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Cytogenetic study of Meriz goat breeds in Iraqi Kurdistan Region

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Abstract

Goats are considered the leading farm animal that has a substantial role in the agricultural sector in the Kurdistan Region of Iraq. No cytological examination has been carried out on them. This experiment aims to identify the Karyotype of the local breeds of domestic goats. This experiment was conducted on the Karyotype and prepared the ideogram of Meriz goats. The determination of the relative length and centromeric index arm ratio of the chromosomes in the breed was achieved by the production of karyotypes. A total of (30)Meriz goats, consisting of (10) males and (20) females, were selected to collect blood samples for a short-term lymphocyte culture. The diploid chromosome count was observed to be (60), consisting of (29) pairs of acrocentric autosomes and one pair of allosomes, specifically the X and Y chromosomes. The acrocentric nature of the X-chromosome and the sub-metacentric nature of the Y-chromosome were identified through scientific investigation. The study observed a variation in the relative length of autosomal chromosomes in Meriz goats, with females ranging from 4.49% to 1.89% and males ranging from (4.53%) to (1.75%). The X-chromosome had a relative length of 3.96 in females, while the Y-chromosome displayed a relative length of (5.05). The findings of this karyological investigation suggest that the chromosomal composition seen in the Meriz goats under examination was within the expected range of normalcy. It is recommended that more cytogenetic analyses be conducted at the population level in order to identify individuals within the Meriz breed population who possesses numerical and/or structural chromosome abnormalities. This research is crucial for enhancing the efficiency of production and reproduction in this breed.

Keywords: Meriz goat, Karyotype, Ideogram, Quinacrine stain

1. Introduction

The Meriz (Kurdi) goats are reared in the elevated regions of the Iraqi Kurdistan mountains and are classified as one of the goat breeds that produce Cashmere. The breeders' lack of familiarity with the importance of Cashmere and its handling results in the undercoat fibers of this particular breed being disregarded [1]. Around 10,000 years ago, goats (Capra hircus) were domesticated in the eastern frontier of Iraq in the Zagros Mountains [2]. In most parts of Iraq, particularly in Kurdistan, it is cultivated primarily for milk and meat consumption, making it an essential animal species. Farmers can start their small projects with these animals that are well-adapted, low-priced, and high-producing, such as meat, milk, and mohair. Goats contribute as much as 19.9% of the national income from producing ruminants and animals. Furthermore, 33.8% of the revenue from the meat and milk of ruminants comes from goat meat and dairy (Ministry of Planning 1991)[3].

The primary objective of growing Meriz goats is to utilize their fibres in the production of traditional Kurdish national attire. On the contrary, the breeders' lack of familiarity with the significance of Cashmere and the potential for processing its hair leads to the disregard of the undercoat fibers [4]. Moreover, it is widely regarded as the principal source of both meat and milk. These diminutive ungulates are easily manageable and possess the ability to withstand adverse environmental circumstances [3]. Regrettably, the characterization of this crucial genetic resource breed has only been accomplished in recent times. Hence, the primary objective of the present investigation was to furnish fundamental insights regarding the Meriz goat. This insight will prove beneficial for researchers, goat breeders, conservationists of animal genetic resources, and students studying animal production.

Local small ruminant breeds are widely recognized as a crucial resource for future international agricultural policies [5]. Low-potential rural areas and wastelands can be exploited through their excellent adaptation to specific environments, which provides rural societies with typical animal-derived products [6]. Furthermore, there have been reports indicating that indigenous goat genotypes, which are well-adapted to the local environmental circumstances, exhibit the ability to yield sufficient milk production and facilitate optimal growth of offspring without the need for additional feeding [7]. Additionally, the indigenous goat population in Iraq holds considerable importance as a spe-

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cies. Their contributions to meat and milk production are particularly noteworthy, particularly within the prevailing agricultural systems of the nation [8].

Understanding the shape and arrangement of chromosomes, as well as their impact on economic features, is advantageous in formulating effective animal breeding methods. According to Basumatary (2003)[9], examining the chromosomal profile in Livestock can provide valuable insights into the reproductive health and fertility status of breeding animals, including those in their early stages of development. The implementation of cytogenetic screening in the assessment of species and breeds is of paramount importance in the conservation and management of animal genetic resources. In the context of "in situ" conservation programmes, detecting and preventing breeding concerns involving chromosomal abnormalities are of utmost significance, primarily due to the restricted population size of the subjects involved. In "ex-situ" programs, it is imperative to verify that the cryopreserved material, including cells, sperm, oocytes, and embryos, originates from animals exhibiting a normal karyotype, due to the reasons mentioned above. In this manner, cryopreserved materials possess the potential for future utilisation in the construction of the breed or the restoration of reproductive capacity in animals. To the best of our knowledge, despite its significant cultural and economic significance, there has been a lack of efforts to characterise this particular goat breed cytogenetically. Previous studies have shown cytogenetic analysis of goats across different species [10–13]. However, there is a shortage of knowledge regarding the Mariz goat breed. The primary objective of the present investigation was to carry out an initial cytogenetic assessment of the Mereiz goat breed, which is raised in Iraq, to ascertain its conformity with the established Karyotype standard for the species (ISCNDB, 2001). Additionally, the study sought to validate the feasibility of commencing a cytogenetic screening program specifically tailored for this particular breed.

According to Mandal et al. (2018), the application of cytogenetic investigation in domestic animals represents a valuable biotechnological approach that can contribute to the genetic enhancement of livestock. This technique enables the identification of animals free from chromosomal aberrations, which are responsible for various issues such as abnormal body conformation, congenital anomalies, reduced fertility (in the case of balanced chromosome abnormalities), or sterility (in the case of sex chromosome abnormalities). In the absence of cytogenetic regulation, the occurrence of chromosome abnormalities in animals can evade the process of natural selection, leading to adverse consequences for reproductive capacity, particularly among female carriers [14].

The utilization of karyotype analysis for local sheep and goat breeds will be highly beneficial in the identification of numerical and structural chromosome aberrations, as well as in establishing the cytotaxonomic link between these species [15, 16]. In accordance with Typylo (2020) [17], the economic effectiveness and profitability of the sheep breeding sector are contingent upon the quality of the product, which is ascertained by its genetic potential. Hence, it is imperative to possess a comprehensive understanding of the genetic composition of both herds and breeds in order to effectively manage and enhance animal production and breeding standards.

Cytogenetic studies in Livestock have been extensively extended in many laboratories to investigate the association between chromosomal aberrations and phenotypic effects, particularly on fertility [18, 19]. Considering the existence of numerous research conducted on the phenotypic characterization of the Mariz goat, there is a scarcity of cytogenetic characterization information available. As a result, we will discuss this breed's chromosomal profile and morphometric traits in this article [20–22].

2. Materials and Methods

A total of thirty Meriz goats, consisting of (10 males and 20 females, were chosen for a karyotype analysis. These goats were randomly picked from a privately owned migrating flock located in Nwawa Village/Betwata in the Rania District of the Sulaimani Governorate, which is situated in the Iraqi Kurdistan region. The chromosomal analysis was conducted in accordance with the technique established by Benn and Delach (2008). A volume of three millilitres of peripheral blood was obtained from each animal and collected in vacuum tubes containing lithium heparin as an anticoagulant (VACUTEST KIMA S.r.l - Italy). Subsequently, 0.5 mL of this blood sample was combined with 4.5 mL of a chromosomal medium P, which was ready for use (Euroclone S.P.A. Italy). The samples underwent incubation for a duration of 71 hrs., at a temperature of 37°C. Approximately one hour before the conclusion of the culture, a volume of 100 µL of colchicine (Gibco, USA) was introduced. Subsequently, the mixture was subjected to centrifugation, and the resulting pellet was treated with a hypotonic solution (0.075 M KCl) and incubated at a temperature of 37°C for 10 minutes. The samples underwent centrifugation and were afterwards fixed using a fixative solution composed of acetic acid and methanol in a volumetric ratio of 1:3. This process was repeated three to four times, after which approximately 2-3 droplets of cell suspension were carefully deposited onto a clean, tilted slide from a height of three feet. The drops were released at a 45° angle, while the edge of the slide was held against the bench. The dried slides were submerged in a trypsin solution comprising 2.5 mL of Trypsin-EDTA 1× in PBS (manufactured by Euroclone S.P.A. Italy) mixed with 50 mL of normal saline for a duration of one minute at a temperature of 37°C. Subsequently, the specimens were subjected to Giemsa staining, a fluorescence-based staining technique that uses quinacrine to detect and characterise individual chromosomes, as well as any associated structural abnormalities, based on the resultant banding pattern. The exact identification of each chromosome can be achieved by the utilisation of the distinctive banding pattern. The chromosome is stained using fluorochrome quinacrine mustard or quinacrine dihydrochloride (atebrin) and thereafter examined under a fluorescence microscope, revealing a distinct banding pattern. The fluorescence intensity is influenced by the arrangement of DNA bases along the chromosomal DNA, which in turn affects the interaction of the dyes with the DNA. In the work of Benn et al. (2008), it has been observed that regions with a high AT content have the ability to enhance fluorescence, whereas regions with a high GC content tend to suppress or quench fluorescence[23].

2.1. The karyological parameters used for chromosome characterization

2.1.1. Measurement of relative length

The calculation of the relative length of each chromosome in relation to the overall genomic length is performed employing the formula outlined by Bhatia and Shanker (1999) and Eroğlu et al. (2021)[24, 25].

Determining the relative lengths of chromosomes is achieved by assessing a specific chromosome's proportional contribution to the haploid genome's overall length.

$$\text{Relativelength} = \frac{\text{Length of individual chromosome}}{\text{The total length of the genome}} \times 100 \ldots\ldots\ldots (\text{Eq. 1})$$

2.1.2. Centromeric index

The centromeric index was calculated through Equation 2.

$$\text{Centromeric index (CI)} = \frac{(\text{SA})}{(\text{LA} + \text{SA})]} \times 100 \ldots\ldots\ldots (\text{Eq. 2})$$

2.1.3. Arm ratio

The arm ratio is determined for the chromosomes with arms by employing the formula outlined by Bhatia and Shanker (1999) and Eroğlu et al. (2021) [24, 25].

$$\text{Arm ratio} = \frac{\text{Length of long arm (q)}}{\text{Length of short arm (p)}} \ldots\ldots\ldots (\text{Eq. 3})$$

3. Results

In the present study, it was observed that all metaphase spreads investigated displayed a diploid number (2n) of 60 chromosomes, consisting of 58 autosomes and two sex chromosomes (XY in males and XX complement in females) (Figures 1 and 2). The acrocentric nature of the 58 autosomes was ascertained. The first six chromosomes exhibited medium acrocentric characteristics, with the X-chromosome being recognized as acrocentric. Determining the arms ratio and centromeric index confirmed that the Y-chromosome displayed a sub-metacentric look.

The Meriz goat population exhibited a range of mean relative length values for autosomes, with females ranging from 4.49 to 1.89 and males ranging from 4.53 to 1.75. The X-chromosome in females had a relative length of 3.96, while the Y-chromosome had a relative length of 5.05. Comparatively, the mean relative length of the X-chromosome was found to be the largest when compared to that of the autosomes, as seen in Tables 1 and 2.

This study examined the average arms ratio of male Meriz goats, which was revealed to be 5.65, 6.08, 6.89, 7.56, 7.96, and 8.39 respectively. Additionally, the arms ratio of all Y-chromosomes was determined to be 1.26. The centromeric index of the goats was also measured, with values of 15.09, 14.16, 12.75, 11.73, 11.24, and 10.74. Furthermore, the centromeric index of all Y-chromosomes was discovered to be 44.80. The observed parameters in

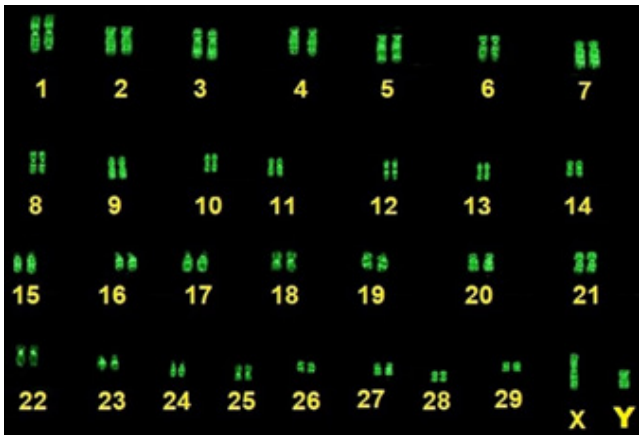

Fig. 1. Normal Male Meriz Goat Karyotype by quinacrine stain.

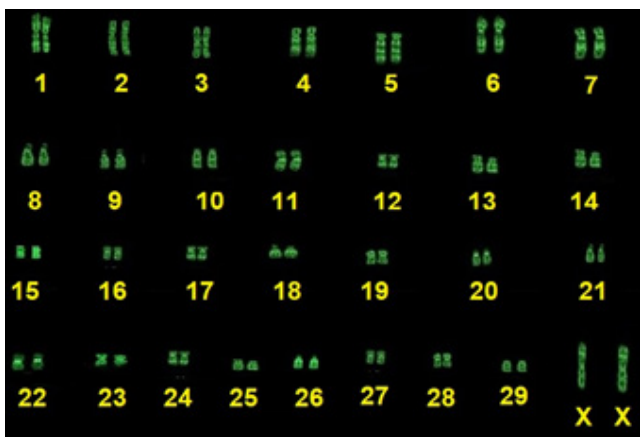

Fig. 2. Normal Female Mariz Goat Karyotype by quinacrine stain.

Table 1. The relative length of the chromosome of Meriz female goat.

Chromosome pair number	Average of relative length (µm)	Type of chromosome
1	4.49	Acrocentric
2	4.43	Acrocentric
3	4.37	Acrocentric
4	4.11	Acrocentric
5	4.16	Acrocentric
6	4.09	Acrocentric
7	3.63	Acrocentric
8	3.59	Acrocentric
9	3.56	Acrocentric
10	3.53	Acrocentric
11	3.41	Acrocentric
12	3.47	Acrocentric
13	3.37	Acrocentric
14	3.33	Acrocentric
15	3.31	Acrocentric
16	3.29	Acrocentric
17	3.26	Acrocentric
18	3.21	Acrocentric
19	3.032	Acrocentric
20	2.98	Acrocentric
21	2.91	Acrocentric
22	2.89	Acrocentric
23	2.83	Acrocentric
24	2.71	Acrocentric
25	2.591	Acrocentric
26	2.55	Acrocentric
27	2.49	Acrocentric
28	2.48	Acrocentric
29	1.89	Acrocentric
X	3.96	Acrocentric
X	3.96	Acrocentric

Table 2. The relative length of the chromosome of Meriz male goat.

Chromosome pair number	Average of relative length (µm)	Type of chromosome
1	4.53	Acrocentric
2	4.23	Acrocentric
3	4.1	Acrocentric
4	4.02	Acrocentric
5	3.94	Acrocentric
6	3.86	Acrocentric
7	3.37	Acrocentric
8	3.31	Acrocentric
9	3.27	Acrocentric
10	3.19	Acrocentric
11	3.14	Acrocentric
12	3.1	Acrocentric
13	3.09	Acrocentric
14	2.99	Acrocentric
15	2.97	Acrocentric
16	2.89	Acrocentric
17	2.85	Acrocentric
18	2.81	Acrocentric
19	2.74	Acrocentric
20	2.69	Acrocentric
21	2.64	Acrocentric
22	2.62	Acrocentric
23	2.58	Acrocentric
24	2.51	Acrocentric
25	2.45	Acrocentric
26	2.43	Acrocentric
27	2.39	Acrocentric
28	2.36	Acrocentric
29	1.75	Acrocentric
X	4.12	Acrocentric
Y	5.06	Submetacentric

Table 3 confirm the submetacentric nature of the Y-chromosome in Meriz goats. Additionally, the arms ratio of female Meriz goats was measured to be 6.24, 6.42, 6.72, 7.10, 7.41, and 8.39, respectively. Furthermore, the arm length ratio of all X-chromosomes was determined to be 17.65, while the centromeric index values were found to be 13.83, 13.50, 12.98, 12.40, 11.97, and 10.85. Lastly, the centromeric index of all X-chromosomes was observed to be 5.43, as presented in Table 4. The aforementioned criteria collectively support the conclusion that the X-chromosome in Meriz goats exhibits a sub-medium acrocentric characteristic.

4. Discussion

Several studies have reported that the number and morphology of autosomes exhibit similarities across various Indian goat breeds, such as Berari [26], Mahabubnagar [27], Karnataka local goats [28], Sangamneri [29], Osmanabadi and Boer bucks[30], as well as native Black Bengal goats (Banani et al., 2018). Contrary to the current research findings, Pattnayak and Patro (1986) discovered that the autosomes exhibited telocentric characteristics in Ganjam and Black Bengal goats[31].

Berari and the current investigation both concur on the acrocentric characteristic of the X-chromosome [26], Mahabubnagar [32], Karnataka local goats [28], Sangamneri [29], Osmanabadi and Boer bucks [30], as well as Native Black Bengal [33]. According to Khavary's study conducted in 1973, the X-chromosome in Tehran goats was seen to be telocentric, which contradicts the more recent research findings. The current investigation revealed that the Y-chromosome had a sub-metacentric morphology. However, previous studies conducted by Khavary (1973)[34], Jayashree (2014), and Bhagat et al. (2014) have discovered that the morphology of the goat in Karnataka native goats and Sangamneri goats was metacentric and had a modest complement. Bunch et al. (1977) have posited that the Y-chromosome has a metacentric or submetacentric structure, but an acrocentric configuration is not observed. According to the study of Umadevi et al. (2011)[32], the Y-chromosome in the Mahabubnagar local goat breed and Black Bengal goat breeds exhibited a smaller and dot-like appearance. The researchers in the study conducted by Banani et al. (2018) observed that the Y-chromosome in Black Bengal goats exhibited a compact, dot-like struc-

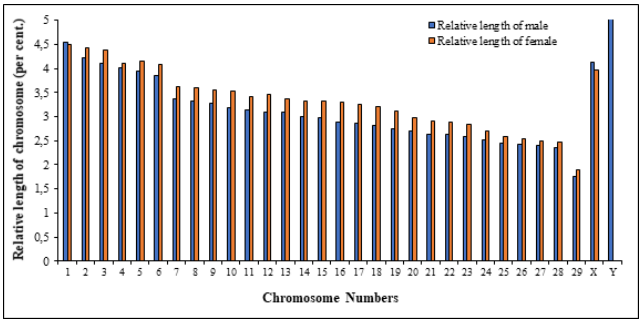

Fig. 3. Idiogram of Meriz goat.

Table 3. Arm ratio and centromere index of the first six chromosomes of Meriz Male goat.

Chromosome pair number	Arm length ratio average (q/p)(µm)	Centromere index average (µm)
1	5.65	15.09
2	6.08	14.16
3	6.89	12.75
4	7.56	11.73
5	7.96	11.24
6	8.39	10.74
Y	1.26	44.80

Table 4. Arm ratio and centromere index of the first six chromosomes of Meriz female goat.

Chromosome pair number	Arm length ratio average (%) (q/p) (µm)	Centromere index average (%) (µm)
1	6.24	13.83
2	6.42	13.50
3	6.72	12.97
4	7.10	12.40
5	7.41	11.97
6	8.31	10.85
X	17.65	5.43

ture, which led them to hypothesise that it may possess sub-metacentric characteristics.

The study conducted on Jayawadagi goats revealed that the average relative lengths of autosomes varied between 1.81±0.08 and 4.79±0.09 percent in females, and between 1.46±0.17 and 4.11±0.44 percent in males. The X-chromosome in females had a relative length of 5.24±0.19, whereas in males, it measured 4.13±0.63. Conversely, the Y-chromosome displayed a relative length of 1.40±0.24. According to Saravanan et al. (2006)[35], the autosomes in Kanniadu goats had relative lengths ranging from 1.61 to 5.49 percent. According to Umadevi et al. (2011)[32], the least-square means for the relative length of autosomes in mono, bi, and multicoloured Mahabubnagar goats varied from 1.997 to 4.742 percent, 2.050 to 5.065 percent, and 2.041 to 4.672 percent, respectively. The study found no statistically significant variation in the relative length of autosomes across these three groups of goats. According to Jayashree (2014), the average relative length (%) of autosomes varied between 1.65±0.11 and 5.69±0.18 in males, and between 1.68±0.13 and 5.26±0.16 in females. Notably, there were substantial disparities in relative length seen between males and females for the 1st, 16th, 17th, 19th, 20th, 21st, 23rd, 24th, and 25th pairs of autosomes. According to Banani et al. (2018), the autosomes in Black Bengal goats exhibited a range of relative lengths, measuring from (1.79 to 5.19)percent in females and (1.78 to 5.25) percent in males (Fig 3).

According to Pattnanayak and Patre (1986), the X-chromosome in Ganjam goats had a relative length ranging from 5.1 to 5.8 percent. The X-chromosome length in Mahabubnagar goats was reported to be 5.86±0.08 by Ekambaram et al. (2011) and 5.16 by Umadevi et al. (2011). In native goats of Karnataka, the X-chromosome length was found to be 6.05±0.15 in females and 6.28±0.31 in males, as reported by Jayashree (2014). Banani et al. (2018) discovered that the X-chromosome had a relative length of 5.95±0.05 in males and 5.57±0.05 in females of Black Bengal goats. The relative length of the Y-chromosome was seen to be 1.36±0.05 percent in Mahabubnagar goats according to a study conducted by Ekambaram et al. (2011)[27]. Similarly, Jayashree (2014) reported a relative length of 1.42±0.13% in native goats of Karnataka, while Banani et al. (2018) found a relative length of 1.47±0.03% in Black Bengal goats. According to a study conducted by Umadevi et al. (2011), the prevalence of a certain condition in Mahabubnagar goats was found to be 1.96%.

In a study conducted by Inamdar et al. (2020), it was observed that the average arms ratio of Jayawadagi goats was 3.09. Additionally, the arms ratio of all Y-chromosomes was found to be greater than 1 and less than 7. The mean centromeric index was determined to be 30.00, and the centromeric index of all Y-chromosomes fell within the range of 12.5 to 50.0.

5. Conclusions

The modal chromosomal number (2n) of the Meriz goat was determined to be 60. From a morphological perspective, it can be observed that all 58 autosomes and the X-chromosome exhibit acrocentric characteristics. The X-chromosome is recognised as the acrocentric chromosome within the chromosomal complement. The Y-chromosome exhibited a submetacentric morphology in the present investigation. The findings of the present study indicate that the animals under investigation had no chromosomal abnormalities. The acquisition of this knowledge holds significant value for goat breeding initiatives aimed at enhancing meat production, bolstering resistance against diseases, and fostering adaptability to environmental stressors, such as climate change. The present investigation yielded no evidence of chromosomal abnormalities in the animals subjected to testing. The existing body of literature about the impact of chromosomal pairs on the relative lengths of chromosomes in Meriz goats is limited, and as a result, definitive conclusions cannot be made. In this study, we have successfully conducted a comprehensive analysis to elucidate the fundamental chromosomal organization of the Meriz species, marking the first instance of such an investigation on this magnitude. The initiation of cytogenetic diagnostics in animals suspected of having chromosomal aberrations or genetic abnormalities is of great importance for future endeavours aimed at preventing the transfer of such conditions to offspring within animal breeding programs.

Conflict of Interests

The author has no conflicts with any step of the article preparation.

Consent for publications

The author read and approved the final manuscript for publication.

Ethics approval and consent to participate

No human or animals were used in the present research.

Informed Consent

The authors declare not used any patients in this research.

Availability of data and material

The data and material are available when requested from corresponding author.

Authors' contributions

DMK and KJK contributed to the idea, design and execution of the study. DMK performed the Karyotype and ideogram analysis, while KJK determined the parametaris of these analysis. DMK and KJK assisted in all animal procedures for the experiment. Both authors contributed equally to the write-up of the final manuscript.

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