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Use of simulation to examine a dairy goat breeding program in Tanzania

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Abstract

This paper discusses selection in a dairy goat population for improved performance by conceptualizing it for a population in Tanzania. Seven strategies (5, 10, 20, 30, 50, 70, 100 test bucks) were simulated. A progeny test based selection breeding program fitting Mgeta (Morogoro, Tanzania) situation was optimized. The selection intensity, accuracy of prediction, and genetic gain of milk yield (kg) per day at heritability 0.1 and 0.2 are discussed. Use of natural mating for 1000 goats, in cooperating villages, were assumed. Three elite bucks were selected for breeding with 12% of the best females. Outlines of essential elements for a local sustainable dairy goat breeding program in Tanzania are included with a schematic figure showing selection steps for dairy goat breeding scheme fitting in Mgeta area. This study found that selection intensity gained when testing many bucks is more important for daily milk yield (DMY) (kg) genetic gain than the extra accuracy gained when testing fewer bucks. Mgeta has a mountainous terrain, small herd sizes per farmer and long distance from one cooperating village to another.

Testing 30 bucks is practical for Mgeta. That gives relatively high (42% or 53%) accuracy of selection and genetic gain (2% or 2.6% for 0.1 or 0.2 heritability). The current results of estimated genetic gain are close to reported findings under other environments. Based on dairy goats of Norwegian breed in Tanzania, milked once daily, if 210 days of milking and an average of 1 litre milk yield is considered, the possible genetic gain per year in this program is equivalent to an increase of 4.2kg for 0.1 heritability and 5.5kg of milk per doe for 0.2 heritability of the trait. Such an increase in amount of milk due to a breeding program under the considered environment is promising. Collaborative efforts from farmers to consumers along the dairy goat market chain remain important elements to realize a sustainable high gain. The proposed breeding program may not be perfect in future because of practical options and accessibility to new knowledge. Thus, it becomes indispensable to revise breeding programs.

Key words: breeding scheme, bucks testing

Introduction

Animal performance is influenced by both genetic (G) and environment (E) factors, and sometimes there is an interaction of the two (G x E – Falconer and Mackay 1996). This implies that the best animal selected under temperate environment may not be the best under tropical conditions.

In 1988, a few breeding females and bucks of Norwegian dairy breed were sent to Mgeta, Tanzania (Mtenga and Kifaro 1993). At different times, replacement has been through importing live dairy bucks or semen for AI (Kifaro et al 2007). However, some of the imported bucks did not perform as expected and some died before mating. AI was an alternative, but a low conception rate and low numbers of new born bucks (6 to 12) were some of the key challenges. For example, out of 46 goats that were inseminated 25 (54%) conceived but only 20 does (43%) completed the gestation period (Kifaro et al 2007). Recruiting breeding bucks from Mgeta is assumed to have a greater genetic impact in Mgeta area than importing from temperate environments mainly because of the G x E effects. The current dairy goat population in seven villages of Mgeta was > 2000 heads (Kifaro et al 2012). This population should be large enough to do selection; however, farmers are scattered so across village breeding schemes may be needed.

Establishing a livestock breeding scheme requires guidance. This study is devoted to develop guidance for a dairy goat breeding scheme through developing recommendations that are building blocks essential for sustainable dairy goat breeding schemes under Tanzanian conditions. To achieve this, a simple simulation technique was used to optimize the number of test bucks per year reflecting Mgeta area breeding scheme conditions. In this study decision on which breeding strategy to opt for, depended on the relationship between intensity of selection (i), accuracy of breeding value prediction (r), and expected genetic gain estimation at a heritability of 0.1 or 0.2. The overall aim was to develop the optimal number of test bucks required in the dairy goat-breeding program including 1000 does, using Mgeta, Tanzania as a case study.

Materials and methods

The projected production environment

Tanzanian dairy goat breeding structures were simulated based on Mgeta production system. The area is of high altitude ranging from 1100 to 1900m above sea level. Mgeta villages are about 50km southwest of Morogoro town. Smallholder farmers are predominantly practicing crop-livestock integrated production systems. They practice low input, high labour, vegetable gardening integrated with small animals like goats, pigs, and poultry. Over 2000 dairy goats are available in the area (Kifaro et al 2012). The goats are stall fed, tethered, and sometimes grazed in both communal and own farm plots. The average number of dairy goats per household is 5. There are buck keepers in the different villages. Annually bucks are rotated within and between villages. Cattle rearing is not common, possibly due to the steep terrain.

Pedigree

Inspired by the available goat population in Mgeta, identities of 1000 female goats were listed in an excel sheet. Only 100 of the females were considered in generation zero to have known parents. The females were assumed to be mated to 100 bucks (i.e. each buck 10 females) at the same time to form generation one. All kids born in generation one had known identity (ID) of their mother and father. The kids' IDs were also listed in the same excel sheet. In later generations the number of kids per buck depended on the number of test bucks considered. Each year a doe was assumed to have a twining rate of 1.1, equivalent to 1100 kids born per generation (550 male and 550 female). Considering 10% mortality, 1000 kids remain (500 female and 500 male, see Figure 3). Culling of kids used an Excel function

"RandomSelection" (<u>http://www.extendoffice.com/documents/excel</u>) to randomize the IDs in the excel sheet, then some were deleted to keep the required number. For does, culling assumed that under natural circumstances the oldest animals in the sheet die before the younger ones. Each year 30% of the oldest does were culled and replaced with weaned female kids. In addition, the non-selected tested young bucks and three elite bucks were replaced yearly.

Four generations followed generation zero, making a pedigree of 4400 individuals (1100 in generation zero, 3000 in first through third generation and 300 in the fourth generation). In each year, 1000 individuals (50%-male and 50%-female) are born and registered with a unique ID.

Age at first mating is one year and kidding is at around 1.5 years. The productive life cycle assumed is 3 to 4 years for both sexes. Generation interval is 4.5 years for elite bucks, and 1.5 years for test bucks. The simulation assumed that all goats come from the same breeding population and have the same conception and survival rates after weaning.

Traits recorded

The DMY of daughters of the tested bucks were used to compare the different breeding strategies possible for the Mgeta area. Milk yield is the most important trait in the breeding goals of dairy goat farmers in Tanzania (Nziku et al 2016). Performance of the 300 progeny of test bucks were used directly to evaluate their sires, but through the pedigree they would contribute to prediction of all relatives' breeding values using BLUP. The Norwegian dairy goats in Mgeta could produce an average of around 210kg of milk through 210 days (seven months) of lactation (Sonola 2015). In the calculations all goats are assumed to have one common mean (fixed effect), that is same environmental effect.

Testing young bucks based on daughters' DMY and selection of three new elite breeding bucks

Seven alternatives for test bucks were simulated (5, 10, 20, 30, 50, 70, and 100 bucks tested per generation). In each strategy, the test bucks produced 1000 (500 male and 500 female) offspring in generation one through three. The test bucks were randomly selected out of the 500 male offspring in a year. When daughters of test bucks have produced milk that is registered in a dairy control, BLUP breeding values are to be calculated for the test bucks, and the three best are selected as elite bucks. The remaining may be sold or slaughtered. The elite bucks become known in the third generation and are included in the mating to produce the fourth generation. So the test bucks only produced 880 (440 males and 440 females) offspring in the fourth generation. The three elite bucks were assumed to contribute 120 offspring (60 males and 60 females). Buck kids for testing were then recruited from the three elite sires. The bucks' testing program was assumed to cut across the three cooperating wards of Nyandira, Tchenzema and Mwarazi in Mgeta division, Tanzania.

Optimization of number of bucks tested

The accuracy (r) and selection intensity (i), leading to genetic gain (ΔG), were the criteria for searching for an optimal number of test bucks per year. Both licensed MatlabR2013a and Excel 2013 computer programs were used for simulation and analyses of data. However, free software like R computer program can be used for similar purposes. Calculations considered the genetic gain for the whole population coming from selection of the three elite sires from the test bucks.

2.7 Accuracy (r a, ã)

The BLUP technique was used to find accuracy of predicted breeding values for test bucks in the alternative breeding schemes. The accuracy of prediction is the correlation between true (a) and predicted (\tilde{a}) additive breeding values and can be found using the coefficient matrix of the mixed model equations based on the Animal Model (Mrode 2014). In the Animal Model 'y' referred to milk records for does:

 $y = Xb + Za + \varepsilon \tag{1}$

var(a) = G = sig2a A, var() = R = sig2e I.

For the calculations here it was assumed just one common mean for all observations, so "X" is just a column of 1s, and the "b" is the common mean (μ) for milk yield.

The vector "a" contains the unknown true breeding values for the trait for all animals included in the pedigree. "A" is the relationship matrix for the animals in the pedigree was calculated by readlongped.m and amatrix.m matlab functions (see appendix), and "Z" assigns the breeding values of the observed animals to their observations. 'I' is an identity matrix of the same size as the number of observations in "y". The additive genetic variance of the trait is sig2a, and the residual and environmental variance of the trait is sig2e.

The solutions for the "b" and "a" of the model are given by the mixed model equations;

$$\begin{bmatrix} \widetilde{\mu} \\ \widetilde{a} \end{bmatrix} = \begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z + G^{-1} \end{bmatrix}^{-1} \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y \end{bmatrix}$$
(2)

Where $G^{-1} = A^{-1} * (sig 2a)^{-1}$ and $R^{-1} = I (sig 2e)^{-1}$ (3)

Since errors are independently distributed with variance sig2e, it is possible to omit them in equation (2) and replace with " α " as in (4) (Mrode 2014).

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + A^{-1}\alpha \end{bmatrix}^{-1} = C = \begin{bmatrix} C^{11} & C^{12} \\ C^{21} & C^{22} \end{bmatrix}$$
(4)
The $\alpha = (1-h^2)/h^2$ (5)

According to Mrode (2014) the diagonal element of the inverse of the coefficient matrix C in equation (4) for animal, the ii element of C $^{22} = C^{ii}$ gives information needed to calculate reliability and accuracy. (The "Offset" function in Excel computer program was used to extract diagonal elements.)

The reliability $(r^2 a, \tilde{a})$ () of evaluation is expressed as = 1- $C^{ii} \alpha$ (6)

The accurancy of predicted breeding value is

$$\sqrt{r^2}_{a,\tilde{a}}$$
 (7)

Genetic gain (AG)

The genetic superiority (ΔG) of selected individuals was estimated by

$$\frac{i * r_{a,\tilde{a}} * \sigma_a}{L} \qquad (8)$$

Where

i = Intensity of selection, the differential expressed as fractions of phenotypic standard deviations (Lynch and Walsh 1998). The intensity of selection () = z/p (9)

Where

z = The height of normal distribution at the truncation point 'x', which is given by z = and is 3.14. (10)

p = Selected individuals/Tested individuals (s/n).

 $(r_{a,\bar{a}}) =$ The accuracy of prediction, which measures how well the true genetic value can be predicted.

- σ_a = Additive genetic standard deviation of the trait (DMY),
- L = Generation interval as the average age in years of parents at the birth of offspring.

The heritabilities adopted were based on variance component estimates in Norwegian dairy goat control test day records for kg milk (Dagnachew et al 2011): 0.0532kg^2 for additive and 0.153kg^2 for the residual for the DMY trait. The residual variance was multiplied by a factor of two: $0.153 \text{kg}^2 * 2 = 0.306 \text{kg}^2$ because it was assumed that there was a lower quality of data in the simulated production system than where estimates were made. These variance components were equivalent to a heritability of 0.148. In the calculations heritability levels of 0.1 (low), and 0.2 (high) for DMY were used.

Further the genetic gain formula was decomposed to:

$$\Delta G / year = \frac{(i_{sse} * r_{BV, BVsse} + pi_{sdt} * r_{BV, BVsdt} + (1 - p)i_{sde} * r_{BV, BVsde} + i_{ms} * r_{BV, BVms} + i_{md} * r_{BV, BVmd}) * \sigma_{BV}}{L_{sse} + pL_{sdt} + (1 - p)L_{sde} + L_{ms} + L_{md}}$$

In this case, the following parameters were used:

Where:

sse = elite buck - son

sde= elite buck - daughter

sdt = test buck - daughter

ms = mother - son

md = mother - daughter

i = selection intensity (for sdt, ms, and md i = 0 = no selection)

 $r_{Bv, B \sim v}$ = correlation between true and estimated breeding values

sBV = genetic standard deviation

L = generation interval

p = proportion of does mated to test bucks

Mothers and test bucks were assumed to be unselected and therefore their i-s are 0. The needed accuracies were therefore for selection of test bucks to become elite bucks only.

Results and discussion

In a breeding program the important phenomenon to understand is the reproductive success maximization of individuals. Bateman's (1948) principle states that the reproductive success variance is low among females and high among males. This principle explains why breeders place a stronger selection on males than on females.

Selection intensity

Table 1 shows change in selection intensity when three elite bucks are selected from a varied number of test bucks per year. Selection intensity is one of the factors in breeding scheme optimizations (Bourdon 2000). As expected, with stronger selection, selection intensity becomes higher. The observed increase in selection intensity comes with the increased number of test bucks while constantly selecting three elite bucks. Testing fewer bucks resulted in decreased intensity of selection. The higher the intensity of selection the better for quick genetic change (Van de Werf 2000, 2006). With 100 tested bucks selection intensity is at its highest in these calculations, and although the accuracy was low the genetic gain was maximized (Figure 1a-b).

test bucks are a	vailable for selection.				
Number of test bucks	Number of elite bucks selected	р	x	z	i
100	3	0.03	1.88	0.07	2.3
70	3	0.04	1.72	0.09	2.1
50	3	0.06	1.55	0.12	2.0
30	3	0.10	1.28	0.18	1.8
20	3	0.15	1.04	0.23	1.6
10	3	0.30	0.52	0.35	1.2
5	3	0.60	-0.25	0.39	0.6

Table 1. Selection intensity (i) for 3 elite bucks when 5, 10, 20, 30, 50, 70, or 100test bucks are available for selection.

p = proportion of individuals selected, x = truncation point, z = the height of normal distribution at the truncation point x, i = intensity of selection

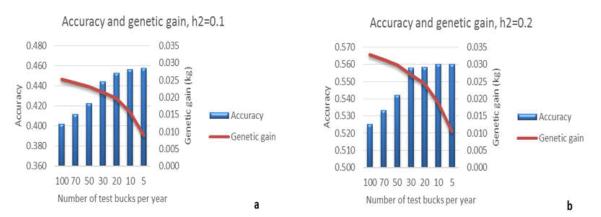
Accuracy

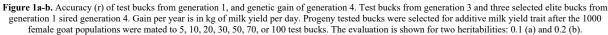
The higher the accuracy the better the prediction of breeding values before selecting the test bucks to become elite bucks. Figure 1a and 1b show that higher accuracy is obtained by testing fewer test bucks per year. This is because the number of daughters per test buck increases (Kahi and Hirooka 2005, Dekkers et al 2004, Van Grevenhof et al 2012; Kahi and Hirooka 2005). Thomas (2014) reminds of the importance of statistical procedure, quantity and quality of data for accuracy determination. Schefers and Weigel (2012) suggested that for a breeding program that involves progeny testing, the accuracy of selection depends on several factors: testing capacity, heritability, and number of offspring per buck. Increasing from

1000 to more goats available in Mgeta would also increase the testing capacity and hence could increase accuracy of prediction in the area if number of test bucks was constant. The effect of heritability on accuracy of prediction is shown by comparing Figure 1a and b, confirming that heritability of a trait is an important factor to consider in a breeding program (Van der Werf 2000). Mgeta should start with few traits of economic importance and with reasonably high heritability, for example, milk yield per day and growth rate.

Genetic gain

Figure 1a and 1b present how good generation 4 goats are expected to be when accuracy of prediction and estimated genetic gain for DMY (kg) trait per year in a population is considered. The result shows that testing 100 bucks gives the highest genetic gain, but suffers from high loss in accuracy. Selection intensity and heritability play a major role for the observed results. Herd effect was assumed not to exist, but is an important factor in real situations so bucks to have connectedness for the analyses. Buck ring (both test and elite) is a recommended practice such that could help to better distribution of progeny among the participating breeding herds. Testing 20-30 bucks per year could be more practical than testing more in Mgeta. Because of the bad land terrain of Mgeta, long distance between one dairy goat keeper and another, and small herd sizes of about 5 goats per farmer, testing 30 bucks is feasible in the area. That also gives relatively high (0.42 or 0.53) accuracy of selection, and genetic gain of DMY (0.020 or 0.026 kg per day, or 4.2 or 5.2 kg per 210 day lactation) - for heritability of 0.1 or 0.2. Testing fewer bucks result in more daughters per buck, therefore the test bucks' breeding values are more accurately predicted. The problem with many bucks will be confounding of buck effect with the effect of the daughters' herd environment. The heterogeneity of the flocks has not been taken into account in the current calculation except as a general lower heritability effect. In an applied breeding scheme dams could have estimated breeding values (EBVs) with lower accuracy than test bucks, and kids to be test bucks could be selected based on mothers' EBVs for amount of milk, and also for own growth ability. This is not included in the presented calculations. The estimated genetic progress obtained by testing 30 bucks per year in the current study is promising. The values were comparable to Shumbusho et al (2013) and Colleau et al (2011). Many factors may affect genetic gain estimation like the population size, testing capacity, heritability, generation interval, use of elite bucks with or without AI, and possibly the evaluation techniques used e.g. selection index (Bijma 2012), BLUP, genomics etc. With emerging new technologies, it is possible to reduce generation interval by use of genomic selection technique (Schefers and Weigel 2012). However, genomic selection has limitations associated with high costs and technology requirements, especially where a 1000 goats' population under conditions like in Mgeta is considered.





Time scale of progeny test selection scheme

The current study shows progeny testing selection schemes for goats requires at least 3.5 years to identify elite bucks and four or so years for sons and daughters of the elite buck to be born (Figure 2). The time scale to identify the elite buck is long and is a natural barrier for faster genetic progress under progeny test schemes. Experience shows that generation interval for buck selection varies between 3 and 5.5 years (Al-Atiyat and Aljumaah 2013; Danchin-Burge 2011; Facó et al 2011). Long generation interval reduces the genetic progress per year. Alternatives that makes it possible to shorten the generation interval by genomic selection or multiple ovulation schemes in dairy animals are developed (Meuwissen et al 2013; Bajagai, 2013; Mapletoft 2013), but are not be feasible for farmers in Tanzania today. Thus, a well-designed mating system, and breeders' commitments over time remain essential. However, a great deal of training will be require to teach farmers to record all milking and to identify animals and keep pedigrees which is crucial. The use of information communication technologies (ICT) such as mobile phone as a tool for recording could help to efficiently record and sharing of goat's records.

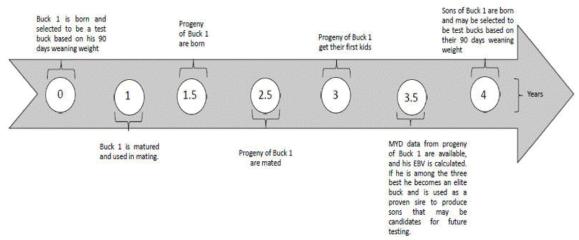


Figure 2. Timescale of progeny testing breeding scheme for dairy bucks based on natural mating. DMY=Daily milk yield, and EBVs=estimated breeding values.

Breeding scheme under cooperating farms (dairy units)

This section proposes an effective progeny testing breeding scheme under cooperative farms from different villages. Cooperation between dairy goat units is proposed because of the small number of goats per unit (~ 5 goats). The strategy is not new in developing countries and has proven to be an efficient breeding scheme (Shumbusho et al 2013; Gizaw et al 2013). The current study recommends a village breeding program and buck rotation (elite and test bucks). The elite buck rotation could make better distribution of the elite bucks' daughters in the cooperating villages in addition to producing sons for future testing (Fernándeza et al 2011; Ådnøy et al 2000). Representatives of the dairy goat association in the area should take the lead in scheduling and controlling buck movements in their areas. Training on why and how buck rotation should be and monitoring would increase efficiency.

Mating plans for Mgeta

In the current study 12% of all does or \sim 120 of the youngest females in the pedigree were mated to elite sires. The remaining 88% \sim 880 of does composed of young and old females were mated to test bucks (Figure 3). Current Mgeta farmers choose buck keepers they like based on the good behaviour and interaction she/he has to members of the association. Buck rotations can be done within villages and between villages. The current study proposes presence of breeding houses – a place where farmers could bring their does for mating. School area can be appropriate areas to construct such houses, because:

· Usually the area is accessible to the majority of communities around.

· These are public premises which give more freedom to farmers to visit.

 \cdot The ongoing activities regarding mating and feeding of goats at such a house is an opportunity for school children to learn about goat management.

 \cdot Feeding of the breeding bucks and does present at the mating house could be managed by a school. In Mgeta some schools are keeping dairy goats managed by the school children.

However, local arrangements are necessary. According to Sonola (2015) peak kidding is in August and September meaning that many conceptions take place in March and April. This is the time when there are plenty of green pastures and good weather for kids to grow.

Data bank for dairy goats

Effective selection breeding scheme requires EBVs of individuals. The available individual information for EBV estimation should be as reliable as possible and efficiently utilized. To achieve that individual performance information should flow in all the time starting from the goat owners to trained performance evaluators. The goat owners are responsible for collecting information of individuals; such as weaning weight, milk yield etc. In Mgeta, this has been found to be somewhat of a challenge (Kifaro et al 2012; Nziku et al 2016). Perhaps working in collaboration with private sectors under the framework of the Private Public Partnerships policy (URT 2009), could help to strengthen the recording process. For example, mobile phones can act as an alternative interface for data transferring from farmers to the server. Technically this can be possible in the near future, as similar techniques seem to be functioning well in most of developing countries e.g. mobile banking. However, farmers' motivation is a key issue in this regard.

Motivation for genetic improvement

A genetic improvement scheme has several demanding requirements. For example, the need for unique animal identification, data to be collected and stored, having parentage file of each animal, understanding statistical techniques for performance evaluations, and possession of computing facilities, are some of the basic requirements. Studies show that

motivation is an essential factor for breeding schemes' success and sustainability (FAO 2010; Philipsson et al 2011; Ogola and Kosgey 2012). Harris and Newman (1994) in a review paper of breeding for profit stated that breeders would be motivated if given assurance that greater income is possible by owning the best animals. Finding elements that could motivate dairy goat farmers like those in Mgeta is indispensable, for example award certificate to farmer with the best buck.

Step by step selection of dairy goat breeding program for Mgeta

Selection of test buck in Mgeta area today could be done by following the simplified diagram in Figure 3. The sketch is a representation and can be adjusted in many ways fitting different situations of selection breeding program of goats.

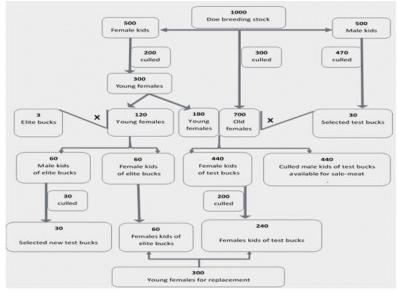


Figure 3. Schematic figure proposed for dairy goat selection breeding scheme in reference to 1000 breeding stock and selection of three elite bucks per year.

Conclusions

Higher genetic gain and scheme sustainability can be expected if farmers and their organizations are able to play major roles in the scheme implementation while working closely with research and academic institutions.

Under Mgeta situation testing 30 young bucks per year may be the current option, however, the proposed breeding program may not be perfect in the future because of the practical options and accessible knowledge. Thus, it becomes necessary to revise breeding programs from time to time.

References

Ådnøy T, Nævdal I and Svendsen M 2000 Buck circles for dairy goat breeding in Norway. In: World Goat Conference Satellite Symp. Gruner L., Chabert Y. (Eds). Institut del'Elevage, INRA, Paris, France, 1047.

Al-Atiyat R M and Aljumaah R S 2013 Simulated breeding scenarios for improving Hejaz goat performance in subtropics. Food, Agriculture & Environment 11 (2): 440-444.

Bajagai Y S 2013 Multiple ovulation and non-surgical embryo transfer in cattle by using intravaginal controlled internal drug release (CIDR) progesterone inserts. Nepal Journal of Science and Technology. 14(1):15-22.

Bateman A J 1948 Inter-sexual selection in Drosophila. Heredity, 2: 349-368.

Bijma P 2012 Accuracies of estimated breeding values from ordinary genetic evaluations do not reflect the correlation between true and estimated breeding values in selected populations. Animal Breeding and Genetics. ISSN 0931-2668.

Bourdon R M 2000 Understanding animal breeding. 2nd ed. Prentice-Hall, Inc. Upper Saddle River, New Jersey 07458. pp 200-216.

Colleau J J, Clément V, Martin P, and Palhière I 2011 Optimized diffusion of buck semen for saving genetic variability in selected dairy goat populations. BMC Genetics. 12-25. <u>http://www.biomedcentral.com/1471-2156/12/25.</u>

Dagnachew B S, Thaller G, Lien S, and Ådnøy T 2011 Casein SNP in Norwegian goats: additive and dominance effects on milk composition and quality. Genetics Selection Evolution. 43:31. <u>http://www.gsejournal.org/content/43/1/31</u>.

Danchin-Burge C 2011 Assessment of genetic variability of 9 races dairy small ruminants and fleece. Account no. 001172004, Livestock Institute collection results, June 2011. Institute Livestock, Paris, France

Dekkers J C M, Gibson J P, Bijma P and van Arendonk J A M 2004 Design and optimisation of animal breeding programmes. Lecture notes for AnS 652 A and B, S05, Iowa State University. <u>http://www.anslab.iastate.edu/Class/AnS652X/chapter1.pdf</u>

Facó O, Lôbo R N B, Gouveia A M G, de Paiva Guimarães M P S L M, Fonsecaa J F, Maciel dos Santos T N, Alves da Silva M A and Villela L C V 2011 Breeding plan for commercial dairy goat production systems in southern Brazil. Small Ruminant Research. 98: 164–169.

Falconer D S and Mackay T F C 1996 Introduction to quantitative genetics, eth Edn. Harlow, London. pp 131-134

FAO (Food and Agricultural Organization) 2010 Breeding strategies for sustainable management of animal genetic resources. Pages 15-87 in FAO Animal Production and Health Guidelines, Version 3. Rome, Italy.

Fernándeza J, Meuwissena T H E, Toroa MA and Mäki-Tanila A 2011 Management of genetic diversity in small farm animal populations. The Animal Consortium. 5 (11):1684–1698.

Gizaw S, Getachew T, Haile A, Rischkowsky B, Sölkner J and Tibbo M 2013 Optimization of selection for growth in Menz Sheep while minimizing inbreeding depression in fitness traits. Genetics Selection Evolution. 45(1):20. doi: 10.1186/1297-9686-45-20.

Harris D L and Newman S 1994 Breeding for profit: synergism between genetic improvement and livestock production (a review). Animal Science. 72(8):2178-200.

Kahi A K and Hirooka H 2005 Genetic and economic evaluation of Japanese Black (Wagyu) cattle breeding schemes. Animal Science. 83(9):2021 –2032.

Kifaro G C, Eik O L, Mtenga L A, Mushi D E, Safari J, Kanuka A A, Kimbita E N, Maeda-Machangu A D, Kanuya N L, Muhikambele V R M, Ndemanisho E and Ulvund M J 2007 The potential use of AI in sustainable breeding of dairy goats in developing countries. A case study of Norwegian dairy goats in Tanzania. Tanzania Journal of Agriculture Sciences. 8(1):19-24.

Kifaro G C, Msalya G, Nziku Z, Ndemanisho E E, Kimbita E N, Mushi D E, Max R A and Mtenga L A 2012 Status of Norwegian dairy goats in two districts of Morogoro region at the start of an up-scaling project. Oral presentation, 1st Annual Conference of the EPINAV Programme, Morogoro, Tanzania, 18 – 19 December 2012.

Lynch M and Walsh J B 1998 Genetics and analysis of quantitative traits. Sinauer Assocs., Inc., Sunderland, MA. pp 26-33.

Mapletoft R J 2013 History and perspectives on bovine embryo transfer. Animal Reproduction. 10(3):168-173.

Meuwissen T, Hayes B and Goddard M 2013 Accelerating improvement of livestock with genomic selection. Annual Review. Animal Bioscience. Vol.1:221-237. doi: 10.1146/annurev-animal-031412-103705. www.annualreviews.org. 22.2.2016

Mrode A R 2014 Linear models for the prediction of animal breeding values. 3rd edn. CABI Nosworthy way Wallingford, Oxfordshire, OX108DE, UK. pp 34-46.

Mtenga L A and Kifaro G C 1993 Dairy goat research and extension at Sokoine University of Agriculture (lowlands) and Mgeta (highlands) areas of Tanzania. In: Kategile J A, Mubi S (editors), Future of livestock industries in East and Southern Africa, Proceedings of a Workshop held at Kadoma Ranch Hotel, Zimbabwe, 20-23 July, 1992. ILCA (International Livestock Centre for Africa), Addis Ababa, Ethiopia, pp 227. http://www.fao.org/wairdocs/ILRI/x5485E/x5485e0d.htm

Nziku Z C, Kifaro G C, Eik L O, Steine T and Ådnøy T 2016 Reasons for keeping dairy goats in Tanzania, and possible goals for a sustainable breeding program. Animal Production Science. <u>http://dx.doi.org/10.1071/AN15423</u>.

Ogola T D O and Kosgey I S 2012 Breeding and development of dairy goats: eastern Africa experience. *Livestock Research for Rural Development*. vol.24, n.21. <u>http://www.lrrd.org/lrrd24/1/ogol24021.htm</u>. 10.09.2014

Philipsson J, Rege J E O, Zonabend E and Okeyo A M 2011 Sustainable breeding programmes for tropical farming systems In: Animal Genetics Training Resource, version 3, 2011. Ojango, J.M., Malmfors, B. and Okeyo, A.M. (Eds).International Livestock Research Institute, Nairobi, Kenya, and Swedish University of Agricultural ciences, Uppsala, Sweden.

Schefers J M and Weigel K A 2012 Genomic selection in dairy cattle: Integration of DNA testing into breeding programs. Animal Frontiers Magazine. 2(1) 4-9. doi: 10.2527/af.2011-0032

Shumbusho F, Raoul J, Astruc J M, Palhierel and Elsen J M 2013 Potential benefits of genomic selection on genetic gain of small ruminant breeding programs. Animal Science. 91:3644–3657. doi:10.2527/jas2012-6205.

Sonola, V S 2015 Evaluation of performance of Norwegian dairy goats in Mgeta, Morogoro. M.Sc. dissertation, Sokoine University of Agriculture, Morogoro, Tanzania. pp.105

Thomas A 2014 Design of Experiments for Analytical Method Development and Validation. BioPharm International. 27(3):56-60.

URT (United Republic of Tanzania) 2009 National Public Private Partnership (PPP) Policy Dar es Salaam Government printers. 10 pp.

Van der Werf J H J 2000 Simple selection theory and the improvement of selection accuracy. In: "Animal Breeding – Use of New Technologies", Kinghorn B.P., Van der Werf, J.H.J. and Ryan, M. (Eds.). The Post Graduate Foundation in Veterinary Science of the University of Sydney. ISBN 0 646 387138. Pages 19-34.

van der Werf J H J 2006 Optimizing design of breeding programs. Armidale animal breeding summer course. pp. 61-96. <u>http://www-personal.une.edu.au/~jvanderw/BPDesignJW.pdf.</u>

Van Grevenhof E M, Van Arendonk J A M and Bijma P 2012 Response to genomic selection: The Bulmer effect and the potential of genomic selection when the number of phenotypic records is limiting. Genetics Selection Evolution. 44:26.

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