GENETIC IMPROVEMENT OF WEANING WEIGHT IN BARKI SHEEP USING NUCLEUS BREEDING SCHEME

El Sayed, Manal; Salwa I. El-Wakil[1]; A. M. Ahmed[1]; R. R. Sadek[2] and A. A. Nigm[2]

Department of Animal Production, Faculty of Agriculture, Ein Shams University, Cairo, Egypt,
1- Animal and Poultry Breeding Department, Desert Research Centre, El Matareya, Cairo, Egypt,
2- Department of Animal Production, Faculty of Agriculture, Cairo University, Giza, Egypt .

SUMMARY

The present study was undertaken to investigate the feasibility of establishing a genetic improvement program for meat production in Barki sheep as a result of selection for weaning weight. The present study utilized an original body weight data collected from the Barki sheep flock raised in the north-western coast of Egypt that belongs to the Desert Research Centre from 1963 to 2005. A total of 1046 animals (542 females and 504 males) progenies of 163 sires and 557 dams were included in the analyses.

The Monte Carlo simulation technique was utilized to construct a three-stratum nucleus breeding scheme consisting of a nucleus flock linked with five multiplier flocks which were consequently linked with commercial flocks of the producers. Such structure was replicated three times for higher accuracy. Moreover, mating was simulated for two successive seasons in the multiplier and commercial flocks and for three successive seasons in the nucleus flock. Two scenarios were simulated whereas the improvement occur without (scenario-1) and with (scenario-2) dissemination of sires from the nucleus flock.

Results indicated that weaning weight breeding values of sires, dams and offspring as well as average weaning weight in the nucleus flocks were generally exceeding those corresponding values in the multiplier and commercial flocks. Breeding values as well as average weaning weight tended to increase as season advanced and being higher in scenario-2 than in scenario-1. Producers of the multiplier and commercial flocks would accomplish higher breeding values as well as average weaning weight in the first season as soon as they shift from scenario-1 to scenario-2. The present study showed that it is technically feasible to implement nucleus breeding schemes in providing improved sires with higher weaning weight breeding values for the genetic improvement of meat production in Barki sheep.

Keywords: nucleus breeding scheme, genetic improvement, simulation, Barki sheep.

INTRODUCTION

Main problems facing the development of Barki sheep dominating the north western coastal (NWC) belt of Egypt could be attributed to the absence of genetic improvement and feed shortage especially during the long dry summer season. Over many generations, selection of ram lambs has been done from within their relatively small flocks on a phenotypic basis which may contribute to low productivity. Kosgey (2004) suggested that nucleus breeding schemes are recommended to optimize the limited available resources. These breeding methods were pioneered in New Zeeland and Australia, but successfully adopted in many countries.

Increasing productivity of Barki sheep can be approached by an organized nucleus breeding scheme through which improved Barki studs can be produced and distributed to the producers 'flocks in order to disseminate the progress achieved in productivity into the producers' flocks throughout the NWC. Nucleus breeding scheme refers to hierarchical structuring of a breeding population composed of a three-tier system embodying nucleus, a multiplier group and the commercial flocks (Hight and Rae, 1970; James, 1984; Turner and Parker, 1985; Galal *et al.*, 2000). Improved sires that have the highest breeding value for the selected traits would be identified to assist in making effective selection decisions (Rae, 1958; Clarke and Rae, 1977). In turn, that would

help increasing productivity and satisfy the increasing demand of animal protein for the coming generations.

Establishing genetic improvement program while it is costly and time consuming, requires lots of information, huge set of data and estimation of many parameters as well as sustainable management procedures for so many years. Although the records available at the Desert Research Centre for body weights in Barki sheep extend for more than 40 years, they did not satisfy the requirements of establishing a nucleus breeding scheme. Thus, the simulation techniques have been recalled in order to create a larger set of data taking into consideration the features of the original data collected on Barki sheep flocks raised under the harsh conditions prevailing in the NWC. The simulation technique would allow investigating the feasibility of various alternatives in order to achieve higher genetic gain. That would also help to furnish a master plan for a breeding structure adequate for improving Barki sheep to be available to the decision maker before its wide-spread implementation. Thus, the present study aimed to construct a nucleus breeding scheme and investigate the impact of disseminating improved sires from the nucleus through multiplier flocks to the commercial flocks of the producers on enhancing genetic gain in Barki sheep.

Earlier results obtained from same original data set indicated that selection based on weaning weight might be more effective, compared with birth and yearling weights, for its higher heritability and higher positive correlated response with yearling body weights (El-Wakil *et al.*, 2009). Hence, weaning weight would be the breeding goal for the constructed nucleus breeding scheme in the present study.

MATERIALS AND METHODS

1. Source of Data

The original body weight data used in the present study were collected from the Barki sheep flock raised at Ras ElHekma (RHRS), from 1963 to 1972, and Maryout Research Stations (MRS), from 1973 to 2005. Both RHRS and MRS are belong to the Desert Research Centre and located at the north-

western coast of Egypt; RHRS 250 kilometers west of Alexandria while MRS 35 kilometers west of Alexandria. In 1972, the sheep flock at RHRS moved to MRS. Flock management was almost the same in RHRS and MRS (El-Wakil *et al.*, 2009). Body weight was recorded at biweekly intervals starting from birth till weaning and at monthly intervals afterwards until the animal was removed from the flock. Adjustments for individual body weights to different exact ages in the original data were carried out by interpolation between the data of two successive ages; growth during the short intervals was assumed to be linear.

The simulated sets of data were generated from the original data obtained from the Barki sheep flock with a total number of 1046 animals (542 females and 504 males) progenies of 163 sires and 557 dams. Attempts were made to simulate the theoretical scheme as closely as possible to the real situation in the field. The present study tried to simulate the actual production system prevailing in the NWC to allow for lambing once a year in October when the new born ram lambs would be available for mating at the age of 16 months.

Results obtained from the original data indicated that selection based on weaning weight might be more effective (El-Wakil *et al.*, 2009). Thus, weaning weight would be the breeding objective of the constructed nucleus breeding scheme in the present study. For the simulated weaning weight data, the present study assumed parametric values shown in table (1).

Table 1. Assumed parametric values of phenotypic, genetic, residual variances and heritability for the simulated data.

Parameter	Estimates
Phenotypic variance (σ_p^2)	19.01
Additive genetic variance (σ_a^2)	7.75
Residual variance (σ_e^2)	11.26
Heritability	0.41

2. Simulation procedure

In order to construct the nucleus breeding scheme, Monte Carlo simulation technique using SAS (2004) with assumed mean (0) and

variance (1) was used to simulate about 140 sets of data to represent the producers flocks, each of them is composed of 3000 ewe lambs with their dams (3000 ewes) and sires (n=100) in addition to their weaning weight and year of birth. According to Analla *et al*. (1995), the expected genetic value of the progeny g_i is assumed to be equal to the average genetic values of the parents [sire (g_s) and dam (g_d)] plus a deviation due to the Mendelian sampling as follows:

$$g_i = 0.5\,(g_s + g_d) + X\sqrt{(0.5\,h^2\,\sigma^2_p)}$$

where:

g_i is equal to the genetic value of an individual i, (g_s) and (g_d) are the genetic values of the parents (sire and dam, respectively),

X is a random number taken from normal distribution with mean 0 and variance 1,

h^2 is the heritability, and

σ^2_p is the phenotypic variance.

The genetic values for the first simulated population (producers' population) were taken randomly from a normal distribution with mean zero and variance $\sigma^2_g = h^2\,\sigma^2_p$ where σ^2_g is the genetic variance and σ^2_p is the phenotypic one. These producer populations were further analyzed using multiple trait animal model (MTDFREML) proposed by Boldman *et al.* (1993) for the fixed (year of birth, 10 levels) and random effects (animal, sire and dam) in order to estimate the heritabilities of weaning weight as well as breeding values for sires, dams and their offspring. The estimation of breeding values based on animal models would allow for optimal use of the information available on nucleus and multiplier flocks (de Vries and Sorensen, 1990). Out of these 140 producers flocks, fifteen of them were assigned as commercial flocks of the producers to be linked with each multiplier flock in the proposed nucleus breeding scheme. The other chosen producers flocks would be used to form the nucleus and multipliers flocks required for the breeding scheme. To simplify the interpretation of including numerous producer flocks in the nucleus breeding scheme, each commercial population was assumed to act as a cooperative comprising a group of breeding producers and would be responsible for distributing the improved sires among the cooperator producers' flocks.

Improved animals produced from the nucleus would be propagated by multiplier flocks and hence would be disseminated to the rest of the non-organized commercial flocks of the producers. Therefore, the multiplier flock for progressive sheep producers is usually regarded to be better than average commercial flocks of the producers. Accordingly, ewes of some chosen producer populations were screened according to their average weaning weights and the top 30% of them were collected and considered as a multiplier flock. Consequently, nine hundred heavier weaning weight ewes were taken from each producer population to form each multiplier flock. Each set of multiplier flock data was analyzed using MTDFREML proposed by Boldman *et al.* (1993) to estimate the breeding values of their sires, dams and offspring. Hence, fifteen sets of data were chosen according to the best estimates of heritability and allocated as multiplier flocks in the present study. As far as sires are concerned, they are screened in some chosen producer populations according to their breeding values, the top thirty percent of them were chosen to be used in each multiplier flock. So, each multiplier flock consists of 900 ewe lambs and 30 sires (Fig. 1).

The initiation of the nucleus flock is usually made through buying distinguished ewes and rams chosen on a phenotypic basis from numerous producers flocks along a vast area of the concerned region. For the optimal efficiency, Rae (1974), James (1977) and Garrick *et al*. (2000) reported that about the top 2% to 10% of the total ewes in the base population should be selected into the nucleus, however, this optimum is not very sharp. Therefore, to form the nucleus flocks in the present study, the top 5% of ewe lambs from some producers populations were screened and chosen according to their average weaning weights, each set composed of 150 ewe lambs. Ten sets of 150 ewe lambs having the best estimates of heritability were chosen to be part of the nucleus flock. Consequently, 1500

heavier weaning weight ewe lambs were collected from ten producer populations to form each nucleus flock. This nucleus flock of 1500 ewe lambs was further analyzed using MTDFREML proposed by Boldman *et al.* (1993) to estimate the heritabilities of weaning weight as well as breeding values for sires, dams and their offspring. Similarly, sires of some producer populations were screened according to their breeding values; the top 5% of these sires were taken from each of ten producers' populations, to account for 50 sires. Hence, each nucleus flock was composed of the best 1500 ewe lambs and 50 sires according to their breeding values.

A three-stratum nucleus breeding scheme was suggested and simulated to contain a nucleus, a group of elite-animals; multipliers, progressive producer flocks and the remaining Barki sheep raisers, the commercial flocks of the producers. The present study constructed a nucleus breeding scheme consisting of a nucleus flock attached with five multiplier flocks and each multiplier flock consequently linked to one commercial flock of the producers. To increase the accuracy of the obtained simulated data, such constructed breeding scheme has been replicated three times.

Based on breeding values, selection in the present study is practiced mainly in sires while selection of females was done in order to maintain the fixed number of nucleus, multiplier and commercial flocks. Mating was simulated at a ratio of 30 ewes per ram for two successive seasons in the multiplier and commercial flocks and for three successive seasons for the nucleus flock. However, to increase the accuracy of estimating the breeding value particularly in the nucleus flock, the distribution of improved sires started after the second season; the first season data would result in less accurate breeding values since they are often lacking any pedigree records from those bought animals. On the other hand, lambs produced from these mating seasons in the nucleus, multiplier and commercial flocks were simulated as males or females by assigning a random number with a sex ratio of 1:1. Within each weaning weight, heavier animals were supposed to be males while lighter ones were assumed as females. On the other hand, a random mortality rate of 5% was suggested in both male and female progenies. Those assumed dead animals were supposed to have the least body weights among the offspring produced since they would be of poor performance and are most likely to die in the normal conditions. Thus, 5% of the least weaning weight progenies produced in each lambing seasons in the nucleus, multiplier and commercial flocks were discarded as dead animals.

Two scenarios of simulation were used to generate data and achieve improvement in weaning weights throughout the nucleus breeding scheme. The proposed scenarios dealt with the improvement occurring without (scenario-1) and with (scenario-2) dissemination of sires from the nucleus. The Monte Carlo simulation technique of SAS (2004) was conducted in both scenarios. The numbers of records utilized in the simulated population in both scenarios were 50, 30 and 100 for sires and 1500, 900 and 3000 for ewes in the nucleus, multiplier and commercial flocks, respectively (Fig. 1).

1. First scenario (scenario-1), without dissemination of sires from the nucleus flock.

In this scenario, the improvement of each nucleus, multiplier and commercial flock occurred as a result of selecting rams and ewes and promoting them from within flock according to their breeding values (Fig. 2). Selection is practiced mainly in rams while little selection of dams was performed just to maintain the fixed number of nucleus (n=1500), multiplier (n=900) and commercial flocks (n=3000). In the first mating season, the available sires of the nucleus (n=50), multiplier (n=30) and commercial flocks (n=100) were mated with the available dams in these flocks using the Monte Carlo simulation technique of SAS (2004) to obtain the breeding values of sires, dams and offspring as well as average weaning weights for the progenies produced in the first season.

To prepare for the second mating season, a mortality rate of 5% was assumed for the offspring produced in the nucleus, multiplier and commercial flocks. The remaining offspring were divided into males and females at a 1:1 ratio. Female progenies of the first season together with those dams from the previous season were screened according to their breeding values. The top females in the nucleus (n=1500), multiplier (n=900) and commercial flocks (n=3000) were selected and prepared to be introduced in the second mating season. Similarly, male progenies of the first season together with their sires from the previous season were screened according to their breeding values. The top sires in the nucleus (n=50), multiplier (n=30) and commercial flocks (n=100) were selected and prepared to be introduced in the second mating season (table 2). The Monte Carlo simulation technique of SAS (2004) was performed to obtain the breeding values of sires, dams and offspring as well as average weaning weights for the progenies produced in the second season in the nucleus, multiplier and commercial flocks.

Table 2. Number of records in the simulated population in both scenarios investigated.

Flock	No. of sires/flock	No. of records/flock
Nucleus flock	50	1500
Multiplier flock	30	900
Commercial flock	100	3000
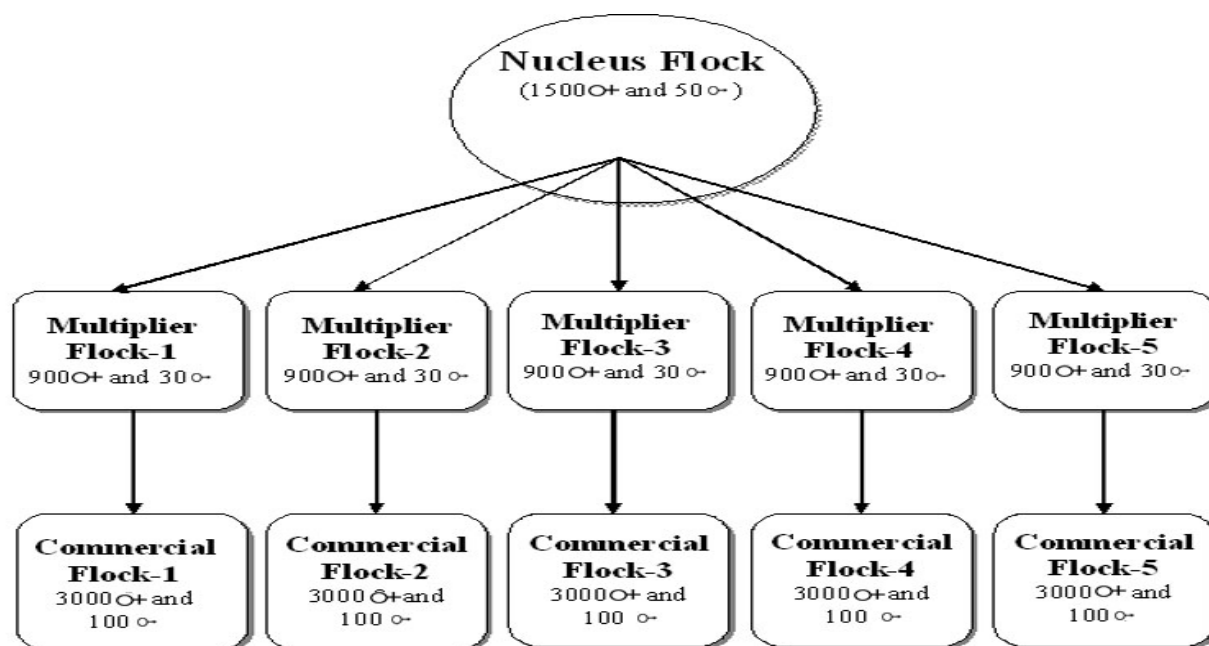
Fig. 1. The simulated nucleus breeding scheme
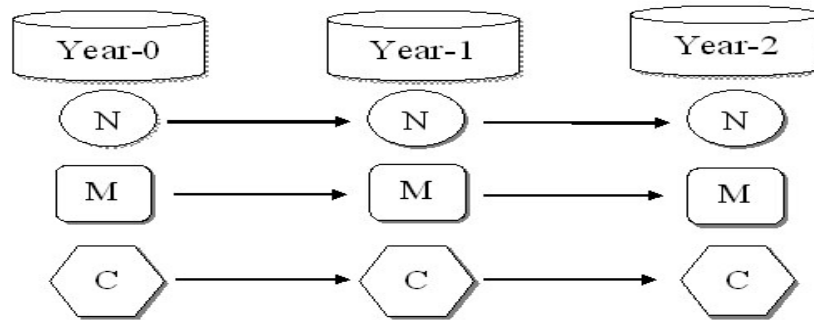
N = nucleus flock, M = multiplier flock, C = commercial flock
Fig. 2. The promotion of improved sires in scenario-1

2. Second scenario (scenario-2), with dissemination of rams from the nucleus flock.

In this scenario, the improvement of multiplier and commercial flocks occurred as a result of introducing superior sires brought in the nucleus flock to the multiplier flocks. Similarly, disseminating superior sires brought in multiplier flocks to commercial flocks (Fig. 3). Mating seasons were conducted and simulated using the Monte Carlo simulation technique of SAS (2004) to obtain the breeding values of sires, dams and offspring as well as average weaning weights for the progenies produced in the studied flocks. In this scenario, the dissemination of improved sires took place from the progenies of the second and third seasons from the nucleus to the multiplier flocks as well as from the multiplier to commercial flocks. It is obvious that there is a time lag of two years from the initiation of disseminating those improved rams brought in the nucleus flocks to show their effects in the multiplier flocks. Similarly, two years lag would occur to reveal the effect of distributing the improved rams from the multiplier flocks to the commercial flocks of the producers.

Male progenies produced from each mating season in the nucleus flock together with their sires from the previous season were screened according to their breeding values. The best 50 sires were retained to be introduced in the following mating season in the nucleus flock, while the next best 50 sires were kept to be disseminated and introduced to the following mating seasons of those five multiplier flocks attached to this nucleus flock, i.e., ten sires will be distributed to each multiplier flock. Consequently, thirty percent of sires available in the multiplier flocks would be replaced each year by improved sires brought from the nucleus flocks. The Monte Carlo simulation technique of SAS (2004) was conducted to obtain the breeding values of sires, dams and offspring as well as average weaning weights for the progenies produced in the nucleus flock.

In the multiplier flock, the ten improved sires received from the nucleus together with those thirty sires available from the previous mating season in addition to the remaining male progenies were screened according to their breeding values. The best 30 sires were introduced in the following mating season in the multiplier flock while the next best 30 sires were distributed to be used in the following mating season in that commercial flock linked to each multiplier flock.

In the commercial flock, those thirty improved sires received from the multiplier flock in addition to the hundred sires available from the previous mating season in the commercial flock together with those remaining male progenies were screened according to their breeding values. The best hundred sires were taken to be introduced in the following mating season of the commercial flock. Thus, thirty percent of sires in the commercial flock have been replaced by improved sires brought from the multiplier flocks.
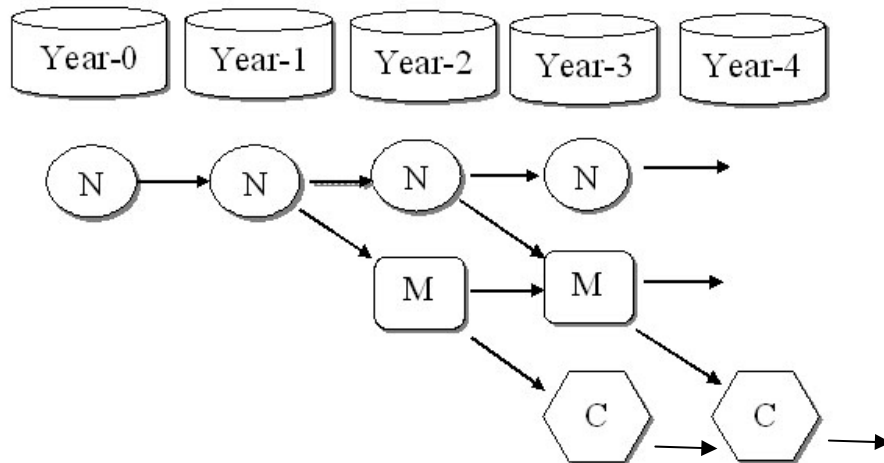
Fig. 3. The dissemination of improved sires in scenario-2

RESULTS AND DISCUSSION

Table (3) presented the overall average weaning weight and its breeding values for sires, dams and offspring in nucleus (3 flocks), multiplier (15 flocks) and commercial flocks (15 flocks) studied in both scenarios in the proposed nucleus breeding scheme. The tabulated results appear to be consistent; a finding which provides confidence in the simulated data obtained. Since the original field data depends on mating once a year, the theoretical genetic responses for weaning weight were estimated on an annual basis for two lambing seasons. The genetic gain achieved was determined as the change in breeding values between two successive seasons since the success of a breeding program can be measured by actual change in breeding value for a selected trait (Hill, 1971; Jurado *et al*., 1994).

Results indicated that weaning weight breeding values of sires, dams and offspring as well as average weaning weight in the nucleus flocks are consistently higher than the corresponding values of the multiplier and commercial flocks.

In nucleus flocks, results showed that second season attained higher increase in weaning weight breeding values compared with that achieved in the first one for sires (10.11 vs 4.80 kg), dams (1.53 vs 0.02 kg) and offspring (5.71 vs 2.48 kg) as well as average weaning weight (22.02 vs 18.79 kg). In the same context, extending the breeding scheme into the third

season appeared to attain higher increases in the weaning weight breeding values for sires (13.30 vs 4.8 kg), dams (3.94 vs 0.02 kg), offspring (8.52 vs 2.48 kg) and average weaning weight (24.83 vs 18.79 kg) compared with that achieved in the first season (Table 3).

Implementing scenario-1 in multiplier flocks showed that second season accomplished more increase over the first one in genetic progress of in terms of an overall average weaning weight breeding values for sires (9.8 vs 2.86 kg), dams (1.25 vs 0.04 kg), offspring (5.52 vs 1.48 kg) and average weaning weight (21.83 vs 17.79 kg) as seen in table (3). Producers of the multiplier flocks would achieve higher overall weaning weight breeding values for their sires (4.64 vs 2.86 kg), offspring (2.42 vs 1.48 kg) and average weaning weight (18.75 vs 17.79 kg) in the first season as soon as they shift to scenario-2 compared with that achieved when they practice scenario-1 as overall averages. Implementing scenario-2 in these multiplier flocks would help producers to obtain improved sires with higher breeding values brought in the nucleus flocks which would result in enhancing the genetic gain of weaning weight in their flocks. In scenario-2, substantial genetic gain is achieved at the second season over the first season of scenario-1, as a base, in those multiplier flocks attached to nucleus ones concerning the overall averages of weaning weight breeding values for sires (12.40 vs 2.86 kg), dams (1.62 vs 0.04 kg), offspring (7.09 vs 1.48 kg) and average weaning weight (23.40 vs 17.79 kg) as seen in table (3).

GENETIC IMPROVEMENT OF WEANING WEIGHT IN BARKI SHEEP USING NUCLEUS BREEDING SCHEME

As far as the commercial flock is concerned, results of scenario-1 showed an increase at the second season over the first one for an overall average weaning weight breeding values of sires and dams of 9.46 kg and 1.41 kg, respectively as well as an increase in the genetic gain for the offspring (5.42 vs 0.06 kg) and average weaning weight (21.73 vs 16.31 kg). Producers of these commercial flocks would attain no or little increase in weaning weight breeding values for their sires, dams and offspring as well as average weaning weights in the first season as soon as they shift to scenario-2 compared with that accomplished when they practice scenario-1. However, implementing scenario-2 in these commercial flocks would allow producers to obtain considerable increase in genetic gain in the second season over the first season of scenario-1 in terms of overall average weaning weight breeding values for sires (12.45 vs 0.00 kg), dams (2.02 vs 0.00 kg), offspring (7.22 vs 0.06 kg) and average weaning weight (23.52 vs 16.31 kg).

Table 3. The overall average weaning weight (Av. WW) and its breeding values (BV) for sires, dams and offspring in the nucleus, multiplier and commercial flocks involved in the proposed nucleus breeding scheme in both scenarios and seasons.

		First Season	Second season	Third season
Nucleus flocks	**Sire BV**	4.80	10.11	13.30
	Dam BV	0.02	1.53	3.94
	Offspring BV	2.48	5.71	8.518
	Av. WW	18.79	22.02	24.83

		Scenario-1		Scenario-2	
		First season	Second season	First season	Second season
Multiplier Flocks	**Sire BV**	2.86	9.80	4.64	12.40
	Dam BV	0.04	1.25	0.04	1.62
	Offspring BV	1.48	5.52	2.42	7.09
	Av. WW	17.79	21.83	18.75	23.40
Commercial flocks	**Sire BV**	00.0	9.46	3.48	12.45
	Dam BV	00.0	1.41	00.00	2.02
	Offspring BV	0.06	5.42	1.78	7.22
	Av. WW	16.31	21.73	18.09	23.52

* Without (scenario-1) and with (scenario-2) dissemination of sires from the nucleus flock.

It is worthwhile mentioning that both scenarios are running together in parallel at the same time. Both scenarios appeared to be efficient in achieving more genetic progress and producing animals with heavier weaning weight and higher breeding values. However, scenario-2 accomplished substantial genetic gains in terms of weaning weight breeding values of sires, dams and offspring as well as average weaning weight compared with that attained through practicing scenario-1 in the same period of time (Table 3). In the long run, adopting scenario-2 would have more advantage by reducing the rate of inbreeding in these flocks.

Although the present study was based on applying the approach of simulation, the results obtained would probably deviate to some extent from what would be expected when implemented in the field. While selection is usually based upon the breeding value or other objective measurements, selection decision in the field may in some cases be affected by other criteria that depend on subjective visual appraisal (e.g. conformation, coat color, health hazards …etc.). On the other hand, the achieved genetic gain depends, among other factors, on selection intensity. The present study has adopted a high proportion of selected animals of 30% in all three levels, since large numbers of improved sires were available, which resulted in enhancing genetic progress. That would minimize the deleterious effects of inbreeding in these flocks, since all available sires would be entirely replaced in three years time. However, in the field, animals brought in the nucleus flock are usually subjected to intensive selection as well as good husbandry compared with those animals of the commercial flocks which had no selection while some degree of selection were practiced in the multiplier flocks. Owners of commercial flocks usually run rams with ewes all year round and could afford neither the effort nor the expense of carrying out pedigree and performance recording required for selection. Genetic improvement under such conditions would not be expected, even with whatever subjective selection that may be practiced. As a result of applying selection with the same intensity at all three levels (nucleus, multiplier and commercial flocks) in the present study, the genetic improvement attained in the commercial flocks was found to be equal or slightly higher in some cases than that achieved in the multiplier flocks (Table 3), which would not be expected to happen in practice. That probably being a clear message to the producers of commercial flocks who would be greatly benefited as soon as they practice selection in their flocks and using genetically improved sires produced in the nucleus and disseminated to the commercial flocks directly, or after being multiplied in the multiplier flocks. Therefore, the use of nucleus breeding schemes is justified for providing genetically improved sires which are lacking at present and desperately needed for the genetic improvement of the indigenous Barki sheep. Moreover, plugging small flocks into the sheep improvement program, would ensure that little insignificant flocks would be plugged into an enormous genetic pool which would allow superior genes to be identified and properly managed to provide more profitable sheep enterprise at a reasonable cost.

CONCLUSION

Since the nucleus can be "closed" (no gene flow into nucleus) or "open" in which case there is gene flow into the nucleus from tiers of lower hierarchy (Roden, 1994), the proposed nucleus breeding scheme could attain higher genetic progress through implementing an open nucleus scheme. That would benefit from promoting animals with high genetic merit produced at the commercial or multiplier levels to the higher tiers, thus enhancing the efficiency of the whole nucleus breeding scheme. The present study indicates the feasibility of implementing nucleus breeding schemes to attain a remarkable genetic improvement of weaning weight in Barki sheep which would lead to improve the genetic potentiality of this breed for meat production.

ACKNOWLEDGEMENT

REFERENCES

Analla, M.; Sanchez, A.; Munaz, A. and Serradilla, J. M. (1995). Simulation analysis with BLUP methodology of different data structure in goat selection schemes in Spain. Small Ruminant Research, 17:51.

Boldman, K. G.; Kriese, L. A.; Van Vleck, L. D. and Kachman, S. D. (1993). A manual for use of MTDFREML a set of programs to obtain estimates of variance and covariance. (Draft). U. S. Department of Agriculture, Agricultural Research Service, 120 pp.

Clarke, J. N. and A. L. Rae (1977). Technical aspects of the national sheep recording scheme

(SHEEPLAN). Proceedings of the New Zealand Society of Animal Production, 37: 183-197.

de Vries, A. G. and D. A. Sorensen (1990). Optimization of present pig breeding programmes. Proceedings of the 4th World Congress on Genetics applied to Livestock Production, Edinburgh 23-27 July, 1990, p.395-404.

El-Wakil, Salwa I. (2009). A simulation study on using nucleus flock for genetic improvement of some production traits in Barki sheep. PhD. thesis, Faculty of Agriculture, Cairo University, Giza, Egypt.

El-Wakil, Salwa I.; ElSayed, Manal; Ahmed, A. M. and Sadek, R. R. and Nigm, A. A. (2009). Genetic and phenotypic parameters of birth, weaning and yearling body weights of Barki sheep raised in the north-western coast of Egypt. Egyptian Journal of Animal Production, 46(1): 43-52.

Galal, S.; J. Boyazoglu and K. Hammond (editors) (2000). Developing breeding strategies for lower input animal production environments. ICAR Technical Series: Cesare Mosconi ISSN: 1563-2504, Publisher: ICAR, Villa del Ragno, Via Nomentana 134, 00162 Rome, Italy, January 2000

Garrick, D. J.; H. T. Blair and J. N. Clarke (2000). Sheep industry structure and genetic improvement. Proceedings of the New Zealand Society of Animal Production, 60: 175-179.

Hight, G.K. and A. L. Rae (1970). Large-scale sheep breeding: its development and possibilities. Sheep farming Annual, 1970, p.73-85.

Hill, W. G. (1971). Investment appraisal for national breeding programmes. Anim. Prod., 13:37-50.

Kosgey, I. S. (2004). Breeding objectives and breeding strategies for small ruminant in the tropics. Ph.D. thesis, Animal Genetics and Breeding Group, Wageningen University. ISBN:90-5808-990-8.

James, J. W. (1984). Mating systems and industry structure in improvement programs. Proceedings of 4th Conference of Austr. Assoc. Anim. Breed. Genetics, 1984: 238-242.

James, J.W. (1977). Open nucleus breeding systems. Anim. Prod., 24: 287-305.

Jurado, J. J.; A. Alonso and R. Alenda (1994). Selection response for growth in a Spanish Merino flock. J. Anim. Sci., 72: 1433-1440.

Rae, A. L. (1958). Genetic variation and covariation in productive characters of New Zealand Romney March sheep. New Zealand J. Agric. Res., 1:104- 123.

Rae, A. L. (1974). The development of group breeding schemes: some theoretical aspects. Sheep farming Annual, p.121-127.

Roden, J. A. (1994). Review of the theory of open nucleus breeding systems. Animal Breeding Abstracts, 62: 151-157.

SAS. (2004). Statistical Analysis System. SAS User's Guide: Statistics. SAS Institute Inc. Editors, Cary, NC.

Turner, R. W. and A. G. H. Parker (1985). New Zealand Group Breeding Schemes. Proceedings 2nd world congress on Sheep and Beef Cattle breeding, Pretoria, South Africa, p. 214-221.

الملخــــص العـــربى

التحسين الوراثي لوزن الفطام في أغنام البرقي بإستخدام نظام التحسين بالنواة

منال السيد، سلوى إبراهيم الوكيل[1]، على مصطفى أحمد[1]، ربيع صادق[2]، على عطية نجم[2]

قسم الإنتاج الحيوانى، كلية الزراعة، جامعة عين شمس، القاهرة، مصر

1- قسم تربية الحيوان والدواجن، مركز بحوث الصحراء، المطرية، القاهرة، مصر.

2- قسم الإنتاج الحيوانى، كلية الزراعة، جامعة القاهرة، الجيزة، مصر

أجريت هذه الدراسة للتعرف على إمكانية عمل برنامج للتحسين الوراثى لزيادة إنتاج اللحوم فى الأغنام البرقى نتيجة للإنتخاب لوزن الفطام. استخدمت بيانات أوزان الجسم التى تم تسجيلها من قطيع الأغنام البرقى المرباة فى الساحل الشمالى الغربى من مصر والتابع لمركز بحوث الصحراء منذ عام 1963 حتى عام 2005، وقد اشتملت البيانات على عدد 1046 حيوان مفرد (542 أنثى& 504 ذكر) وهم أبناء لعدد 163 أب و 557 أم.

استخدمت فى الدراسة طريقة مونت كارلو للمحاكاة فى عمل برنامج التحسين الوراثى بالنواة يتكون من ثلاثة طبقات، وقد اشتمل هذا البرنامج على قطيع النواة ويرتبط به خمسة قطعان للإكثار والتى ترتبط بدورها بخمسة قطعان تجارية للمنتجين بالمنطقة. كما تم عمل ثلاثة تكرارات لهذا البرنامج لزيادة الدقة فى البيانات المتحصل عليها من المحاكاة. كذلك تم عمل محاكاة لموسمين للتلقيح فى قطعان الإكثار وقطعان المنتجين التجارية بالإضافة إلى ثلاثة مواسم للتلقيح فى قطعان النواة. كما تم عمل محاكاة لسيناريوهين للتحسين الوراثى حيث يعتمد السيناريو الأول على تحسين قطعان النواة وقطعان

الإكثار وقطعان المنتجين التجارية من داخل هذه القطعان، بينما يعتمد السيناريو الثانى على توزيع كباش محسنة من قطيع النواة وإكثارها فى قطعان الإكثار لتوزيعها على القطعان التجارية للمنتجين بالمنطقة.

أوضحت النتائج تفوق القيم التربوية لوزن الفطام لكل من الكباش والنعاج والأبناء وكذلك متوسط وزن الفطام المتحصل عليها من قطيع النواة مقارنة بقطعان الإكثار والقطعان التجارية للمنتجين. كما حدثت زيادة فى القيم التربوية لوزن الفطام وكذلك متوسط وزن الفطام بتقدم المواسم وكذلك عند تطبيق السيناريو الثانى مقارنة بالسيناريو الأول. حقق كبار المربين فى قطعان الإكثار وقطعان المنتجين زيادة فى القيم التربوية وكذلك متوسط وزن الفطام فى الموسم الأول فور تحولهم من السيناريو الأول إلى السيناريو الثانى. خلصت الدراسة إلى أن تطبيق السيناريو الثانى للتحسين الوراثى بالنواة سوف يؤدى إلى توفير حيوانات محسنة ذات أوزان أثقل عند الفطام وبقيم تربوية عالية مما يجعلها قادرة على إحداث تحسين وراثى لزيادة إنتاج اللحوم فى الأغنام البرقى المحلية.