population, period 1961-2018



Source of reference: (Food and Agriculture Organization of the United Nations, 2020)

Global goat milk production was estimated at 19.1 million t in 2019 (Food and Agriculture Organization of the United Nations, 2020). In Asia, governments and developmental agencies identified the dairy goat sector as a resilient alternative in the face of climate change and have invested in many projects over the last decade (Asian-Australasian Dairy Goat conference, 2018). Therefore, 55.4% of the world's goat inventory is located on the Asian continent (Table 1), with China, India, Sudan, Bangladesh, and Pakistan as its main livestock concentrating countries (Liang and Paengkoum, 2019). Asia also represents the highest production of goat milk (56.2% worldwide), with India producing 3,767,866 t, followed by Sudan with 1,104,620 t, Bangladesh with 1,051,493 t, and Pakistan with 824, 098 t (Miller and Lu, 2019).

Table 1. Goat distribution in different areas of the world, 2018

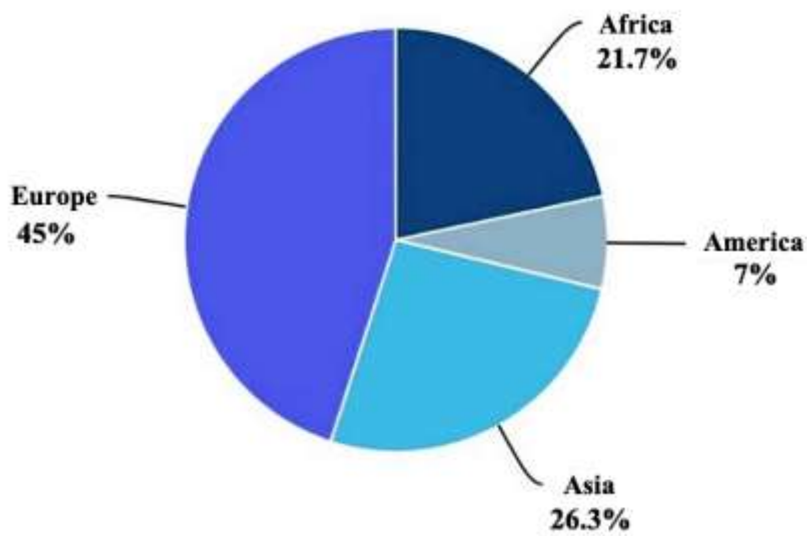
Continent	Heads (million)	Percentage (%)	Number of countries
Asia	556	55.4	48
Africa	388	38.7	59
Europe	17	1.7	42
Americas	38	3.8	47
Oceania	4	0.4	14
Total	1,003	100	201

Source of reference: (Statistics Division of the Food and Agriculture Organization of the United Nations, 2020)

Dairy goat farming in China has increased especially in the Shaanxi, Shandong, and Henan provinces, due to government recognition of the sector and its financial incentives (Liang and Paengkoum, 2019). However, Chinese production cannot meet the demand of its consumers; therefore, China is the world's largest importer of goat milk powder and whey for the manufacture of infant formula (Ribeiro and Ribeiro, 2010). Africa reached 38.7% of the world's goat inventory, despite the fact that its research, extension, and marketing plans, led by the African government, have prioritized cattle and overlooked small ruminants (Monau *et al*., 2020).

Significant goat milk production is found in many African countries, including Nigeria, Sudan, Chad, Ethiopia, and Kenya (Kahi and Wasike, 2019). However, although most of the world's production and consumption of goat milk is found in Asia, the most organized market for its industrialization is in Europe, mainly in cheeses (Figure 2), where production reached 483 thousand t in 2019, with France as the main contributor at the European level, followed by Spain, Greece, Germany, Italy, and the Netherlands (Dubeuf, 2010). Thus, during 2018, Europe participated with 17 million goats, with Russia, Spain, Romania, Greece, and Italy representing the five countries with the largest goat populations (Ruiz *et al*., 2019). Dairy goat production has a different origin in the Americas because goats are not indigenous to the Western Hemisphere (Ginja *et al*., 2017). European breeds were introduced by the Spanish during the colonial period, and today they remain the most popular dairy breeds (Lu and Miller, 2019). Nubian goats from Egypt have also been introduced through England and Nigerian goats through Africa, but Swiss and other European breeds remain dominant (Sponenberg, 2020). With respect to its goat inventory, the Americas represented 3.8% of the world's goats (Table 1), while Brazil, Mexico, Argentina, Haiti, and Bolivia stood out with the largest goat population on this continent (Lu and Miller, 2019).

Figure 2. Goat cheese production and distribution worldwide, 2019



Source of reference: (Statistics Division of the Food and Agriculture Organization of the United Nations, 2020)

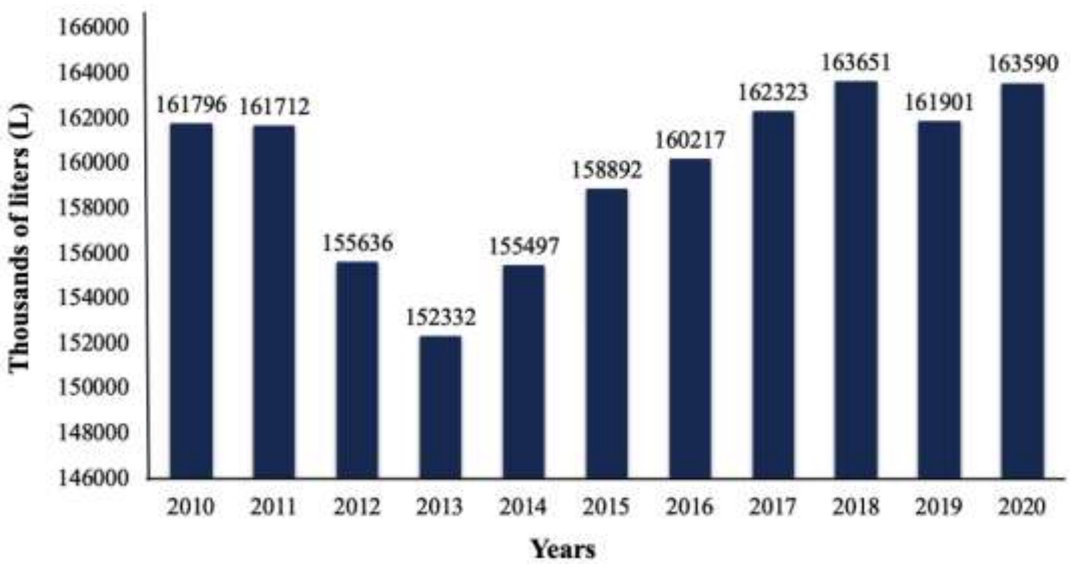
Finally, Oceania participated with 4 million goats, while Australia, Fiji, New Zealand, Vanuatu, and French Polynesia stood out as its main concentrating countries (Miller and Lu, 2019). Consequently, global goat milk production is concentrated in a few countries, mainly in Asia and Africa, with production systems located in tropical or arid regions. Goat milk is most likely consumed locally, while cow milk enters formal markets for processing (International Goat Association, 2021).

2. National production of goat milk

The national land area covers 1,964,375 km^2, of which 108.9 million hectares are used for livestock production, with the participation of 250,000 families whose primary or complementary productive activity is goat production (National Institute of Statistics and Geography, 2020). It represents 8.8 million goats (Statistics Division of the Food and Agriculture Organization of the United Nations, 2020), distributed across 494,000 Livestock Production Units (**LPU**), which, during 2020, reached a production of 163,590 L of goat milk (Figure 3), with a producer price of \$6.46/L (Agri-Food and Fisheries Information and Statistics Service, 2020), an annual per capita consumption of 1.3 L, and a share in national livestock production of 0.7% (Ministry of Agriculture and Rural Development, 2021).

Mexican goat farming represents 9 out of every 1,000 L of the world's total (Food and Agriculture Organization of the United Nations, 2020). It maintains a seasonal regime, due to the fact that goats are ruminants that present reproductive seasonality and multiple births (Maldonado *et al.*, 2018), as well as the availability of food during the rainy season and agricultural residues from seasonal crops (Clark and Mora, 2017).

Figure 3. Goat milk production in Mexico, 2010-2020 period



Source of reference: (Agri-Food and Fisheries Information and Statistics Service, 2020)

Production systems in the northeastern and central-western regions (arid-semiarid zones) of the states of Coahuila, Durango, Nuevo Leon, San Luis Potosi, and Zacatecas make up 64% of the total national goat inventory (Table 2). The remaining 36% is located in the central-temperate regions of the states of Guanajuato and Queretaro (Agri-Food and Fisheries Information and Statistics Service, 2021).

Table 2. Main goat milk producing states in Mexico, 2019

Ranking	Federal State	Thousands of liters (L)
1	Coahuila	45,065
2	Guanajuato	42,196
3	Durango	25,181
4	Jalisco	9,015
5	Chihuahua	7,341
6	Zacatecas	5,895
7	San Luis Potosi	4,769
8	Baja California Sur	4,123
9	Michoacan	4,036
10	Nuevo Leon	3,897
	Rest of Federal States	10,383
	Total	161,901

Source of reference: (Agri-Food and Fisheries Information and Statistics Service, 2020)

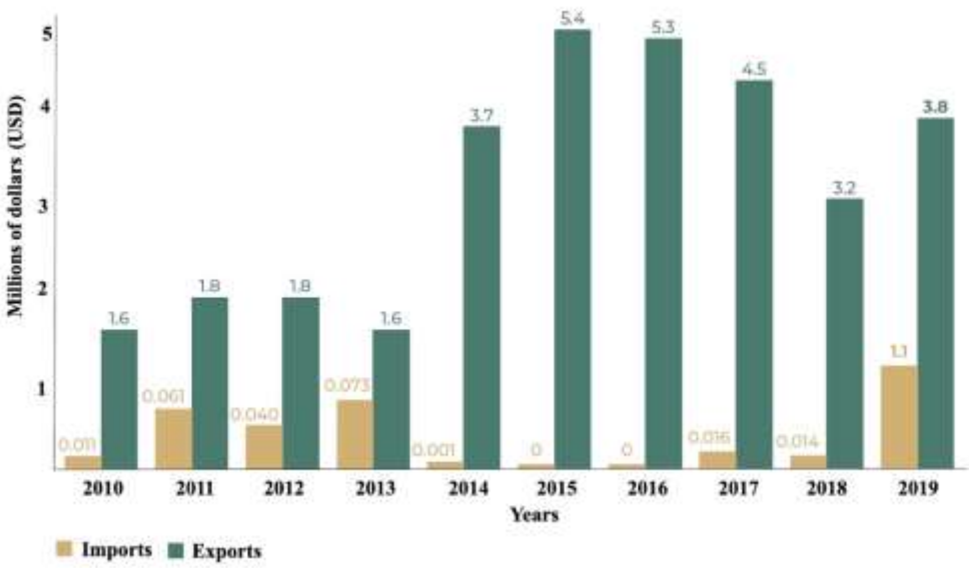
Coahuila and Guanajuato (Figure 4), are the largest producers of goat milk, together accounting for 53.9% of the country's production, equivalent to 87.259 million L (Ministry of Agriculture and Rural Development, 2021). Therefore, they contribute 52.2% of the total value of national production, equivalent to $515.6 million (Agri-Food and Fisheries Information and Statistics Service, 2021). National production is maintained by animals without a defined phenotype; however, in the Comarca Lagunera region, there seems to be a predominance of the dairy genotype (e.g., Alpine, Saanen and Nubian breeds) (Maldonado *et al*., 2018).

Figure 4. Main goat milk producing states in Mexico, 2019

Source of reference: (Agri-Food and Fisheries Information and Statistics Service, 2021)

Access of Mexican goat milk to cross-border trade circuits is mainly via dairy derivatives (e.g., curd and cheese) (Ministry of Agriculture and Rural Development, 2021). In this sense, Mexico exports only to the United States of America (USA), registering a flow of 3.8 million USD during 2019 (Figure 5). During the same year, imports reached 1.1 million USD, and came mainly from the USA, Spain, France, Portugal, and the Netherlands (Ministry of Economy, 2021).

Figure 5. International trade of goat milk derivatives in Mexico, period 2010-2019



Source of reference: (Ministry of Economy, 2021)

3. Dairy goat breeds

Alpine Breed

The Alpine is a French breed that is medium to large in size, with upright ears and a variety of colors. The hair is medium to short, and the face is straight.

Figure 6. Alpine breed specimen

Source of reference: (American Dairy Goat Association, 2020)

Alpine colors are described by using the following terms:

– **Cou Blanc (coo blanc):** “White neck” – white front quarters and black hindquarters, with back or gray markings on the head;

– **Cou Clair (coo clair):** “Clear neck” – front quarters are tan, saffron, off-white, or shading to gray with back hindquarters;

– **Cou Noir (coo nwah):** “Black neck” – black forequarters and white hindquarters;

– **Sundgau (sundgow):** “Black neck” – black front quarters and white hindquarters;

– **Pied:** Spotted or mottled;

– **Chamoisee (shamwahzay):** Brown or bay, distinctive markings are the black face and dorsal stripe; feet and legs sometimes with a martingale running along the withers and down to the chest;

– **Two-Tone Chamoisee:** Light front quarters with brown or gray hindquarters. This is not a *cou blanc* or *cou clair*, as these terms are reserved for animals with black hindquarters; and

– **Broken Chamoisee:** A solid chamoisee color, broken with another color by being banded or splashed. Any variation in the above patterns broken with white should be described as a broken pattern, such as a broken cou blanc (American Dairy Goat Association, 2020).

Alpine females are at least 76 cm tall and weigh 61 kg, while males are at least 81 cm tall and weigh 77 kg. They have upright ears and come in many colors and color combinations (Figure 6). The hair is medium to short, and the bridge of the nose is smooth. Alpines are known to be a hardy and adaptable animal that thrives in any climate while maintaining good health and excellent production (American Dairy Goat Association, 2020).

Florida Breed

The Florida goat is a dairy goat breed native to the Lower Guadalquivir Valley, Spain. Its origin dates back to the beginning of the 20th century, but it wasn’t until 1997 when it became an official breed recognized by the Official Catalog of Livestock Breeds of Spain (American Dairy Goat Association, 2020). Its origin comes from the contribution of Nubian-type animals to the Alpine-Pyrenean stock native to the Guadalquivir Valley. It owes its name to the particular characteristics of its mottled red-on-white background or vice versa, so that it resembles a flowery field.

Florida goats are an attractive animal that embodies vigor, strength, and femininity, with a morphostructural conformation suitable for milk production (American Dairy Goat Association, 2020). It is a hypermetric, longilinear breed with a subconvex profile with arched and backward horns. The coat is mottled white on a red background or vice versa but mottled white on a black background is also acceptable (Figure 7).

Figure 7. Florida breed goats bred in Spain

Source of reference: (National Association of Florida Goat Breeders, 2012)

Both the presence and absence of mammaries is allowed (National Association of Florida Goat Breeders, 2012). The head is long with a convex or subconvex profile, with a not very broad forehead. The ears are large in size and set back, parallel in alertness and drooping at rest. The trunk should be long and deep, which determines a great respiratory and digestive capacity. Withers are fine and slightly prominent, chest broad at the base and manifest sternal keel. The flanks are deep, arched, and refined. The rump has a strong union with the back, being broad, strong, long, and slightly sloping. The tail is set slightly above the tip of the ischium (Figure 8).

Figure 8. Florida breed females bred in Spain

Source of reference: (National Association of Florida Goat Breeders, 2012)

The limbs are strong, well-separated, and conformed. The forelegs are straight and well-plumb, and the hind legs are parallel, well-separated, and almost perpendicular from the hock to the fetlock, when viewed from the side. The mammary system presents good capacity and a strong insertion, with a well-developed and well-implanted udder, but of medium depth and with well-positioned and defined teats. Males belonging to the Florida breed have a shorter head length and more accentuated convexity of the front, with a strong and developed neck, without losing length (Figure 9).

Figure 9. Florida stallions bred in Spain

Source of reference: (National Association of Florida Goat Breeders, 2012)

The Florida goat breed is mainly used for milk production and is characterized by high production, with high fat and protein content (Table 3).

Table 3. Milk production characteristics of the Florida breed

Number of births	No. lactations	Lactation duration (d)	Milk production (kg)	Fat (%)	Protein (%)
Primiparous	1086	256	496.08	5.08	3.64
Multiparous	2085	282	699.16	4.99	3.62
Mean	3171	273.48	629.61	5.02	3.63

Source of reference: (National Association of Florida Goat Breeders, 2012)

Another remarkable product of this breed is the suckling kid, where it shows a good productive potential. Due to the size of this breed, kids present an average birth weight of 3.2 kg, and an average daily gain of 180 g. The average slaughter weight of 8 and 9 kg is reached quickly between 25 and 30 days of life, with a carcass weight of 4.5 to 5 kg (International Goat Association, 2021).

Nubian breed

The Nubian breed descends from the crossbreeding of regional English, Irish, and Swiss goats (Saanen) with imported males from Egypt (Nubia Zaraibe), Ethiopia, Syria, Iran, and India (Jamna Pari) (De Gea, 2006).

Figure 10. Nubian breed specimen

Source of reference: (American Dairy Goat Association, 2020)

In 1910, the Anglo Nubian was recognized as a breed in Great Britain and registration began with 459 goats accepted as the nucleus of the Anglo Nubian section of the studbook (Stemmer *et al*., 2009). The Nubian is relatively large and of Asian, African, and European origin. They are known for milk with high fat content. Females are at least 76 cm tall and weigh 61 kg, while males are at least 81 cm tall and weigh 77 kg (American Dairy Goat Association, 2020).

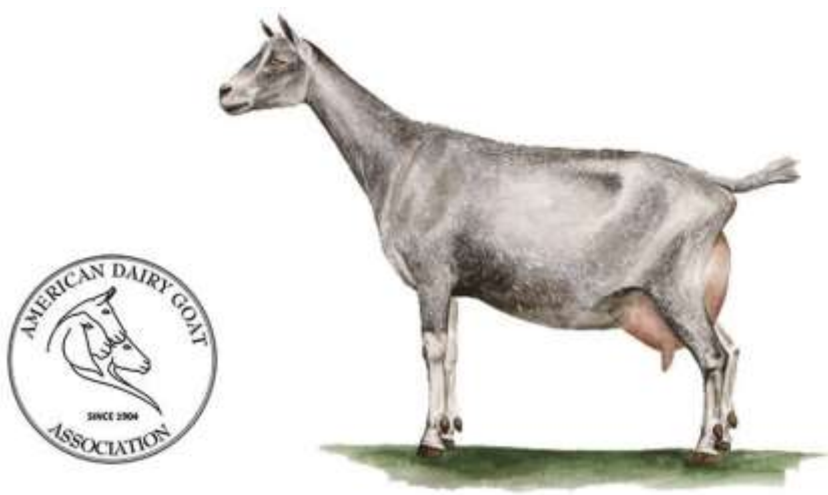
The head is the distinguishing feature of the breed, with the facial profile between the eyes and the muzzle being strongly convex, often referred to as the "Roman nose". The ears are long (extending at least an inch beyond the muzzle when held flat along the face), broad, and pendulous (Figure 10). They lie close to the head at the temple, flaring slightly and well-forward at the rounded tip, forming a “bell”. The ears are not thick, with well-defined cartilage.

The hair is short, fine, and shiny. Any color or colors, solid or patterned, are acceptable. The breed standard accepts specimens of any color or combination of colors, although the predominant colors are tan (red), dark brown, overo and dark (black) (De Gea, 2006). It was introduced in the USA and Canada. Later, by means of selection, they began to specialize in milk production, and it was in the USA where the greatest emphasis was placed on genetic improvement, which led to better developed production.

Sable breed

This breed comes from pure Saanen animals that presented colors other than white and creamy white (Figure 11). Breeders in the USA selected and fixed the color coat characteristic by crossing between the animals that presented these “anomalies”.

Figure 11. Sable breed specimen



Source of reference: (American Dairy Goat Association, 2020)

To differentiate it from the traditional Saanen, it has received the name Sable, given that the first animals selected had colored hairs between the white coat (as is the sable color in other animals), with these animals being of a grayish color (as if they were dirty), light brown, or black with markings of the Alpine and Toggenburg type (International Goat Association, 2021).

The phenotype (physical characteristics) in purebred or full-blood animals is virtually the same as traditional Saanen, with the exception of the coat color. However, because it is a relatively recent breed, it still has an open pedigree book, so there are different grades of Sable recognized by the American Dairy Goat Association (ADGA) (American Dairy Goat Association, 2020).

The Sable grades recognized by the ADGA are as follows:

- Purebred Sable;
- American Sable;
- Grade Sable; and
- Experimental Sable.

According to some Sable breeders, heat and humidity tolerance characteristics, as well as fertility and production in tropical areas, are superior to those shown by traditional, pure Saanen. In Mexico, it is believed that there is little presence of this breed; however, the influence of the lines carrying Saanen genetics is greater than what is thought. Therefore, even though it has not been recognized as an official breed in Mexico, the Sable is a great option for use in tropical dairy herds (American Dairy Goat Association, 2020).

Saanen breed

Saanen is a Swiss breed. It is medium to large in size and the bones are rough. However, females should be smooth and not coarse. Saanens are all white or light cream in color, white being preferred (Figure 12).

Figure 12. Saanen breed specimen

Source of reference: (American Dairy Goat Association, 2020)

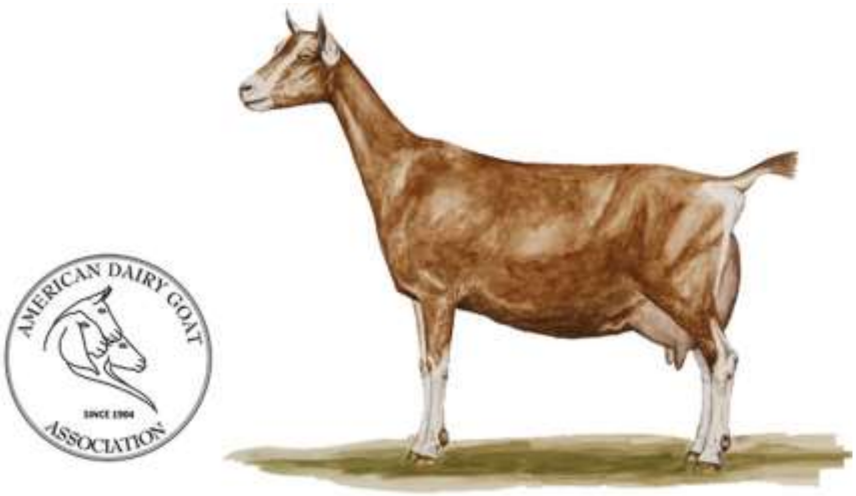
Its hair is short and fine, although a fringe over the spine and thighs is often present. The ears should be erect and carried attentively, preferably pointing forward. The face should be straight or domed. A “Roman nose” tendency is discriminated against (International Goat Association, 2021). Female goats are at least 76 cm tall and weigh 61 kg, while males are at least 81 cm tall and weigh 77 kg. The Saanen breed is distinguished by its solid white or light cream-colored hair. Skin patches may be present and a spot in the coat up to 3.8 cm wide is permitted. Saanen ears are erect and the bridge of the nose is straight or convex. The Saanen is a favorite for commercial dairies, due to its high milk production and calm temperament (American Dairy Goat Association, 2020).

Toggenburg breed

Toggenburg is a Swiss breed. This breed is of medium size. The hair is short to long, soft, and fine. Its color is solid, varying from light beige to dark chocolate with no preference for any shade (Figure 13). Distinctive white markings are as follows: White ears with a dark spot in the middle; two white stripes down the face from above each eye to the muzzle; white hind legs from the hocks to the hooves; white front legs from the knees down, with dark vertical stripes below the knee being acceptable; a white triangle on each side of the tail; white spots may be present at the root of the wattles or in that area, if no wattles are present (International Goat Association, 2021).

Varying degrees of cream markings, rather than pure white, are acceptable, but not desirable. Ears are erect and carried forward. Facial lines may be concave or straight, but never blunt. The bridge of the nose may be straight or convex (American Dairy Goat Association, 2020).

Figure 13. Toggenburg breed specimen



Source of reference: (American Dairy Goat Association, 2020)

Female Toggenburgs are at least 66 cm tall and weigh 54 kg, while males are at least 71 cm tall and weigh 68 kg. Toggenburgs were among the first purebred dairy goats imported into the USA and registered (American Dairy Goat Association, 2020).

4. Heritability (h^2) generalities in goat genetic improvement

The objective of breeding programs involves the identification and utilization of the best individuals within a herd, so that the next generation will show a better performance in the selected traits, with respect to the average of the previous generation (Biffani *et al.*, 2020). In that sense, the breeder needs information on the phenotype of the animals for the proper selection of parents, evaluation methods, selection methods, and mating systems (Scholtens *et al.*, 2020).

The phenotype of an individual is mainly influenced by a number of genetic and environmental factors, so that a specific quantitative trait not only describes the genetic differences between animals in a given population, but also the variability of the trait corresponding to the effect of the environment in which these animals develop (Schultz *et al.*, 2020). The genetic and environmental components of phenotype (P) can be divided into additive genetic effects (G_A), dominance effects (G_D), and epistatic effects (G_E), in addition to both permanent environmental effects (E_P) and temporary environmental effects (E_T) (Arnal *et al.*, 2020).

$$P = G_A + G_D + G_1 + E_P + E_T \quad (1)$$

In selection programs, permanent environmental effects present a disadvantage to the breeder, when the environmental influence of a mother has a significant impact on the behavior of her progeny (Scholtens *et al.*, 2020). For example, a young female develops mastitis and loses function in a certain environment, resulting in reduced weaning weights of subsequent offspring. In this regard, genetic evaluation methods implement contemporary groups to explain some of the environmental effects and adequately predict the additive genetic component (fraction heritable from parents to progeny) (from Araujo Neto *et al.*, 2018).

Several strategies have been developed to accurately characterize the proportion of variation in a trait in a population that can be attributed to heritable genetic factors (MacNeil *et al.*, 2021). Heritability is the specific concept that encompasses this proportion, defined as the average phenotypic differences or superiority that is likely to be genetically transmitted to the next generation and is calculated as follows (Kocevska *et al.*, 2021):

$$h^2 = \sigma^2 A / \sigma^2 P \quad (2)$$

Where:

h^2 = Heritability of a trait in a given population;
σ^2_A = Genetic variance (genetic potential of an animal that can be transmitted to its progeny); and
σ^2_P = Phenotypic variance of a trait in that population (variability of phenotypes in the population).

The heritability estimate ranges from 0 to 1; it is often expressed as a percentage (Ginja *et al.*, 2017). A number close to 1 indicates that a trait is highly heritable in a population. This aspect gives it great importance in selective breeding and behavioral genetics (Kocevska *et al.*, 2021).

Heritability plays an important role in the selection of polygenic traits, especially those related to animal production and behavior (Chen *et al.*, 2020). It may also increase if genetic variation increases, causing individuals to show more phenotypic variation, such as showing different levels of maternal production (Schmid *et al.*, 2021). Furthermore, heritability may also increase if environmental variation decreases, causing herd individuals to show less phenotypic variation, such as similar maternal characteristics among females in the herd (Asadi-Fozi *et al.*, 2020).

5. Applications of heritability in the selection and improvement of goat herds

Heritability indicates to the breeder how much confidence to place in the phenotypic behavior of an animal when choosing breeding parents for the next generation (Schmid *et al.*, 2021). Some of the traits reported in the literature for meat and dairy goats are presented in Tables 4, 5, and 6. In highly-heritable traits, where h^2 exceeds 0.40, the animal's phenotype is a good indicator of genetic merit or breeding value (Martin *et al.*, 2016). On the other hand, traits where the h^2 is less than 0.15, the performance value of an animal is much less useful for identifying individuals with the best genes for the trait of interest (Garcia-Peniche *et al.*, 2012).

Table 4. Heritability values for productive and reproductive traits in dairy goats

Trait	h^2	Breeds	Source of reference
Supernumerary nipples	0.40 0.44	Alpine Saanen	Martin *et al.* (2016)
Age at first birth (days)	0.22 0.28 0.32 0.61 0.16 0.32	Alpine Lamancha Nubian Oberhasli Saanen Toggenburg	Garcia-Peniche *et al.* (2012)
Interval between births (days)	0.06 0.04 0.02 0.02 0.06 0.08	Alpine Lamancha Nubian Oberhasli Saanen Toggenburg	Garcia-Peniche *et al.* (2012)

When the trait is highly heritable, selection is more important than crossbreeding and handling, but when the trait is low in heritability, selection is not appropriate, in lieu of crossbreeding and handling (Ginja *et al.*, 2017). In other words, having this knowledge provides an idea of the possibilities of achieving genetic improvement through selection (Schmid *et al.*, 2021).

Table 5. Heritability values for productive and reproductive traits in dairy and dual purpose goats

Trait	h^2	Breeds	Source of reference
Milk production (kg)	0.36 0.48 0.44 0.61 0.36 0.47 0.29 0.45	Alpine Lamancha Nubian Oberhasli Saanen Toggenburg Aradi Damascus	Garcia-Peniche *et al.* (2012) Kahi and Wasike (2019)
Fat production (kg)	0.36 0.43 0.40 0.60 0.34 0.44	Alpine Lamancha Nubian Oberhasli Saanen Toggenburg	Garcia-Peniche *et al.* (2012)
Protein production (kg)	0.36 0.54 0.45 0.59 0.38 0.49	Alpine Lamancha Nubian Oberhasli Saanen Toggenburg	Garcia-Peniche *et al.* (2012)
Fat production (%)	0.51 0.50 0.56 0.42 0.46 0.59 0.23 0.22	Alpine Lamancha Nubian Oberhasli Saanen Toggenburg Aradi Damascus	Garcia-Peniche *et al.* (2012) Kahi and Wasike (2019)
Protein production (%)	0.46 0.66 0.57 0.46 0.43 0.57	Alpine Lamancha Nubian Oberhasli Saanen Toggenburg	Garcia-Peniche *et al.* (2012)

Research conducted by Ginja *et al.* (2017) indicated that heritability estimates are lower in extensive handling systems, given the scarcity of dietary energy for the expression of genetic variation under extensive handling conditions; therefore, the breeder should take into account the origin of these heritability estimates. However, the absence of a significant difference between the different handling levels in the present finding could be due to the fact that most of the heritability estimates for the intensive handling levels were estimated using an animal model, and most of the heritability estimates in extensive and semi-intensive handling were calculated using the parent-offspring relationship (Garcia-Peniche *et al.*, 2012; Kahi and Wasike, 2019).

Table 6. Heritability values for reproductive traits in meat and dual purpose goats

Trait	h^2	Breeds	Source of reference
Birth weight	0.15 0.41 0.08 - 0.18	Ardi Damascus Boer	Mohammed *et al.* (2018) Menezes *et al.* (2016)
Weaning weight	0.26 0.35 0.23	Ardi Damascus Boer	Mohammed *et al.* (2018) Menezes *et al.* (2016)
Weight at 180 days	0.45 0.18	Ardi Damascus	Mohammed *et al.* (2018)
Daily weight gain	0.17 0.31	Criolla goat Boer	Menezes *et al.* (2016) Josiane *et al.* (2020)
Body length	0.14	Boer	Zhang *et al.* (2008)
Litter weight at birth	0.05	Boer	Menezes *et al.* (2016)
Child survival	0.02	Criolla goat	Josiane *et al.* (2020)
Interval between births	0.10	Boer	Menezes *et al.* (2016)

Breeders should rely on heritability values from herds that have handling, genetic, and environmental similarities; otherwise, one needs to keep in mind that this value will act more as a partial guideline on which to base decisions to select and improve the herd (Ginja *et al.*, 2017).

6. Molecular technologies in goat genetic improvement

Until the mid-1960s, markers used in genetics and animal breeding were controlled by genes associated with polymorphic traits, generally easy to identify visually (Mukherjee *et al.*, 2019). Only a small number of morphological markers and phenotypic characteristics of easy visual identification allowed finding significant associations between these and economically important characteristics (Mukherjee *et al.*, 2019). However, due to their limitations, isoenzymatic markers emerged – biochemical markers that distinguish homozygous from heterozygous genotypes – becoming accessible to a greater number of species, consequently providing better results in the differentiation of individuals (Ramesh *et al.*, 2020).

The application of molecular techniques as an additional support for the selection of animals has gained importance, since it is possible to identify genes with favorable effects for productive characteristics, as well as detrimental alleles for the productive behavior of carrier animals (Arnal *et al.*, 2020). In this sense, the development of different techniques for the realization of such identification has allowed its application in various areas of livestock production, and different molecular markers have been developed for this purpose (Biffani *et al.*, 2020).

Molecular markers are defined as fragments of deoxyribonucleic acid (DNA), with specific, identifiable locations, which inheritance can be traced at the genomic level and correspond to expressed or unexpressed regions of the genome (Zonaed Siddiki *et al.*, 2020). Currently, the molecular markers most commonly used in the livestock sector are classified into two groups: i) Microbial Source Tracking (MST), and ii) direct markers, also known as linked markers (LM) (Wakchaure *et al.*, 2015). MSTs are short sequences of one to four nucleotides repeated 10 to 50 times throughout the genome of the species and flanked by highly conserved regions (Ramesh *et al.*, 2020).

The most well-known MSTs are randomly amplified DNA polymorphisms, restriction fragment length polymorphisms, amplified fragment length polymorphisms, and simple, repeated sequences, better known as microsatellites (Xia *et al.*, 2018). Microsatellites are mostly used in breed conservation studies, being a fundamental tool in understanding the genetic structure of Criolla goat populations, as part of the improvement of national programs aimed at the rescue, conservation, and use of any breed (Asroush *et al.*, 2018).

LM are specific loci along the genome of the species in charge of encoding genes corresponding to certain well-defined characteristics. Baumung *et al.* (2004) indicate the presence of about three million LM; a little more than 700,000 have been validated in humans and cattle. For these markers, variants of the polymerase chain reaction (PCR) technique have been developed, based on different physicochemical properties of DNA (Biffani *et al.*, 2020).

The development of DNA sequencing led to the discovery of single nucleotide polymorphisms (SNP) (Eck *et al.*, 2009), considered the most widely used trait-linked markers of livestock interest today. The abundant presence in the genome, genetic stability, and high capacity for inclusion in automated analyses make SNPs a useful tool in genotyping (Asroush *et al.*, 2018), genome-wide association study (GWAS), and genomic evaluations (Biffani *et al.*, 2020).

7. Uses and applications of molecular markers

Techniques based on molecular markers have been widely used in several animal species, obtaining important results for the development of crossbreeding schemes, breed conservation, and the application of this knowledge in genomic preventive medicine (Al-Samarai and Al-Kazaz, 2015). Commercially, the most widely used chip in animal genotyping is the 50k chip with 54,609 SNP-type markers (Chhotaray *et al.*, 2020).

The continuous advance and development of techniques based on molecular markers, as well as their increasingly routine application, have allowed the costs of such tests to become more and more affordable (Bouwman *et al.*, 2018). Thus, applications in livestock today include paternity testing, with exclusion probabilities > 90%, validation of pedigree records, measurement of genomic response to selection, identification of individuals carrying (or free of) genetic diseases, as well as disease-resistant animals, marker-assisted selection, and introgression (Sudrajad *et al.*, 2020).

Pedigree verification is an important aspect of the use of molecular markers in several programs (Eck *et al.*, 2009), as they provide substantial opportunities to increase the accuracy of estimated genetic values and gain (Ginja *et al.*, 2017). Likewise, the identification of possible carriers of lethal or detrimental genes allows the breeder to include only healthy animals, with ideal genetic profiles, in accordance with the established selection objectives (Vargas *et al.*, 2018).

Several goat breeder associations worldwide have implemented, to a greater or lesser extent, DNA testing to validate their reproductive animals and establish genetic fingerprints that allow, in the medium term, to increase the accuracy of the genetic values of their animals. For example, the American Dairy Goat Association (2020) has, since 2015, implemented mandatory DNA testing to obtain genetic profiles of all registered and unregistered males before the offspring are eligible for registration.

Paternity testing is also offered as part of this service. In addition, tests performed include: Carrier identification for G6 sulfatase deficiency, scrapie (transmissible, spongiform encephalopathy), and alpha S1 casein type, in addition to genetic fingerprinting and paternity testing (American Dairy Goat Association, 2020). This has allowed the global implementation of genetic improvement strategies in production, reproduction, and health.

The differences in the scopes and reports of the DNA tests of the different associations depend on their correct interpretation during decision making at the time of selection, generating, to a greater or lesser extent, the need for training of both the team of technicians and the breeders themselves (Table 7).

Table 7. Interpretation of DNA test data

Code	Meaning	Interpretation
SQ	DNA-qualified stallion	Suitable male qualified by DNA, third generation
DQ	DNA-qualified womb	Suitable female qualified by DNA, third generation
PQ	Qualified sires	Suitable male or female qualified by DNA, second generation
OT	Original DNA proof	Suitable male or female qualified by DNA, first generation
SE	Stallion excluded by DNA	Male not suitable for breeding, qualified by DNA
DE	Womb excluded by DNA	Female not suitable for breeding, qualified by DNA
DNA	With DNA test	Animal with genetic fingerprint and paternity test available
N/N	Normal	G6S free
N/G	Carrier	G6S carrier
G/G	Affected	G6S affected
NN QQ	Affected	No resistance to classical scrapie
NN QK	Highly-susceptible carrier	One copy of protective variant K222, increased resistance to classical scrapie
NN KK	Moderately-susceptible carrier	Two copies of protective variant K222, increased resistance to classical scrapie
NS QQ	Highly-susceptible carrier	One copy of protective variant S146, increased resistance to classical scrapie
SS QQ	Moderately-susceptible carrier	Two copies of protective variant S146, increased resistance to classical scrapie
NS QK	Very low-susceptible carrier	One copy each of protective variant S146 and K22, increased resistance to classical scrapie
A, B	High alpha S1 casein production (CSN1S1)	Any combination is associated with high volumes of CSN1S1 production
E, F, N	Low production of alpha S1 casein (CSN1S1)	Any combination is associated with high production volumes of CSN1S1
O1	No production of alpha S1 casein (CSN1S1)	No production of CSN1S1
A, B, E, F, N	Medium production of alpha s1 casein (CSN1S1)	Any combination is associated with medium CSN1S1 production volumes

Source of reference: (American Dairy Goat Association, 2020)

8. Marker-assisted selection

Marker-assisted selection (MAS) is an auxiliary tool for genetic evaluations in cattle herds, as it allows greater genetic progress, in combination with conventional methods (Zheng *et al.*, 2021). The use of genetic identification techniques for MAS of high-quality animals has gained importance in the identification of genes related to productive characteristics, as well as genes with detrimental effects on the productive behavior of carrier animals (Petrović *et al.*, 2018).

MAS is used in several countries to determine polymorphisms in the alleles that make up the genotypes of milk proteins, which have direct effects on the composition and technological properties of milk (Al-Samarai and Al-Kazaz, 2015) – a fact that Amills *et al.* (2017) demonstrated by reporting the influence of genetic characteristics of animals on the physicochemical behavior of milk. Asroush *et al.* (2018) and Zonaed Siddiki *et al.* (2020) established the theoretical basis for animal selection based on genomic evaluations, gaining popularity in animal production. Such evaluations are based on considering the parts of the genome that animals inherited from their parents.

The concept behind marker-assisted selection is that there may be genes with significant effects that can be specifically targeted in selection (Martin *et al.*, 2016). Some traits are controlled by single genes (e.g., hair color), but most economically important traits are quantitative traits that are usually controlled by a fairly large number of genes (Ginja *et al.*, 2017). However, some of these genes may have a major effect, and can be referred to as major effect genes, located in QTL (Al-Samarai and Al-Kazaz, 2015). Although the term QTL is strictly applied to genes of any effect, in practice, it refers only to major genes, since only these will be large enough to be detected and mapped in the genome (Ramesh *et al.*, 2020).

When making selection decisions based on marker genotypes, it is important to know what information can be inferred from the marker genotypes (Menezes *et al.*, 2016). The use of direct markers is straightforward, as the marker genotype provides a direct indication of the QTL genotype (Ginja *et al.*, 2017). The problem is how to base decisions on indirect markers. When there is a direct marker (DNA test) for a QTL, we can use direct marker-assisted selection, sometimes known as Genotyping Assisted Selection (**GAS**) (Isik and Bilgen, 2019). Where only linked markers exist for a QTL, we must use indirect MAS-assisted selection. In either case, the goal is to determine QTL genotypes to aid selection (Menezes *et al.*, 2016).

The value of this depends on several factors: i) When heritability is low, the value of individual QTL information tends to be higher, because the precision of the genetic values increase by a relatively larger amount (Al-Samarai and Al-Kazaz, 2015); ii) when the traits of interest cannot be measured in a gender, the marker information provides a basis for classifying animals of that gender (Xia *et al.*, 2018); iii) if the trait cannot be measured prior to sexual maturity, the marker information can be used to select at a juvenile stage (Chhotaray *et al.*, 2020); and iv) if a trait is difficult to measure or requires sacrifice (as is the case with many corpse traits), the information from the marker can be used (Asroush *et al.*, 2018).

Conclusions

Some considerations regarding the goat livestock system for milk production and commercialization were reviewed through the lens of integral management of the national and international market, including an analysis of its main genetic improvement indicators. It is considered that the evaluation of dairy goats by heritability in selection, assisted by molecular markers, is a methodology that interprets the interests of the producer. In addition, the use of DNA tests provided by genetic evaluation services should be accompanied by breeding values for individual traits, thus facilitating breeders who wish to apply their own weighting criteria to achieve sustainable development of the dairy goat.

References

Agri-Food and Fisheries Information and Statistics Service. (2020). *SIAP. Agrifood industry*. Retrieved 22 Oct from http://nube.siap.gob.mx/cierre_pecuario/

Agri-Food and Fisheries Information and Statistics Service. (2021). *SIAP. Agri-food Information Consultation System (SIACON)*. Retrieved 20 Oct from https://www.gob.mx/siap/documentos/siacon-ng-161430

Al-Samarai, F., R,, and Al-Kazaz, A., A,. (2015). Molecular markers: an introduction and applications. *Eur j mol biotechnol, 9*(3), 118-130. https://doi.org/10.13187/ejmb.2015.9.118

American Dairy Goat Association. (2020). *AGDA. The breed standards*. Retrieved 25 Sep from https://adga.org/breed-standards/

Amills, M., Capote, J., and Tosser-Klopp, G. (2017). Goat domestication and breeding: a jigsaw of historical, biological and molecular data with missing pieces. *Anim Genet, 48*(6), 631-644. https://doi.org/10.1111/age.12598

Arnal, M., Larroque, H., Leclerc, H., Ducrocq, V., and Robert-Granie, C. (2020). Estimation of genetic parameters for dairy traits and somatic cell score in the first 3 parities using a random regression test-day model in French Alpine goats. *J Dairy Sci, 103*(5), 4517-4531. https://doi.org/10.3168/jds.2019-17465

Asadi-Fozi, M., Bradford, H. L., and Notter, D. R. (2020). Direct and correlated responses to selection for autumn lambing in sheep. *Genet Sel Evol, 52*(1), 56. https://doi.org/10.1186/s12711-020-00577-z

Asian-Australasian Dairy Goat conference. (2018). *Fourth Asian-Australasian Dairy Goat conference.* Retrieved 20 Sep from https://www.iga-goatworld.com/blog/conference-report-4th-asian-australasian-dairy-goat-conference

Asroush, F., Mirhoseini, S. Z., Badbarin, N., Seidavi, A., Tufarelli, V., Laudadio, V., Dario, C., and Selvaggi, M. (2018). Genetic characterization of Markhoz goat breed using microsatellite markers. *Arch Anim Breed, 61*(4), 469-473. https://doi.org/10.5194/aab-61-469-2018

Baumung, R., Simianer, H., and Hoffmann, I. (2004). Genetic diversity studies in farm animals–a survey. *J Anim Breed Genet, 121*(6), 361-373. https://doi.org/10.1111/j.1439-0388.2004.00479.x

Biffani, S., Tiezzi, F., Fresi, P., Stella, A., and Minozzi, G. (2020). Genetic parameters of weeping teats in Italian Saanen and Alpine dairy goats and their relationship with milk production and somatic cell score. *J Dairy Sci, 103*(10), 9167-9176. https://doi.org/10.3168/jds.2020-18175

Bouwman, A. C., Daetwyler, H. D., Chamberlain, A. J., Ponce, C. H., Sargolzaei, M., Schenkel, F. S., Sahana, G., Govignon-Gion, A., Boitard, S., Dolezal, M., Pausch, H., Brondum, R. F., Bowman, P. J., Thomsen, B., Guldbrandtsen, B., Lund, M. S., Servin, B., Garrick, D. J., Reecy, J., Vilkki, J., Bagnato, A., Wang, M., Hoff, J. L., Schnabel, R. D., Taylor, J. F., Vinkhuyzen, A. A. E., Panitz, F., Bendixen, C., Holm, L. E., Gredler, B., Hoze, C., Boussaha, M., Sanchez, M. P., Rocha, D., Capitan, A., Tribout, T., Barbat, A., Croiseau, P., Drogemuller, C., Jagannathan, V., Vander Jagt, C., Crowley, J. J., Bieber, A., Purfield, D. C., Berry, D. P., Emmerling, R., Gotz, K. U., Frischknecht, M., Russ, I., Solkner, J., Van Tassell, C. P., Fries, R., Stothard, P., Veerkamp, R. F., Boichard, D., Goddard, M. E., and Hayes, B. J. (2018). Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals. *Nat Genet, 50*(3), 362-367. https://doi.org/10.1038/s41588-018-0056-5

Chen, S. Y., Oliveira, H. R., Schenkel, F. S., Pedrosa, V. B., Melka, M. G., and Brito, L. F. (2020). Using imputed whole-genome sequence variants to uncover candidate mutations and genes affecting milking speed and temperament in Holstein cattle. *J Dairy Sci, 103*(11), 10383-10398. https://doi.org/10.3168/jds.2020-18897

Chhotaray, S., Panigrahi, M., Pal, D., Ahmad, S. F., Bhushan, B., Gaur, G. K., Mishra, B. P., and Singh, R. K. (2020). Ancestry informative markers derived from discriminant analysis of principal components provide important insights into the composition of crossbred cattle. *Genomics, 112*(2), 1726-1733. https://doi.org/10.1016/j.ygeno.2019.10.008

Clark, S., and Mora, G., M. B. (2017). A 100-year review: Advances in goat milk research. *J Dairy Sci, 100*(12), 10026-10044. https://doi.org/10.3168/jds.2017-13287

de Araujo Neto, F. R., Pegolo, N. T., Aspilcueta-Borquis, R. R., Pessoa, M. C., Bonifacio, A., Lobo, R. B., and de Oliveira, H. N. (2018). Study of the effect of genotype-environment interaction on age at first calving and production traits in Nellore cattle using multi-trait reaction norms and Bayesian inference. *Anim Sci J, 89*(7), 939-945. https://doi.org/10.1111/asj.12994

De Gea, G. S. (2006). *Breeds of goats in production in Argentina. Argentine Site of Animal Production*. Retrieved 25 Sep from https://www.produccionanimal.com.ar/produccion_ovina/ovina_y_caprina_curso_fav/33-razas_cabras.pdf

Dubeuf, J. P. (2010). Characteristics and diversity of the dairy goat production systems and industry around the world. Structural, market and organisational conditions for their development. *Tecnol & Ciên Agropec, 4*(5), 25-31. https://hal.inrae.fr/hal-02813363

Eck, S. H., Benet-Pages, A., Flisikowski, K., Meitinger, T., Fries, R., and Strom, T. M. (2009). Whole genome sequencing of a single Bos taurus animal for single nucleotide polymorphism discovery. *Genome Biol, 10*(8), R82. https://doi.org/10.1186/gb-2009-10-8-r82

Food and Agriculture Organization of the United Nations. (2020). *FAO. World production statistics*. Retrieved 22 Sep from http://www.fao.org/fishery/statistics/es

Garcia-Peniche, T. B., Montaldo, H. H., Valencia-Posadas, M., Wiggans, G. R., Hubbard, S. M., Torres-Vazquez, J. A., and Shepard, L. (2012). Breed differences over time and heritability estimates for production and reproduction traits of dairy goats in the United States. *J Dairy Sci, 95*(5), 2707-2717. https://doi.org/10.3168/jds.2011-4714

Ginja, C., Gama, L. T., Martínez, A., Sevane, N., Martin, B. I., Lanari, M. R., Revidatti, M. A., A., A. M. J., Bedotti, D. O., Ribeiro, M. N., Sponenberg, P., Aguirre, E. L., Álvarez, F. L. A., Menezes, M. P. C., Chacon, E., Galarza, A., Gómez, U. N., Martínez, L. O. R., Pimenta, F. E. C., da Rocha, L. L., Stemmer, A., Landi, V., and Delgado, B. J. V. (2017). Genetic diversity and patterns of population structure in Creole goats from the Americas. *Anim Genet, 48*(3), 315-329. https://doi.org/10.1111/age.12529

International Goat Association. (2021). *IGA. Little Rock, AR, EE. UU.* Retrieved 20 Sep from https://www.iga-goatworld.com/

Isik, R., and Bilgen, G. (2019). Associations between genetic variants of the POU1F1 gene and production traits in Saanen goats. *Arch Anim Breed, 62*(1), 249-255. https://doi.org/10.5194/aab-62-249-2019

Josiane, M., Gilbert, H., and Johann, D. (2020). Genetic parameters for growth and kid survival of indigenous goat under smallholding system of Burundi. *Animals (Basel), 10*(1), 1-13. https://doi.org/10.3390/ani10010135

Kahi, A. K., and Wasike, C. B. (2019). Dairy goat production in sub-Saharan Africa: current status, constraints and prospects for research and development. *Asian-Australas J Anim Sci, 32*(8), 1266-1274. https://doi.org/10.5713/ajas.19.0377

Kapaj, A., and Deci, E. (2017). World milk production and socio-economic factors effecting its consumption. In W. R. Ross, J. R. Collier, and R. V. Preedy (Eds.), *Dairy in human health and disease across the lifespan* (1ª illustrated ed., Vol. 1, pp. 107-115). Academic Press.

Kocevska, D., Barclay, N. L., Bramer, W. M., Gehrman, P. R., and Van Someren, E. J. W. (2021). Heritability of sleep duration and quality: A systematic review and meta-analysis. *Sleep Med Rev, 59*, 101448. https://doi.org/10.1016/j.smrv.2021.101448

Kubicová, Ľ., Predanocyová, K., and Kádeková, Z. (2019). The importance of milk and dairy products consumption as a part of rational nutrition. *Potr S J F Sci, 13*(1), 234-243. https://doi.org/10.5219/1050

Liang, J. B., and Paengkoum, P. (2019). Current status, challenges and the way forward for dairy goat production in Asia - conference summary of dairy goats in Asia. *Asian-Australas J Anim Sci, 32*(8), 1233-1243. https://doi.org/10.5713/ajas.19.0272

Lu, C. D., and Miller, B. A. (2019). Current status, challenges and prospects for dairy goat production in the Americas. *Asian-Australas J Anim Sci, 32*(8), 1244-1255. https://doi.org/10.5713/ajas.19.0256

MacNeil, M. D., Berry, D. P., Clark, S. A., Crowley, J. J., and Scholtz, M. M. (2021). Evaluation of partial body weight for predicting body weight and average daily gain in growing beef cattle. *Transl Anim Sci, 5*(3), txab126. https://doi.org/10.1093/tas/txab126

Maldonado, J. J. A., Salinas, G. H., Torres, H. G., Becerril, P. C. M., and P., D. R. (2018). Factors influencing milk production of local goats in the Comarca Lagunera, Mexico. *Livest Res Rural Dev, 30*(7), 2-7. https://lrrd.cipav.org.co/lrrd30/7/glat30132.html

Martin, P., Palhiere, I., Tosser-Klopp, G., and Rupp, R. (2016). Heritability and genome-wide association mapping for supernumerary teats in French Alpine and Saanen dairy goats. *J Dairy Sci, 99*(11), 8891-8900. https://doi.org/10.3168/jds.2016-11210

Menezes, L., Sousa, W., Cavalcanti-Filho, E., and Gama, L. (2016). Genetic parameters for reproduction and growth traits in Boer goats in Brazil. *Small Rumin Res, 136*(1), 247-256. https://doi.org/10.1016/j.smallrumres.2016.02.003

Miller, B. A., and Lu, C. D. (2019). Current status of global dairy goat production: an overview. *Asian-Australas J Anim Sci, 32*(8), 1219-1232. https://doi.org/10.5713/ajas.19.0253

Ministry of Agriculture and Rural Development. (2021). *SADER. Agrifood Newsletter*. Retrieved 20 Oct from https://www.gob.mx/agricultura

Ministry of Economy. (2021). *SE. Tariff Information System*. Retrieved 22 Oct from http://www.economia-snci.gob.mx/

Mohammed, K. M., El–Den, M. A. K., and Dahmoush, A. Y. (2018). Heritability and variance components estimates for growth traits in Saudi Ardi goat and Damascus goat and their crosses. *Asian Pac J Reprod, 7*(1), 39. https://doi.org/10.4103/2305-0500.220984

Monau, P., Raphaka, K., Zvinorova, C. P., and Gondwe, T. (2020). Sustainable utilization of indigenous goats in Southern Africa. *Diversity, 12*(1), 20-30. https://doi.org/10.3390/d12010020

Mukherjee, S., Huda, S., and Sinha Babu, S. P. (2019). Toll-like receptor polymorphism in host immune response to infectious diseases: A review. *Scand J Immunol, 90*(1), e12771. https://doi.org/10.1111/sji.12771

National Association of Florida Goat Breeders. (2012). *ACRIFLOR. Specimens of the Florida breed bred in Spain*. Retrieved 25 Sep from http://www.acriflor.org/datos.html

National Institute of Statistic and Geography. (2020). *INEGI. Dirección General de Estadísticas Sociodemográficas*. Retrieved 22 Oct from https://www.inegi.org.mx

Organisation for Economic Cooperation and Development. (2020). Dairy and dairy products. In Food and Agriculture Organization (Ed.), *OECD-FAO Agricultural Outlook 2020-2029* (1a illustrated ed., Vol. 1, pp. 174-183). Food and Agriculture Organization. http://www.fao.org/documents/card/es/c/ca8861en/

Petrović, M. P., Selionova, M. I., Caro-Petrović, V., Ružić-Muslić, D., Maksimović, N., Ilić, Z. Z., and Pavlović, I. (2018). The application of modern molecular techniques in animal selection. *Biotechnol Anim Husb, 34*(4), 371-386. https://doi.org/10.2298/BAH1804371P

Ramesh, P., Mallikarjuna, G., Sameena, S., Kumar, A., Gurulakshmi, K., Reddy, B. V., Reddy, P., and Sekhar, A. C. (2020). Advancements in molecular marker technologies and their applications in diversity studies. *J Biosci, 45*(1), 1-15. https://doi.org/10.1007/s12038-020-00089-4

Ribeiro, A. C., and Ribeiro, S. D. A. (2010). Specialty products made from goat milk. *Small Rumin Res, 89*(2-3), 225-233. https://doi.org/10.1016/j.smallrumres.2009.12.048

Ruiz, M. F. A., Castel, G. J. M., and Guerrero, Y. M. (2019). Current status, challenges and the way forward for dairy goat production in Europe. *Asian-Australas J Anim Sci, 32*(8), 1256-1265. https://doi.org/10.5713/ajas.19.0327

Schmid, M., Imort-Just, A., Emmerling, R., Fuerst, C., Hamann, H., and Bennewitz, J. (2021). Genotype-by-environment interactions at the trait level and total merit index level for milk production and functional traits in Brown Swiss cattle. *Animal, 15*(1), 100052. https://doi.org/10.1016/j.animal.2020.100052

Scholtens, M. R., Lopez-Villalobos, N., Garrick, D., Blair, H., Lehnert, K., and Snell, R. (2020). Genetic parameters for total lactation yields of milk, fat, protein, and somatic cell score in New Zealand dairy goats. *Anim Sci J, 91*(1), e13310. https://doi.org/10.1111/asj.13310

Schultz, E. B., Santana, T. E. Z., Silva, F. F., Garcia, A. O., Oliveira, H. R., Rodrigues, M. T., and Brito, L. F. (2020). Short communication: Genetic parameter estimates for caprine arthritis encephalitis in dairy goats. *J Dairy Sci, 103*(7), 6407-6411. https://doi.org/10.3168/jds.2019-17740

Sponenberg, D. P. (2020). Local goat breeds in the United States. In S. Kukovics (Ed.), *Goats (Capra) from ancient to modern* (1ª illustrated ed., Vol. 1, pp. 34-42). IntechOpen.

Statistics Division of the Food and Agriculture Organization of the United Nations. (2020). *FAOSTAT. Production. Primary livestock.* Retrieved 25 Sep from http://faostat3.fao.org/download/Q/*/S

Stemmer, A., Scgultz, M. S., Gall, C., and Zarate, A. (2009). Develompnet and wordwide, distribution of the anglo nubian goat. *Trop Subtrop Agroecosyst, 11*(2), 185-188.

Sudrajad, P., Subiharta, S., Adinata, Y., Lathifah, A., Lee, J. H., Lenstra, J. A., and Lee, S. H. (2020). An insight into the evolutionary history of Indonesian cattle assessed by whole genome data analysis. *PLoS One, 15*(11), e0241038. https://doi.org/10.1371/journal.pone.0241038

Vargas, G., Neves, H. H. R., Camargo, G. M. F., Cardoso, V., Munari, D. P., and Carvalheiro, R. (2018). Genome-wide association study and functional analysis of feet and leg conformation traits in Nellore cattle. *J Anim Sci, 96*(5), 1617-1627. https://doi.org/10.1093/jas/sky079

Wakchaure, R., Ganguly, S., Praveen, P., Kumar, A., and Sharma, S. (2015). Marker Assisted Selection (MAS) in Animal Breeding: A Review. *J Drug Metab Toxicol, 6*(1), e127. https://doi.org/10.4172/2157-7609.1000e127

Wesley, E., and Peterson, F. (2017). The role of population in economic growth. *Sage Open, 7*(4), 1-15. https://doi.org/10.1177/2158244017736094

Xia, Y., Luo, W., Yuan, S., Zheng, Y., and Zeng, X. (2018). Microsatellite development from genome skimming and transcriptome sequencing: comparison of strategies and lessons from frog species. *BMC Genomics*, *19*(1), 886. https://doi.org/10.1186/s12864-018-5329-y

Zhang, C., Yang, L., and Shen, Z. (2008). Variance components and genetic parameters for weight and size at birth in the Boer goat. *Livestock Science, 115*(1), 73-79. https://doi.org/10.1016/j.livsci.2007.06.008

Zheng, J., Deng, T., Jiang, E., Li, J., Wijayanti, D., Wang, Y., Ding, X., and Lan, X. (2021). Genetic variations of bovine PCOS-related DENND1A gene identified in GWAS significantly affect female reproductive traits. *Gene, 802*(1), 145867. https://doi.org/10.1016/j.gene.2021.145867

Zheng, Z., Wang, X., Li, M., Li, Y., Yang, Z., Wang, X., Pan, X., Gong, M., Zhang, Y., Guo, Y., Wang, Y., Liu, J., Cai, Y., Chen, Q., Okpeku, M., Colli, L., Cai, D., Wang, K., Huang, S., Sonstegard, T. S., Esmailizadeh, A., Zhang, W., Zhang, T., Xu, Y., Xu, N., Yang, Y., Han, J., Chen, L., Lesur, J., Daly, K. G., Bradley, D. G., Heller, R., Zhang, G., Wang, W., Chen, Y., and Jiang, Y. (2020). The origin of domestication genes in goats. *Sci Adv, 6*(21), 5216-5221. https://doi.org/10.1126/sciadv.aaz5216

Zonaed Siddiki, A., Miah, G., Islam, M. S., Kumkum, M., Rumi, M. H., Baten, A., and Hossain, M. A. (2020). Goat genomic resources: The search for genes associated with Its economic traits. *Int J Genomics, 2020*(1), 5940205. https://doi.org/10.1155/2020/5940205