

Research Application Summary

Genetic variability in registered Alpine dairy goat population in Kenya

Kimitei, R.K.,^{1,2} Muasya, T.K.¹ & Wasike, C.B.³

¹Department of Animal Science, Egerton University, P.O. Box 536 - 20015, Egerton, Kenya

²Dairy Training Institute, P.O. Box 449 - 20117, Naivasha, Kenya

³Department of Animal Science, Maseno University, Private Bag
Maseno, Kenya

Corresponding Author: ronaldkimitei@gmail.com

Abstract

A total of 6893 individuals were used to evaluate the population structure and genetic variability of registered Alpine dairy goats in Kenya. Parameters estimated were pedigree completeness, maximum generations traced, complete generations, equivalent generations, generation interval, inbreeding coefficient, effective population size and population structure. The average level of pedigree completeness for registered Alpine dairy goats was 10% with 65.9% of individuals having known parents while 16.1%, 2.3 and 0% had information on their grandparents and great grand-parents. None of the individuals had known great-great-grand parents known. The average generation interval was 10.6 years. The longest generation interval was reported for sire-sire pathway (15.9 years) while the dam-sire pathway had the shortest (5.7 years). Out the 6398 individuals in the pedigree, only 26 were inbred, and had an inbreeding level of 23.1%. Inbreeding level was higher among inbreds, when estimated based on complete generations rather than maximum traced generations. As average inbreeding level for the entire population was low, its trend was not estimated. Maximum traced generations, complete generations, equivalent generations were 8, 2 and 2.1, respectively. The associated rates of inbreeding and effective population size estimates were 0.09, 0.17 and 0.16; 579.8, 296.1 and 315.9, respectively. Pedigree completeness in the registered Alpine population in Kenya is low, leading to over- or under-estimation of measures of genetic diversity. Rate and level of inbreeding increased with increasing pedigree completeness. The Alpine dairy breeding programme in Kenya should be strengthened by enhancing pedigree recording to enable long-term management of genetic variability and genetic improvement.

Key words: Alpine dairy goats, genetic diversity, gene origin, Kenya

Résumé

Un total de 6893 individus ont été utilisés pour évaluer la structure de la population et la variabilité génétique des chèvres laitières alpines enregistrées au Kenya. Les paramètres estimés étaient l'exhaustivité du pedigree, les générations maximales tracées, les générations complètes, les générations équivalentes, l'intervalle de génération, le coefficient de consanguinité, la taille effective de la population et la structure de la population. Le niveau moyen d'exhaustivité du pedigree des chèvres laitières alpines enregistrées était de 10 %, 65,9 % des individus ayant des parents connus tandis que 16,1 %, 2,3 et 0 % avaient des informations sur leurs grands-parents et arrière-grands-parents. Aucun des individus n'avait connu d'arrière-arrière-grands-parents connus. L'intervalle moyen entre les générations était de 10,6 ans. L'intervalle de génération le plus long

a été signalé pour la voie père-père (15,9 ans) tandis que la voie mère-père avait la plus courte (5,7 ans). Sur les 6398 individus du pedigree, seuls 26 étaient consanguins et avaient un niveau de consanguinité de 23,1%. Le niveau de consanguinité était plus élevé chez les consanguins, lorsqu'il était estimé sur la base des générations complètes plutôt que sur le nombre maximal de générations tracées. Comme le niveau moyen de consanguinité pour l'ensemble de la population était faible, sa tendance n'a pas été estimée. Le nombre maximal de générations tracées, de générations complètes et de générations équivalentes était de 8, 2 et 2,1, respectivement. Les taux associés de consanguinité et les estimations de la taille effective de la population étaient de 0,09, 0,17 et 0,16 ; 579,8, 296,1 et 315,9, respectivement. L'exhaustivité de la généalogie de la population alpine enregistrée au Kenya est faible, ce qui conduit à une surestimation ou à une sous-estimation des mesures de la diversité génétique. Le taux et le niveau de consanguinité augmentaient avec l'augmentation de la complétude du pedigree. Le programme de sélection laitière alpine au Kenya devrait être renforcé en améliorant l'enregistrement des pedigrees pour permettre une gestion à long terme de la variabilité génétique et de l'amélioration génétique.

Mots clés : Chèvres laitières alpines, diversité génétique, origine des gènes, Kenya

Introduction

Dairy goats have continued to gain popularity over the years in Kenya. This is because goats are cheap to acquire compared to cattle, require little land, reproduce quickly, and are able to feed on a wide range of forages (Peacock, 2005). Goat milk is a more suitable alternative to cow milk due to its beneficial and therapeutic effects especially on the young, elderly and people with cow milk allergy (Ribeiro and Ribeiro, 2010). Dairy goat production therefore offers a viable option of addressing the millennium development goals of alleviating extreme poverty and hunger (Peacock, 2005). However, there is a general decline in performance in advanced generations of crossbred Kenyan dairy goat populations. The decline in performance has partly been attributed to poor husbandry practices, recombination losses and increase in inbreeding levels (Muasya *et al.*, 2006; Mugambi *et al.*, 2007; Ogola *et al.*, 2010). Inbreeding levels have been reported to significantly affect birth weight, weaning weight, kidding interval and age at first service and first kidding in goats (Muasya *et al.*, 2006; Marete *et al.*, 2011). In the study by Marete *et al.* (2011), quality of pedigree recording and its effect on measures of genetic diversity were not assessed. In populations where pedigree recording is not consistent, levels of inbreeding are underestimated (Muasya *et al.*, 2013; Mwangi *et al.*, 2016) and its effects on performance may not be easily quantified (Marete *et al.*, 2011).

Apart from reduced performance, inbreeding diminishes additive genetic variance (Falconer and Mackay, 1996), leads to emergence of lethal alleles in homozygous form, eventually leading to loss of fitness and viability of populations (FAO, 1998; Franklin and Frankham, 1998). The rate of inbreeding for the Alpine dairy goat in Kenya of 0.019% per year translates to a rate per generation of 0.1% (Marete *et al.*, 2011) which is recommended by Franklin and Frankham (1998) beyond which a population loses its long-term viability. The estimate was within the limit of 1% beyond which a population loses its fitness. However, the study by Marete *et al.* (2011) did not explore the influence of pedigree quality and depth, though these two aspects are known to affect estimates of inbreeding and effective population size (Muasya *et al.*, 2013; Mwangi *et al.*, 2015). In addition the increasing trend of rate of inbreeding indicates the need to put in place a strategy to plan matings which result in the least coancestry between mates (Fernandez *et al.*, 2011). The objective of this study was therefore to assess the population structure and genetic variability of dairy goats in Kenya.

Materials and Methods

Data on identity of each individual, sire, dam, sex and date of birth were obtained from the Kenya Stud Book, which is the organization officially mandated to record pedigree of all registered animals in Kenya.

Estimation of demographic parameters

Pedigree completeness. The pedigree completeness level of the reference populations was evaluated by using four parameters: (1) the pedigree completeness index, (2) the maximum number of traced generations, (3) the number of equivalent complete generations, and (4) The complete generations. Pedigree completeness index (PEC) which is the proportion of ancestors known per generation for each offspring will be calculated using the method proposed by MacCluer *et al.* (1983), to assess the quality of the pedigree data used to estimate inbreeding and relatedness. This was done by describing the completeness of each ancestor in the pedigree upto the 4th generation. Pedigree completeness index (PEC) was calculated as follows;

$$PEC_{\text{individual}} = \frac{4C_{\text{sire}} \times C_{\text{dam}}}{C_{\text{sire}} + C_{\text{dam}}} \quad [1]$$

C_{sire} and C_{dam} are paternal and maternal line contributions respectively calculated as;

$$[2] \quad C = 1/d \sum_{i=1}^d a_i$$

where; d is the total number of generations considered, $i=1, 2 \dots$ and a_i is the fraction of ancestors present in generation i in the current study. 4 generations will be considered therefore $d=4$.

The maximum number of traced generations, number of equivalent generations and complete generation equivalent were calculated as per the methods described by Gutiérrez and Goyache (2005). The maximum number of traced generations is defined as the generations separating the offspring from its furthest known ancestor in each path, where ancestors with no known parent shall be considered founders and assigned to generation 0. Number of equivalent generations is defined as the number of generations (n) separating the individual from each known ancestor. It will be computed as the sum of $(1/2)^n$, where n is the number of generations separating the individual from each known ancestor (parent=1, grandparent=2 etc.). The complete generation equivalent refers to the furthest generation for which all ancestors are known.

Generation interval. Generation interval (GI) was calculated across the four selection pathways; sires of sires (ss), sires of dams (sd), dams of sires (ds), and dams of dams (dd), after Falconer and Mackay (1996) as:

$$G. I. = \frac{L_{ss} + L_{sd} + L_{ds} + L_{dd}}{4}$$

Parameters measuring genetic diversity

Inbreeding coefficient. The level of heterozygosity of the population will be assessed using inbreeding coefficient (F) and average relatedness coefficient (AR). Inbreeding coefficient, defined as the probability of an individual having two alleles identical by descent, will be computed using the algorithm of Meuwissen and Luo (1992). The rate of inbreeding will be estimated using the

method described in Falconer and Mackay (1996). Each generation's increase in inbreeding (ΔF) will be calculated as;

$$\Delta F = \frac{F_n - F_{n-1}}{1 - F_{n-1}}$$

F_i is the average inbreeding in the i^{th} generation. Future trends in inbreeding will be estimated using the rate of increase in inbreeding. The increase in inbreeding between two generations ($F_n - F_{n-1}$) will be obtained from the product of regression coefficient (b) of the average inbreeding over the year of birth obtained in the last 8 years and the average generation interval (l) i.e.

$$F_n - F_{n-1} = l \times b$$

F_{n-1} was calculated from the mean inbreeding in the last year studied (F_{ly}) as follows;

$$F_{n-1} = F_{ly} - l \times b$$

Effective population size. The effective population size (N_e) refers to the size of an idealized population which would give rise to the rate of inbreeding. It will be obtained from the product of the annual rate of inbreeding per generation (ΔF_y) and the generation interval (L) as follows;

$$N_e = \frac{1}{2\Delta F_y \times L} \quad [8]$$

Effective population size was also estimated by regressing individual inbreeding coefficients over the number of fully traced generations, maximum number of generations and equivalent complete generations since N_e can be overestimated for shallow pedigree populations.

Population structure. Genetically important flocks and the effective population size was used to determine the direction of gene flow and the possible structuring within and between the populations. These flocks consist of individuals who are most utilized as breeding animals and was identified by calculating the marginal contribution of the top 100 ancestors to each reference population of females born in 2014. The marginal contribution of an individual quantifies its contribution to the reference population, which has in the past been unexplained by greater contributing individuals (Mc Parland *et al.*, 2007).

Results

The level of pedigree completeness for Alpine dairy goats recorded with the dairy goat association of Kenya (DGAK) was 10%. Figure 1 shows that 65.9% of individuals had known parents while 16.1%, 2.3 and 0% had information on their grandparents and great grand-parents. None of the individuals had known great-great-grand parents known.

Table 1 shows parameters for the Alpine dairy goats registered with DGAK in Kenya. The entire population had an inbreeding coefficient of 0.09%. Mean average relatedness was 0.14%. Mean traced, complete and equivalent generations were 1.32, 0.56 and 0.86, respectively. Rate of inbreeding based on maximum traced, complete and equivalent generation was 0.09, 0.17 and 0.16%, respectively. Effective population size estimated based on maximum, complete and equivalent generations was 579.8, 296.1 and 315.9, respectively.

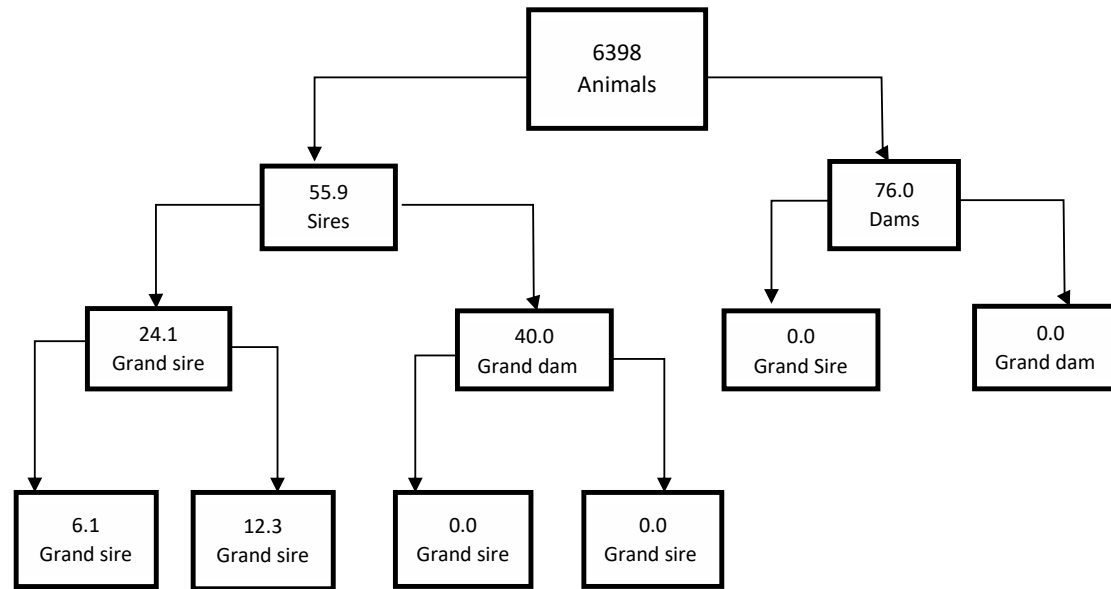


Figure 1. Pedigree completeness (%) for registered Alpine dairy goats in Kenya

Table 1. Number of animals, average inbreeding coefficient (F %), and average complete generation equivalents for registered Alpine dairy goats of Kenya

	N	Parameter	Maximum	Mean	Average F (%)	Increase in inbreeding	Effective population size
Whole population	6398	Traced generations	8	1.32	0.01	0.09	579.8
		Complete generations	2	0.56	0.17	296.1	
		Equivalent generations	2.1	0.85	0.16	315.9	
Inbreds	26	Traced generations		2.5	23.1		
		Complete generations		1.00			
		Equivalent generations		1.49			

*goats in the reference population with complete pedigree information for at least 3 generations

The level of inbreeding increased with maximum traced generation from 0 in the first generation to 0.24% in the third generation, then decreased gradually to 0 in generation 8 (Table 2a). Out of a total of 6398 individuals in the pedigree, only 26 were inbred, and had an inbreeding level of 23.1% (Table 2b). Inbreeding level was higher among inbreds, when estimated based on complete generations than maximum traced generations (Tables 2a,b). As average inbreeding level for the entire population was low, its trend was not estimated.

Effective population sized for maximum traced and complete generations with non-zero inbreeding ranged from 209.5 to 448.0 (Tables 2a,b). Average relatedness ranged from 0.06 to 0.48% in the most recent maximum generation and was always higher than the corresponding average inbreeding level (Table 2a).

Table 2a. Mean inbreeding (F), average relatedness (AR) and effective population size (Ne) by maximum generations for alpine goats in Kenya

Maximum traced generation	N	F	% inbred	Average F for inbred	AR	NE
0	1527	0		0.06		
1	2301	0		0.12		
2	1781	0.24	0.95	25.00	0.19	209.5
3	632	0.24	1.11	21.43	0.22	210.7
4	118	0.21	0.85	25.00	0.23	236.0
5	28	0.11	3.57	3.13	0.24	448.0
6	1	0		0.41		
7	2	0		0.36		
8	8	0		0.48		

Table 2b. Mean inbreeding (F), average relatedness (AR) and effective population size (Ne) by complete generations for Alpine goats in Kenya

Complete generations	N	F	% inbred	Average F for inbred	AR	NE
0	2832	0			0.08	
1	3565	0.17	0.73	23.20	0.18	295.5
2	1	0.00		0.22		

Generation intervals for the various pathways are shown in Table 3. The longest generation interval was associated with sire pathways, while dam pathways had intervals less than 6 years.

Table 3. Estimates of generation interval for different pathways for registered Alpine dairy goats in Kenya

Pathway	N	Generation interval	sd
Fat_Son	925	15.9	2.1
Fat_Dau	3938	13.7	4.2
Mot_Son	922	5.7	5.7
Mot_Dau	2652	5.9	5.4
Mean	8437	10.6	6.2

The longest generation interval was reported for Sire-sire pathway (15.9 years) while the Dam-Sire pathway had the shortest (5.7 years)

Discussion

The mean generation interval of 10.6 for the Alpine population in Kenya was higher than that of 2.77 reported for the Spanish Murciano-granadina goats (Oliviera *et al.*, 2016). Lower values were reported of 3.55 years for Iranian Markhoz breed (Rashidi *et al.*, 2015). Although higher generation intervals are desirable in order to maintain original genetic diversity, the high value for the Kenyan population could partly be due to overuse of a few superior sires. Quality of pedigree determines the accuracy of estimated population parameters and therefore the genetic diversity of a population. According to Boichard *et al.* (1997) equivalent generations is a good indicator of the integrity of pedigree data. The number of equivalent generations reported for the Kenyan Alpine population of 0.85. This was lower than 1.61 reported for South Khorosan Cashmere goats (Joezy-Shekalgorabi *et al.*, 2016). The low values obtained in the current study indicate incomplete pedigrees and low pedigree depth.

The average inbreeding found in the current study was similar to that of 0.012 reported by Marete *et al.* (2011) for the same population. A higher value of average inbreeding 0.18% were reported for the Murciano-Granadini goat breed in Spain. Average relatedness was also lower than 0.03% for same population of (Oliviera *et al.*, 2016). Joezy-Shekalgorabi *et al.* (2016) reported a value of 0.85% for Cashmere goats in South Khorosan. The average inbreeding of inbred animals of 23.1% was similar to that of 24.7% for the Murciano-Granadini goat breed (Oliviera *et al.*, 2016; Deroide *et al.*, 2016). The low value of average inbreeding is consistent with the high effective population size of 579.8 reported in the current study. Nevertheless, when average inbreeding was estimated based on complete generation and equivalent generations, the parameter almost doubled, implying that the current estimated of the population was underestimated due to poor pedigree quality. Similar results were reported by Muasya *et al.* (2013) for the Kenyan Holsten-Friesian population. This means that the level of inbreeding in the Alpine population in Kenya is higher than that estimated using the current population structure.

Over the years and generations, average inbreeding and effective population size increased and decreased, respectively, a trend similar to that reported for the Murciano-Granadini breed in Spain (Oliviera *et al.*, 2016). Whereas the effective population size of 579.8 was high, those estimated based on equivalent and complete generations were 315.9 and 296.1, respectively. The later 2 values are lower than the threshold of 500 required for a population to maintain its evolutionary

potential (Franklin and Frankham, 1998). Therefore despite the low quality of pedigree, measures of diversity estimated in the current study reveal a general decline in genetic diversity in the Alpine goat population in Kenya. This is emphasized by the rates of inbreeding of 0.16 and 0.17% for the two parameters which are above the level of 0.1% set by Franklin and Frankham (1998).

Conclusion

The registered Alpine population has low pedigree completeness, leading to overestimation of effective population size and underestimation of rate and level of inbreeding. Inbreeding level increased with increasing pedigree completeness. The breeding programme should be strengthened by enhancing pedigree recording to enable long-term management of genetic variability and genetic improvement.

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