Managing Genetic Variation to Conserve Genetic Diversity in Goats and Sheep

J. N. B. Shrestha[1]   **G. H. Crow**[2]   **M.I. Soysal**[3]

[1]Dairy and Swine Research and Development Centre, Agriculture and Agri-Food, Sherbrooke, Canada,
[2]Department of Animal Science, University of Manitoba, Winnipeg, Manitoba, Canada
[3]Namık Kemal University, Department of Animal Science, Tekirdağ, Turkiye

Domestic goat and sheep populations maintained for many generations with small numbers of male and female parents, or declining in total numbers, not only endure accumulated genetic drift but also a steady rise in inbreeding, which can be directly attributed to dispersive forces of evolutionary significance that influence gene frequency. Increasing effective population size shows theoretical promise in lessening the impact on erosion of biodiversity from genetic drift. For example, doubling the effective numbers of parents which increases effective population size reduces rate of inbreeding by nearly one-half in many of the scenarios in the present study. Similarly, equalizing the number of male and female parents can decrease the variance among progeny of each parent, which in turn increases effective population size. The recurring erosion of domestic goat and sheep diversity has contributed to decreased fecundity, reduced fitness and poor adaptability, all known to influence efficiency of production. The potential loss in performance of livestock and poultry following many generations of accumulated genetic drift, which often goes unnoticed, can be predicted for specific populations from precise estimates of their mean value, additive genetic variance and heritability along with their effective number of male and female parents. For example, when the effective population size decreases from 200 to 40, the potential reduction in mean performance for economically important traits of goat and sheep populations following 20 generations of accumulated genetic drift will nearly double. In contrast, increasing effective population size from 200 to 600 will have the potential reduction in mean performance. The accumulation of favourable mutations could imply an effective population size of 100 or more, which is equal to a rise in rate of inbreeding of 0.5% or less, may be acceptable in sustaining genetic response to artificial selection in commercial breeding populations. The application of quantitative genetic principles related to inbreeding and genetic drift make it possible to safeguard against erosion of genetic diversity in endangered breeds, populations and landraces while lessening the impact from potential loss in their performance. Conservation of domestic animal diversity can be achieved by managing the erosion of genetic variation based on breeding strategies which promote the mating of sires to all dams, in either 'random bred' or 'balanced pedigreed' breeding structure for populations of endangered domestic goats and sheep. Obviously, the *in-situ* and *ex-situ* conservation of live animals, along with cryogenic preservation of their gametes, stem cells, somatic cells, blood and gonads will be complementary to conservation breeding.

Keywords: Conservation; Endangered breeds; Genetic drift, Inbreeding, Effective population size

Koyun ve Keçilerdeki Genetik Çeşitliliği Korumak İçin Genetik Varyasyonun Yönetimi

Küçük sayıda erkek ve dişi ebeveynlerle birçok generasyon sürdürülen ya da toplam sayı azalışı gösteren populasyonlar sadece birikimli genetik drift etkisine maruz kalmaz aynı zamanda düzenli bir şekilde yükselen akrabalı yetiştirmeye maruz kalır. Bu durum ise gen frekansını etkileyen evrimsel anlamlı dağıtıcı kuvvetlerin sonucudur. Artan etkili populasyon büyüklüğü genetik driften ötürü biyoçeşitlilik erezyonunu azaltma konusunda teorik bir beklenti yaratmaktadır. Söz gelimi bu çalışmada sonuçları benzeştirme senaryoları ile etkili ebeveyn sayısını iki katına çıkarmanın etkili populasyon büyüklüğünü azalttığı akrabalı yetiştirme hızını ise neredeyse yarı yarıya yavaşlattığı gösterilmiştir. Benzer şekilde erkek ve dişi sayısını eşitlemenin her ebeveynin dölleri arasındaki varyasyonu azalttığı neticede etkili populasyon büyüklüğünü arttırdığı gösterilmiştir. Evcil koyun ve keçi çeşitliliğinde meydana gelen erozyon verime etkili olan azalan fekundite, uyum ve zayıf adaptasyon olgusuna katkıda bulunmaktadır. Eklemeli genetik drift sonucu birçok generasyonun ardından evcil çiftlik hayvan ve

3Corresponding author

kanatlılardaki potansiyel verim düşmesi çoğunlukla fark edilemeyebilir. Ancak bu değerler bazı özel populasyonlarda etkili erkek ve dişi ebeveyn sayısı ile birlikte kalıtım derecesi, eklemeli genetik varyans ve bunların isabetli ortalama tahminlerinden belirlenebilir. Söz gelimi etkili populasyon büyüklüğü 200 den 40 a düştüğünde koyun ve keçi populasyonlarında 20 generasyon eklemeli genetik drift ardından ekonomik bakımdan önemli özellikler için ortalama verimdeki potansiyel azalma iki misline yakın olacaktır. Buna karşılık etkili populasyon büyüklüğü 200 den 600 e çıkınca, ortalama verimdeki potansiyel azalma yarı yarıya olacaktır. Ticari üretim populasyonlarında arzu edilen mutasyonlardaki birikim etkili populasyon büyüklüğünü 100 veya daha fazla kılıp böylece akrabalı yetiştirme hızını % 0,5 ya da daha az yaptığında yapay seleksiyon sürdürülebilir, makul genetik ilerlemeye yol açabilecektir. Akrabalı yetiştirme ve genetik dirifte ilişkin kantitatif genetik prensiplerin uygulanması nesli tükenme tehlikesindeki ırklarda populasyonlarda ve karasal ırklarda verim bakımından potansiyel düşme etkisinin azalmasına karşın genetik çeşitliliğin erozyonuna karşı korunmasını mümkün kılar. Belirlenmiş erkek ve dişi eşleştirmenin ister tesadüfi ister soy kütüğüne kayıtlı evcil hayvan çeşitliliğinin korunması süreci belirli bir yetiştirme stratejisine dayalı yürütülmesi halinde nesli tükenmekte olan populasyonlarda genetik varyasyonun erozyonunda kontrol sağlanabilir. Açık bir şekilde canlı hayvanların *in-situ* ve *ex-situ* korunması ve bununla beraber bunların gametlerinin, kök hücrelerinin, somatik hücrelerinin, kan ve gonadlarının dondurularak muhafazası ile koruma amaçlı programlara tamamlayıcılık sağlayacaktır.

Anahtar kelimeler: Koruma, Tehlikedeki Irklar, Genetik Dirift, Akrabalı Yetiştirme, Etkili Populasyon Büyüklüğü

Introduction

The erosion of domestic goat and sheep diversity due to creative human activity and natural causes is of serious concern and may be of a sizable threat to a nations' food security if current production levels are to be sustained and the changing demands of future markets need to be addressed. Creative human activities promoting globalization continue to impact domestic animal genetic resources worldwide as a result of ongoing habitat loss to urbanization, abandonment of family farms in favour of agri-business, replacement of indigenous breeds, populations and landraces with highly productive animals, and the selection of individuals, families and populations with inherent potential for increased productivity (Shrestha et al., 2008). Forces of nature such as fire, earthquakes, war, diseases and climate change create dispersive forces of evolutionary significance which cause fluctuations in parent numbers across generations, influencing gene frequencies and resulting in genetic death and genetic bottle necks. Furthermore, the random nature of allele transmission which results from the assortment of chromosomes during meiosis is a function of the normal gene flow from one generation to the next (Fisher, 1930; Wright, 1931; 1945). This sampling of genes within animals, and also the sampling of animals from families, and families from populations is responsible for recurrent genetic drift. Endangered breeds, populations and landraces raised over many generations with small numbers of male and female parents, or decreasing total numbers have a sizeable loss of genetic variability from accumulated genetic drift which is associated with a steady rise in inbreeding along with loss of productivity.

Conservation of domestic animal diversity has received international attention in the last two decades because domestic animal genetic resources offer the best opportunity to meet the current and future market requirements for food, commodities, trade, employment, energy, and recreation. The Food and Agriculture Organization of the United Nations (Anon., 1998) reported that nearly 800 farm animal breed populations in the world have become extinct, and among those that remain, about 30% were endangered (Scherf, 2000). The risk status in actual number of breeds, worldwide for different livestock species have been estimated as 27% in goats and 22% in sheep (Galal, 2005). These estimates were based on prevailing risk criteria that tend to vary over time, such as breed populations with less than 1000 females, or 20 males, or 1200 in total numbers, decreasing and less than 80% females. Managing genetic diversity of endangered animal populations using techniques based on conservation planning, genetics, ecological studies, and *in-situ* and *ex-situ* conservation of live animals including preservation of their gametes, stem cells, somatic cells, blood

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and gonads has achieved limited success. Attempts to implant cloned embryos or zygotes from the wild Mouflon sheep into domestic sheep have achieved success permitting expansion of populations at risk of extinction. Thus breeds that are not endangered may act as surrogates to reproduce implants from zygotes or clones.

Material and Method

The subject of the present study is to compare breeding strategies that can lessen the erosion of domestic goat and sheep genetic diversity and to demonstrate their effectiveness in conserving breeds, populations and landraces that are at risk of becoming endangered and possibly extinct. The equation regarding these calculation given below.

Results

Effective population size and genetic drift

Population size is a measure of the number of breeding males and females and has a significant influence on genetic drift. This is because each generation there is the sampling of families in breed populations, individual goats and sheep from those families, and genes within animals. This sampling causes gene frequencies to drift from their initial values and contribute towards increased homozygosity. When the degree of inbreeding is minimal in a population, there is a tendency to maintain gene frequencies at their historical values.

When mating is random each parent has an 'equal chance' of contributing to the next generation and the number of progeny per parent follows a Poisson distribution. According to Wright (1931) the effective number of parents (N_e) is $\dfrac{4N_m N_f}{N_m + N_f}$, where N_m and N_f are the number of male and female parents, respectively, or $\dfrac{1}{N_e} = \dfrac{1}{4N_m} + \dfrac{1}{4N_f}$. The inbreeding rate per generation (ΔF) which depends upon effective population size is $= \dfrac{1}{2N_e} = \dfrac{1}{8N_m} + \dfrac{1}{8N_f}$.

In a balanced pedigreed breeding population the distribution of progeny numbers per parent does not follow a Poisson distribution as is assumed above. Any attempt to equalize the number of offspring from each parent will decrease the

variance of progeny number and increase the effective number of parents. The exact balancing of differences in progeny numbers per parent would reduce sampling variance to zero, while drift variance would be one-half of that derived from the usual formula.   To illustrate this, Gowe et al. (1959) described a balanced pedigree breeding population in poultry where each male has one male offspring and N_f/N_m female offspring, and each female has one female offspring and a probability of N_m/N_f of having one male offspring in the next generation, resulting in $\Delta F = \dfrac{3}{32N_m} + \dfrac{1}{32N_f}$ (Hill, 1972).

In breeding populations that may vary in effective number of parents from generation to generation, the average value of N_e in a specific generation is estimated as $\bar{N}_e = t /(\dfrac{1}{N_{e1}} + \dfrac{1}{N_{e2}} + ... + \dfrac{1}{N_{et}})$, where 't' is the number of generations (Wright, 1939). The ΔF in 't' generation can be estimated by $1-(1-\Delta F)^t$. Thus homozygosity will be attained in

$$\dfrac{\log[1-\{1-(1-\Delta F)^t\}]}{\log(1-\Delta F)}$$ generations.   The

effective number of male and female parents, N_e, ΔF and number of generations to attain homozygosity in randombred and pedigreed populations have been presented in Table 1.

As a consequence of drift, the mean performance of the population under constant environmental conditions will show changes. Any change in gene frequency has a variance of $\dfrac{q(1-q)}{2N_e}$, where q is the gene frequency of the favourable allele and N_e is the effective number of parents. The change in mean performance from one generation to the next has variance due to genetic drift ($\hat{\sigma}_d^2$) $= \dfrac{\hat{\sigma}_g^2}{N_e}$, where $\hat{\sigma}_g^2$ is additive genetic variance, which may be rewritten as $\hat{\sigma}_d^2 = 2\Delta F \hat{\sigma}_g^2$ (Gowe et al. 1959).   The genetic parameters for body weights, milk yield, wool characteristics, reproduction and survival obtained from previously published estimates from several

breeds of goats and sheep have been utilized to estimate the influence of 20 generations of accumulated drift on production performance (Tables 2 and 3).

The repeated mating of all the sires in the populations may be considered as an alternate breeding strategy to allow for no increase in inbreeding. In this breeding procedure all sires mate with each dam or group of dams (Figure 1), inbreeding would start to occur after one cycle of 's' generations of using sires from 's' families,

estimated as $\Delta F = \dfrac{4}{3}\left(\dfrac{1}{2s+3}\right)$, where s is the number of male parents (Smith, 1977). The ongoing human activity associated with potential loss of domestic animal genetic resources may be overcome by employing breeding strategies when repeat mating of sires is complemented with either the random or balanced pedigreed breeding populations, while minimizing detrimental influence occurring from rise in ΔF.

Table 1. Effective number of male and female parents, effective population size (N_e), inbreeding rate per generation (ΔF) and number of generations to homozygosity in balanced pedigreed population.

Effective parents			ΔF (%)								Generations to
Male	Female	N_e	1	5	10	15	20	25	30	50	homozygosity
1	1	4	12.50	48.71	73.69	86.51	93.08	96.45	98.18	99.87	66
2	2	8	6.25	27.58	47.55	62.02	72.49	80.08	85.57	96.03	137
3	3	12	4.17	19.17	34.66	47.19	57.31	65.49	72.11	88.09	207
4	4	16	3.13	14.68	27.20	37.89	47.01	54.78	61.42	79.56	278
5	5	20	2.50	11.89	22.37	31.60	39.73	46.90	53.21	71.80	348
5	10	23	2.19	10.47	19.84	28.23	35.75	42.47	48.50	66.91	399
10	10	40	1.25	6.10	11.82	17.19	22.24	26.98	31.43	46.68	700
10	20	46	1.09	5.35	10.41	15.21	19.74	24.04	28.10	42.30	801
12	12	48	1.04	5.10	9.94	14.54	18.90	23.03	26.96	40.76	841
15	15	60	0.83	4.10	8.03	11.80	15.41	18.88	22.20	34.19	1053
20	20	80	0.62	3.09	6.08	8.98	11.78	14.51	17.15	26.91	1405
20	40	91	0.55	2.70	5.34	7.90	10.39	12.81	15.17	23.98	1606
25	25	100	0.50	2.48	4.89	7.24	9.54	11.78	13.96	22.17	1757
25	50	114	0.44	2.17	4.29	6.37	8.40	10.38	12.33	19.69	2009
50	50	200	0.25	1.24	2.47	3.69	4.88	6.07	7.23	11.76	3518
50	100	229	0.22	1.09	2.17	3.23	4.29	5.33	6.36	10.37	4021
100	100	400	0.12	0.62	1.24	1.86	2.47	3.08	3.68	6.06	7040
100	200	457	0.11	0.55	1.09	1.63	2.16	2.70	3.23	5.32	8046
100	300	480	0.10	0.52	1.04	1.55	2.06	2.57	3.08	5.08	8449
200	200	800	0.06	0.31	0.62	0.93	1.24	1.55	1.86	3.08	14084
200	400	914	0.05	0.27	0.55	0.82	1.09	1.36	1.63	2.70	16096
250	250	1000	0.05	0.25	0.50	0.75	1.00	1.24	1.49	2.47	17606
250	500	1143	0.04	0.22	0.44	0.65	0.87	1.09	1.30	2.16	20122
300	300	1200	0.04	0.21	0.42	0.62	0.83	1.04	1.24	2.06	21128
300	600	1371	0.04	0.18	0.36	0.55	0.73	0.91	1.09	1.81	24147

Pedigreed population: $\Delta F = (3/32N_m) + (1/32N_f)$;
Rate of inbreeding in generation = $1-(1-\Delta F)^t$;
Generations to attain homozygosity$=\log[1-\{1-(1-\Delta F)^t\}]/\log(1-\Delta F)$.

Table 2. Effective number of parents, and maximum expected change (±) from drift in the mean performance after 20 generations for balanced pedigreed population of goat.

Effective No. of parents (n)		West African Dwarf[1] Body wt. (kg) at			Boer[2] Body wt. (kg) at				Angora[3]			Skopelos dairy[4] Milk yield (kg) at	
Male	Female	Birth	120d	360d	Birth	100d	6-mo	12-mo	Grease fleece wt. (kg)	Mean fiber diameter (µg)	Medulated fiber (%)	90d	Total
1	1	0.19	3.95	7.50	0.96	2.48	8.77	8.12	0.55	3.7	0.67	28.2	37.1
2	2	0.17	3.49	6.62	0.84	2.19	7.74	7.16	0.48	3.3	0.59	24.9	32.8
3	3	0.15	3.10	5.89	0.75	1.95	6.89	6.37	0.43	2.9	0.52	22.2	29.1
4	4	0.13	2.81	5.33	0.68	1.76	6.24	5.77	0.39	2.6	0.47	20.1	26.4
5	5	0.12	2.58	4.90	0.63	1.62	5.73	5.30	0.36	2.4	0.44	18.5	24.3
5	10	0.12	2.45	4.65	0.59	1.54	5.44	5.03	0.34	2.3	0.41	17.5	23.0
10	10	0.09	1.93	3.67	0.47	1.21	4.29	3.97	0.27	1.8	0.33	13.8	18.1
10	20	0.09	1.82	3.46	0.44	1.14	4.04	3.74	0.25	1.7	0.31	13.0	17.1
15	15	0.08	1.61	3.05	0.39	1.01	3.57	3.30	0.22	1.5	0.27	11.5	15.1
20	20	0.07	1.41	2.67	0.34	0.88	3.12	2.89	0.19	1.3	0.24	10.0	13.2
20	40	0.06	1.32	2.51	0.32	0.83	2.93	2.71	0.18	1.2	0.22	9.4	12.4
25	25	0.06	1.27	2.40	0.31	0.79	2.81	2.60	0.17	1.2	0.21	9.0	11.9
25	50	0.06	1.19	2.25	0.29	0.75	2.64	2.44	0.16	1.1	0.20	8.5	11.1
50	50	0.04	0.91	1.72	0.22	0.57	2.01	1.86	0.13	0.9	0.15	6.5	8.5
50	100	0.04	0.85	1.61	0.21	0.53	1.88	1.74	0.12	0.8	0.14	6.1	8.0
100	100	0.03	0.64	1.22	0.16	0.40	1.43	1.32	0.09	0.6	0.11	4.6	6.1
100	200	0.03	0.60	1.14	0.15	0.38	1.34	1.24	0.08	0.6	0.10	4.3	5.7
100	300	0.03	0.59	1.12	0.14	0.37	1.31	1.21	0.08	0.5	0.10	4.2	5.5
200	200	0.02	0.46	0.87	0.11	0.29	1.01	0.94	0.06	0.4	0.08	3.3	4.3
200	400	0.02	0.43	0.81	0.10	0.27	0.95	0.88	0.06	0.4	0.07	3.1	4.0
250	250	0.02	0.41	0.78	0.10	0.26	0.91	0.84	0.06	0.4	0.07	2.9	3.8
250	500	0.02	0.38	0.73	0.09	0.24	0.85	0.79	0.05	0.4	0.06	2.7	3.6
300	300	0.02	0.37	0.71	0.09	0.23	0.83	0.77	0.05	0.4	0.06	2.7	3.5
300	600	0.02	0.35	0.66	0.08	0.22	0.78	0.72	0.05	0.3	0.06	2.5	3.3
Genetic parameters													
Mean±SE		1.57±0.01	5.75±0.05	8.04±0.08	4.4±0.02	17.8±0.11	22.7±0.14	36.9±0.20	1.52±0.01	24.7±0.07	1.37±0.02	156±1.3	224±2.4
$\hat{\sigma}_g^2$		0.0047	2.1002	7.5601	0.123	0.827	10.34	8.85	0.04	1.77	0.06	107.12	185.08
$\hat{h}^2$ ±SE		0.50±0.05	0.43±0.07	0.30±0.07	0.36±0.14	0.60±0.12	0.60±0.17	0.36±0.19	0.25	0.33	0.15±0.04	0.14±0.04	0.07±0.06

$\hat{\sigma}_d^2 = \hat{\sigma}_g^2 / N_e = 2\Delta F \hat{\sigma}_g^2$, where $\hat{\sigma}_d^2$ = drift variance, $\hat{\sigma}_g^2$ = additive genetic variance, N_e = effective population size, and ΔF = rate of inbreeding per generation.

Source: [1] Bosso et al. (2007); [2] Schoeman et al. (1997); [3] Taddeo et al. (1998); [4] Kominakis et al. (2000).

Table 3. Effective number of parents, and maximum expected change (±) from drift in the mean performance after 20 generations for balanced pedigreed population of sheep.

Effective No. of parents (n)		Dorper[1] Body wt. (kg) at			Turkish Merino[2] Body wt. (kg) at			Grease	Djallonké[3] Body wt. (kg) at			Lacuane[4] Yield		
Male	Female	Birth	42d	100d	Birth	90d	12-mo	fleece wt. (kg)	Birth	120d	360d	Milk (l)	Fat (kg)	Protein (kg)
1	1	0.67	3.40	5.34	0.61	4.89	9.33	0.61	0.22	7.74	9.57	11.9	2.96	2.57
2	2	0.59	3.00	4.71	0.54	4.31	8.23	0.54	0.20	6.83	8.44	10.5	2.62	2.27
3	3	0.52	2.67	4.19	0.48	3.84	7.32	0.48	0.17	6.07	7.51	9.4	2.33	2.02
4	4	0.47	2.41	3.80	0.43	3.47	6.63	0.43	0.16	5.50	6.80	8.5	2.11	1.83
5	5	0.44	2.22	3.49	0.40	3.19	6.09	0.40	0.14	5.06	6.25	7.8	1.94	1.68
5	10	0.41	2.11	3.31	0.38	3.03	5.78	0.38	0.14	4.80	5.93	7.4	1.84	1.60
10	10	0.33	1.66	2.61	0.30	2.39	4.56	0.30	0.11	3.78	4.68	5.8	1.45	1.26
10	20	0.31	1.56	2.46	0.28	2.25	4.30	0.28	0.10	3.56	4.41	5.5	1.37	1.19
15	15	0.27	1.38	2.17	0.25	1.99	3.79	0.25	0.09	3.15	3.89	4.9	1.21	1.05
20	20	0.24	1.21	1.90	0.22	1.74	3.32	0.22	0.08	2.75	3.40	4.2	1.05	0.92
20	40	0.22	1.13	1.78	0.20	1.63	3.12	0.20	0.07	2.59	3.20	4.0	0.99	0.86
25	25	0.21	1.09	1.71	0.20	1.57	2.99	0.20	0.07	2.48	3.06	3.8	0.95	0.82
25	50	0.20	1.02	1.60	0.18	1.47	2.80	0.18	0.07	2.32	2.87	3.6	0.89	0.77
50	50	0.15	0.78	1.22	0.14	1.12	2.14	0.14	0.05	1.77	2.19	2.7	0.68	0.59
50	100	0.14	0.73	1.15	013	1.05	2.00	0.13	0.05	1.66	2.05	2.6	0.64	0.55
100	100	0.11	0.55	0.87	0.10	0.80	1.52	0.10	0.04	1.26	1.56	1.9	0.48	0.42
100	200	0.10	0.52	0.81	0.09	0.75	1.42	0.09	0.03	1.18	1.46	1.8	0.45	0.39
100	300	0.10	0.51	0.80	0.09	0.73	1.39	0.09	0.03	1.15	1.42	1.8	0.44	0.38
200	200	0.08	0.39	0.62	0.07	0.56	1.08	0.07	0.03	0.89	1.11	1.4	0.34	0.30
200	400	0.07	0.37	0.58	0.07	0.53	1.01	0.07	0.02	0.84	1.03	1.3	0.32	0.28
250	250	0.07	0.35	0.55	0.06	0.51	0.96	0.06	0.02	0.80	0.99	1.2	0.31	0.27
250	500	0.06	0.33	0.52	0.06	0.47	0.90	0.06	0.02	0.75	0.93	1.2	0.29	0.25
300	300	0.06	0.32	0.50	0.06	0.46	0.88	0.06	0.02	0.73	0.90	1.1	0.28	0.24
300	600	0.06	0.30	0.47	0.05	0.43	0.82	0.05	0.02	0.68	0.85	1.1	0.26	0.23
Genetic parameters														
Mean±SE		3.98±0.02	11.9±0.06	25.6±0.12	4.30±0.02	31.2±0.15	53.3±0.21	5.26±0.03	2.01±0.01	8.51±0.08	14.8±0.14	140±1.3	9.43±0.09	7.57±0.07
$\hat{\sigma}_g^2$		0.06	1.55	3.83	0.05	3.21	11.68	0.05	0.0066	8.0458	12.2897	19.1	1.18	0.89
$\hat{h}^2$ ±SE		0.11±0.04	0.28±0.04	0.20±0.07	0.08±0.03	0.12±0.04	0.25±0.05	0.08±0.04	0.39±0.06	0.54±0.08	0.21±0.11	0.27±0.10	0.23±0.09	0.22±0.09

$\hat{\sigma}_d^2 = \hat{\sigma}_g^2 / N_e = 2\Delta F \hat{\sigma}_g^2$, where $\hat{\sigma}_d^2$ = drift variance, $\hat{\sigma}_g^2$ = additive genetic variance, N_e = effective population size, and ΔF = rate of inbreeding per generation.

Source: [1] Nese et al. (2001); [2] Ozcan et al. (2004); [3] Bosso et al. (2007); [4] Barillet and Boichard (2001).
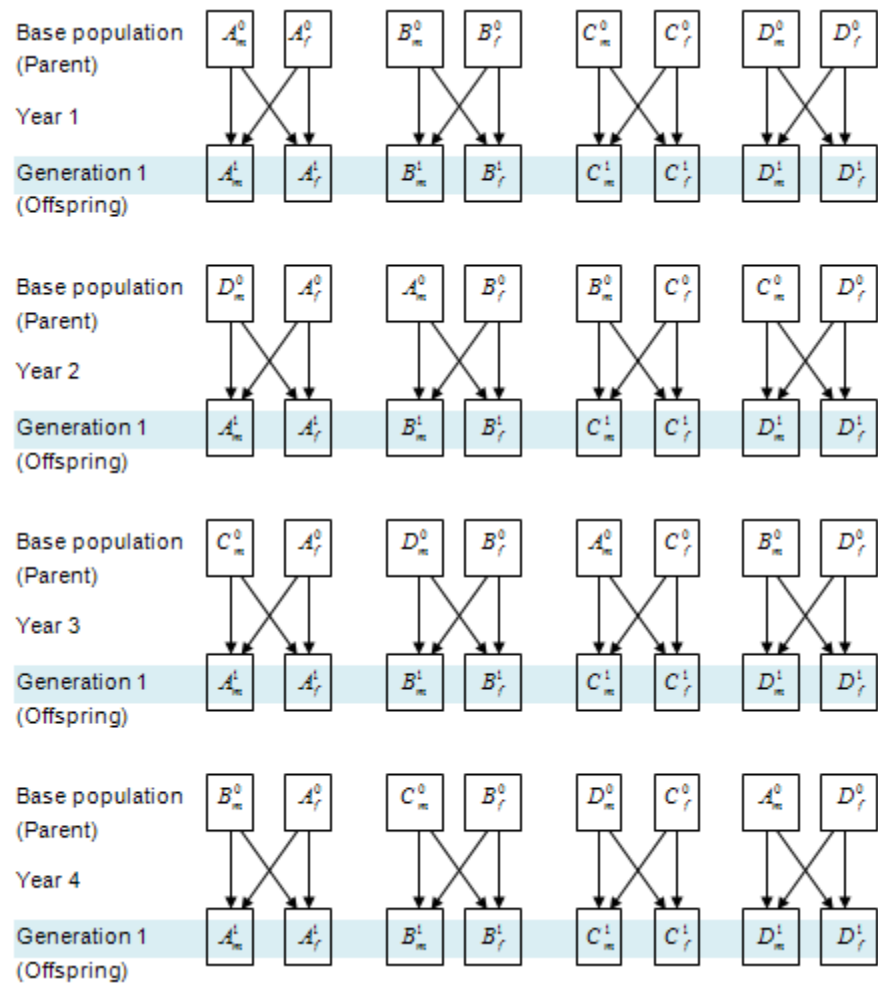
Figure 1. Breeding scheme with repeated mating of sire.
No inbreeding until all sires (s) mate with each dam or group of dams, thereafter, inbreeding

$$= \frac{4}{3}\left(\frac{1}{2^{s+3}}\right) \text{ (Smith, 1977).}$$

Potential loss of productivity from genetic drift

Balanced pedigreed populations with equal number of male (N_m) and female (N_f) ranging from 1 to 300 show ΔF varied from 12.5 to 0.04% in generation 1, from 73.69 to 0.42% in generation 10, from 93.08 to 0.83% in generation 20, and from 98.18 to 1.24% in generation 30 (Table 1). When the number of female parents is twice the number of male parents with $N_m = 5$ and $N_f = 10$ to $N_m = 300$ and $N_f = 600$ female, ΔF varied from 2.19 to 0.04% in generation 1, from 19.84 to 0.36% in generation 10, from 35.75 to 0.73% in generation 20, and from 48.5 to 1.09% in generation 30. There was an increase in number of generations to attain homozygosity from 66 generations for 1 male and 1 female

parent to 7,040 generations for 100 male and 100 female parents, and 24,147 generations for 300 male and 600 female parents.

In a balanced pedigreed breeding population of Boer goats (Schoeman et al. 1997), 20 generations of genetic drift changed mean body weights at birth, 100d, 6- and 12-mo which varied from $N_m = N_f = 1$ (0.96, 2.48, 8.77 and 8.12 kg, respectively), to $N_m = N_f = 100$ (0.16, 0.40, 1.43 and 1.32 kg, respectively), and $N_m = 300$ and $N_f = 600$ (0.08, 0.22, 0.78 and 0.72 kg, respectively). Correspondingly in Angora goats (Taddeo et al. 1998), mean grease fleece weight, fiber diameter and medulated fiber varied from $N_m = N_f = 1$ (0.55 kg, 3.7 µg and 0.67%, respectively), to $N_m = N_f = 100$ (0.09
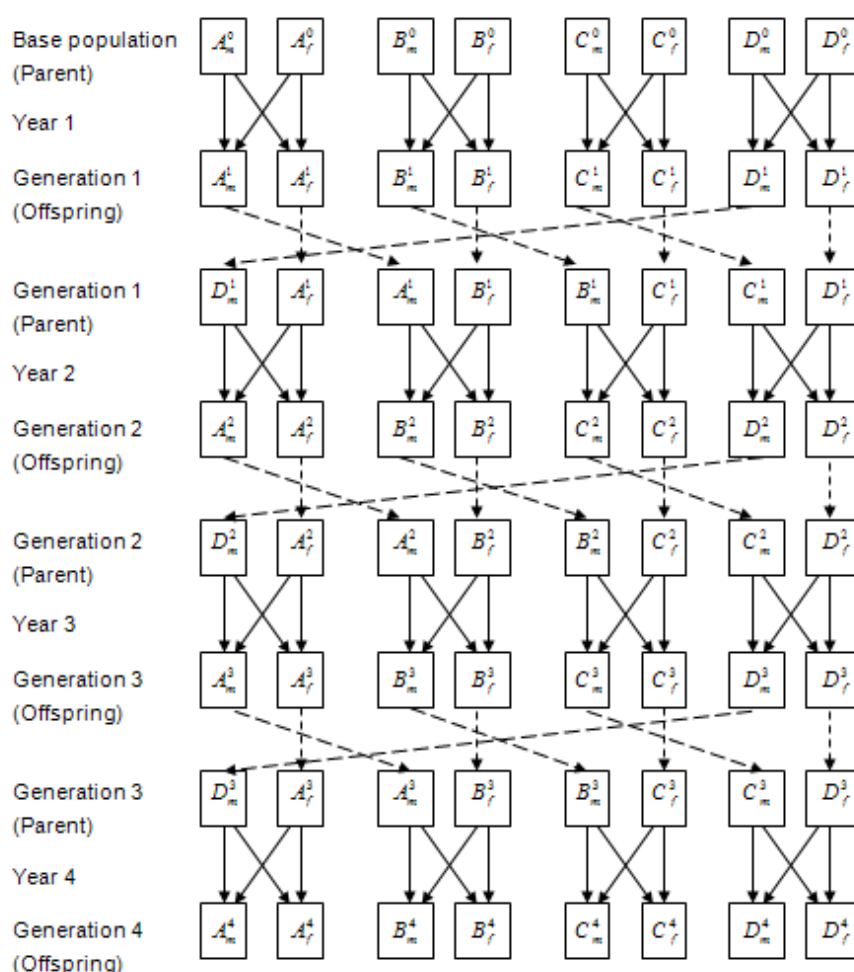
Figure 2. Breeding scheme for pedigreed population with repeat mating of sire.
Each sire mated to a dam of group of dams will contribute a replacement male and female offspring that will be selected at random to become parents for the succeeding generations. Each generation, a female or group of females assigned to a specific male for breeding. $\Delta F = (3/32N_m) + (1/32N_f)$ Hill (1972).

kg, 0.6 µg and 0.11%, respectively), and N_m = 300 and N_f = 600 (0.05 kg, 0.3 µg and 0.06%, respectively); in Skopelos dairy goats (Kominakis et al. 2000), mean 90d and total milk yield varied from $N_m = N_f = 1$ (28.2 and 37.1 kg, respectively), to $N_m = N_f = 100$ (4.6 and 6.1 kg, respectively), and $N_m = 300$ and N_f = 600 (2.5 and 3.3 kg, respectively); in West African Dwarf (Bosso et al. 2007), mean body weights at birth, 120d and 360d varied from $N_m = N_f = 1$ (0.19, 3.95 and 7.5 kg, respectively), to $N_m = N_f = 100$ (0.03, 0.64 and 1.22 kg, respectively), and $N_m = 300$ and $N_f = 600$ (0.02, 0.35 and 0.66 kg, respectively).

In a balanced pedigreed breeding population of Lacuane sheep (Barillet and Boichard,. 1987), 20 generations of genetic drift changed mean yield of milk, fat and protein which varied from $N_m = N_f = 1$ (11.9 *l*, 2.96 and 2.57 kg, respectively), to $N_m = N_f = 100$ (1.9 *l*, 0.48 and 0.42 kg, respectively), and $N_m = 300$ and N_f = 600 (1.1 *l*, 0.26 and 0.23 kg, respectively). Correspondingly in Dorper sheep (Neser et al. 2001), mean body weights at birth, 42 and 100d varied from $N_m = N_f = 1$ (0.67, 3.40 and 5.34 kg, respectively), to $N_m = N_f = 100$ (0.11, 0.55 and 0.87 kg, respectively), and $N_m = 300$ and N_f = 600 (0.06, 0.3 and 0.47 kg, respectively); in
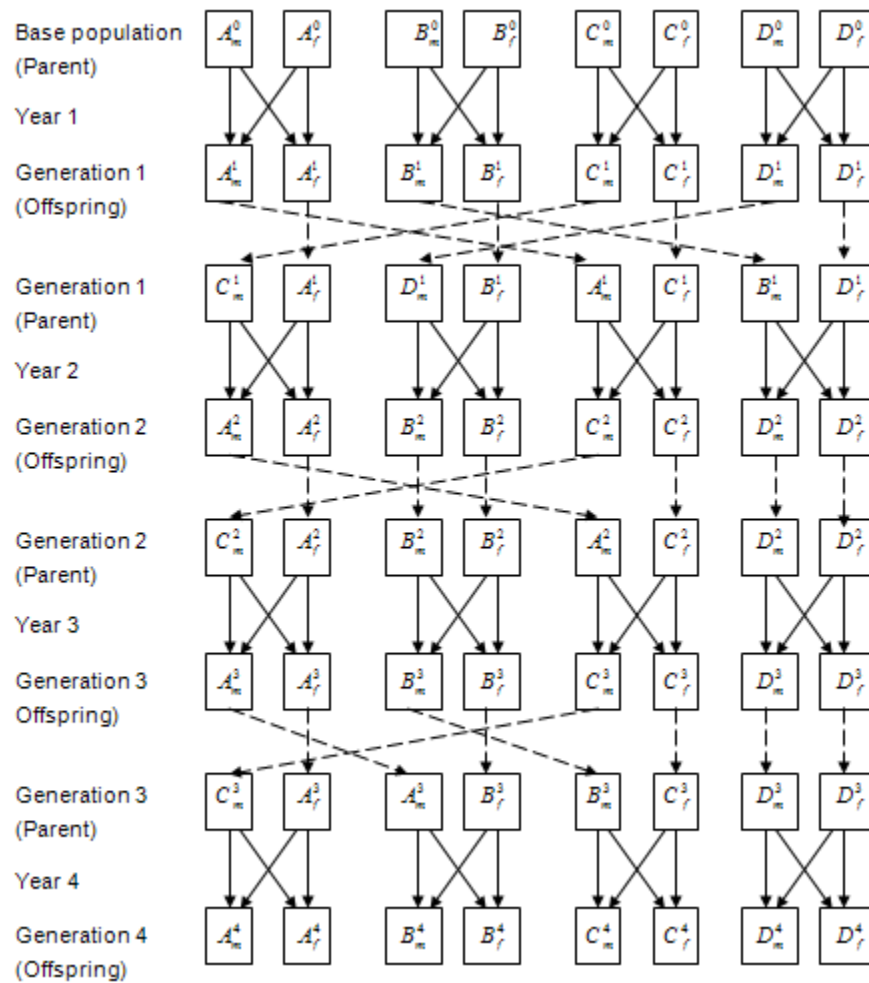
Figure 3. Breeding scheme for randombred population.

Each sire mated to a dam of group of dams will contribute a replacement male and female offspring that will be selected at random to become parents for the succeeding generations. Each generation, a female or group of females assigned to a male at random for breeding. $\Delta F = (1/8N_m) + (1/8N_f)$ Crow (1954), Crow and Morton (1955).

Turkish Merino sheep (Ozcan et al. 2005), mean body weights at birth, 90d and 12-mo, and grease fleece weight varied from $N_m = N_f = 1$ (0.61, 4.89 and 9.33 kg, and 0.61 kg, respectively), to $N_m = N_f = 100$ (0.10, 0.80 and 1.52 kg, and 0.10 kg, respectively), and $N_m = 300$ and $N_f = 600$ (0.05, 0.43 and 0.82 kg, and 0.05 kg, respectively).

Discussion

Erosion of domestic animal diversity can be reduced in theory by increasing N_e which depends on the number of breeding male and female parents, and in so doing there is a reduction in ΔF. Developing countries share 98% of 792 million goats and 73% of 1161 goat breed populations and 75% of 1,051 million sheep and 59% of 2386 sheep breed populations (Anon., 2008; Anon., 2009). Therefore the introduction of improved genetic procedures to manage indigenous breed populations could help reverse the culture of promoting breeds for their productivity alone (Smith, 1984). Evidence presented here for goats and sheep illustrates that increasing the number of male and female breeding parents from 10 to 20 decreased the rate of inbreeding in generation 1 and 10 from 2.5 and 22.37%, respectively, to 1.25 and 11.82%, respectively. Thus, doubling the number of male and female parents doubled

N_e and halved ΔF. At the same time when increasing the number of female parents, the rate of inbreeding in generations 1 and 10 for a breeding population with 100 male and 100 female parents that was 0.25 and 2.47%, respectively decreased with 100 male and 200 female parents to 0.19 and 1.86%, respectively, and with 100 male and 300 female parents to 0.17 and 1.65%, respectively. In general, increasing the number of female parents relative to male parents by two or three fold increased N_e from 200 to 267 and 300, respectively, resulting in ΔF to decrease by about 0.24 and 0.32%, respectively.

The effective number of parents will decrease with an increase in the variance of progeny numbers per parent which arises from real differences that occur in the reproductive ability of the parents. It is possible to decrease the variance of progeny numbers per parent and increase effective number of parents by equalizing the number of male and female parents. The significant advantage of increasing N_e is to minimize loss of productivity as well as increasing the number of generations necessary to attain homozygosity. In conservation breeding, the impact from erosion of domestic animal diversity can be lessened by modifying the current management practice of keeping only a few sires in contrast to keeping more males for subsequent breeding whilst increasing the sire to dam ratio. Furthermore there is opportunity to re-establish goat and sheep breeds at the verge of extinction by implanting their zygotes into common breeds of the same species. This approach will certainly increase the number of breeding animals within the breed, population and landrace.

The influence of genetic drift is cumulative, therefore expected change in performance can continue over several generations. In goats and sheep, there is evidence to suggest that the change in mean performance expected from drift following 20 generations will vary with the effective number of male and female parents. In goats, maximum influence expected from genetic drift by decreasing N_e from 10 male and 100 female parent to 25 male and 25 female parents nearly doubled the possible change in mean performance for body weights of the Boer breed, fleece characteristics of the Angora breed, milk yield of the Skopelos dairy breed,

and body weights of the West African Dwarf breed. Correspondingly in sheep, possible changes in mean performance were estimated for yield of milk, fat and protein of the Lacuane breed, body weights of the Dorper breed, body weights and grease fleece weight of the Turkish Merino, and body weights of the Djallonké breed. In general, decreasing N_e from 100 male and 100 female parents to 20 male and 20 female parents could lead to a doubling in possible change in performance, this is about triple for 10 male and 10 female parents, and only one-half for 300 male and 600 female parents (all relative to performance changes shown by populations with 100 males and 100 females). These estimates clearly demonstrate the association of N_e to the magnitude of potential loss in mean performance for economically important production performance in goats and sheep. In general, average values from a number of publications may be used to predict potential loss in performance for specific objectives.

Strategies to manage genetic variation could involve a breeding population with or without pedigree records where each sire mated to a dam, or a group of dams contribute replacement male and female offspring which are selected at random to become parents in the following generation. In the absence of pedigree records, a randombred breeding population based on random selection of male and female offspring in successive generations will maintain genetic authenticity of a breed, population and landrace at risk of endangerment. Each sire and dam has an equal chance of mating with one another in a randombred population. Therefore the change in ΔF which is a function of N_e can be predicted. Nevertheless, mating of half-sibs and full-sibs is possible, which will contribute towards an increase in ΔF. In contrast, a balanced pedigreed breeding population has an advantage over a randombred breeding population because the mating of related individuals is avoided by design. The ΔF can be reduced by 50% in a balanced pedigreed population by avoiding full- and half-sib mating. Consequently, possible change in mean performance from genetic drift can be halved in a balanced pedigreed breeding population compared to a randombred breeding population. There have been many selection studies in the past five decades that have utilized either

randombred or pedigreed breeding populations to monitor environmental trends in a genetically stable population (Shrestha et al., 1996).

5.Conclusion

Strategies based on randombred and balanced pedigreed breeding populations demonstrate potential merit in maintaining genetic authenticity of breeds, populations and landraces at risk of endangerment or extinction by avoiding loss in mean performance associated with genetic drift. Developing countries with a greater proportion of

indigenous breed populations of goats and sheep maintained in small numbers could

benefit from randombred or pedigreed breeding populations with repeat mating of sires in order to maintain genetic authenticity. This will not only minimize the loss of genes from families in populations, but also the loss of individuals within families and of genes within individuals. Breeding strategies influence the variance of gene frequencies as a result of genetic sampling from generation to generation and also influence the rate of inbreeding per generation and potential loss in production performance.

References

Anonymous, 1998. Secondary Guidelines: Management of small populations at risk. Food and Agriculture Organization of the United Nations, Rome, Italy, 219 p.

Anonymous, 2008. Food and Agriculture Organization of the United Nations, Rome, Italy, accessed July 2008.

Anonymous, 2009. http://www.fao.org/dad-is/ accessed 23 Feb. 2009

Barillet, F., Boichard, D., 1987. Studies on dairy production of milking ewes. I. Estimates of genetic parameters for total milk composition and yield. Génét. Sél. Evol. 19, 459-474.

Bosso, N.A., Cissé, M.F., van der Waaij, E.H., Fall, A., van Arendonk, J.A.M., 2007. Genetic and phenotypic parameter estimates of body weight in West African Dwarf goat and Djallanké sheep. Small Rumin. Res. 67, 271-278.

Crow, J.F., 1954. Breeding structure of populations. II. Effective population number. In: Kempthorne, O., Bancroft, T.A., Gowen, J.W., Lush, J.L., (Eds.), Statistics and Mathematics in Biology. Iowa State College Press, Ames, Iowa, USA, pp. 543-556.

Crow, J.F., Morton, N.E., 1955. Measurement of gene frequency drift in small populations. Evolution 9, 202-214.
.
Fisher, R.A., 1930. The genetic theory of natural selection. Clarendon Press, Oxford, UK.

Galal, S. 2005. Biodiversity in goats. Small Rumin. Res. 60, 75-81.

Gowe, R.S., Robertson, A., Latter, B.D.H., 1959. Environment and poultry breeding problems. 5. The design of poultry control strains. Poult. Sci. 38, 462-471.

Hill, W. G., 1972. Estimation of genetic change. I. General theory and design of control populations. Anim. Breed. Abstr. 40, 1-15.

Kominakis, A., Rogdakis, E., Vasiloudis, Ch., Liaskos, O., 2000. Genetic and environmental sources of variation of milk yield of Skopelos dairy goats. Small Rumin. Res. 36, 1-5.

Neser, F.W.C., Erasmus, G.J., van Wyk, J.B., 2001. Genetic parameter estimates for pre-weaning weight traits in Dorper sheep. Small Rumin. Res. 40, 197-202.

Ozcan, M., Ekiz, B., Yilmaz, A., Ceyhan, A., 2005. Genetic parameter estimates for lamb growth traits and greasy fleece weight at first shearing in Turkish Merino sheep. Small Rumin. Res. 56, 215-222.

Scherf, B. D., (Editor) 2000. World watch list of domestic animal diversity. Third Edition, Food and Agriculture Organization of the United Nations, Rome, Italy, 726 pp.

Schoeman, S.J., Els, J.F., van Niekerk, M.M., 1997. Variance components of early growth traits in the Boer goat. Small Rumin. Res. 26, 15-20.

Shrestha, J. N. B., Peters, H. F., Heaney, D. P., Van Vleck, L. D., 1996. Genetic trends over 20 years of selection in the three synthetic Arcotts, Suffolk and Finnish Landrace sheep breeds. 1. Early growth traits. Can. J. Anim. Sci. 76, 1-6.

Shrestha, J.N.B., Galal, S., Mariante, A. da S., Kotze, A., Delgardo, J.V., Devendra, C., 2008. Impact of globalization on livestock and poultry genetic resources in the world. Proc. Seventh Global Conference on Conservation of Domestic Animal Genetic Resources, National Institute of Animal Husbandry and Rare Breeds International, Hanoi, Vietnam.

Smith, C., 1977. The use of frozen semen and embryos to measure genetic trends in farm

livestock. Z. Tierzucht. Zuchtungsbiol. 94, 119-130.

Smith, C., 1984. Genetics aspects of conservation in farm livestock. Livest. Prod. Sci. 11, 37-48.

Taddeo, H.R., Allain, D., Mueller, J., Rochambeau, H., Manfredi, E., 1998. Genetic parameter estimates of production traits of Angora goats in Argentina. Small Rumin. Res. 28, 217-223.

Wright, S., 1931. Evolution in Mendelian populations. Genetics 16, 97-159.

Wright, S., 1939. Statistical genetics in relation to evolution. Exposes de Biometrie et de Statistique Biologique, Hermann and Cie, Paris, No. 802, 63pp.

Wright, S., 1945. The differential equation of the distribution of gene frequencies. Proc. Nat. Acad. Sci. 31, 382-389.