



Genetic gain in open nucleus breeding scheme to improve milk production in Egyptian buffalo

S.A. Abdel-Salam¹, A.I. Sayed¹, Manal Elsayed² & S. Abou-Bakr²

¹Department of Animal Production, Faculty of Agriculture, Cairo University, Gamaa Street, Giza, Egypt Egypt

²Department of Animal Production, Faculty of Agriculture, Ain Shams University, Shubra El-Khema, Cairo, Egypt

Abstract

Populations of buffaloes with one milk record for each buffalo were generated using Monte Carlo simulation with assumed mean (0) and variance (1). Four different population sizes (z): 10000, 25000, 50000 and 100000 animals were obtained. Four generations of progeny were obtained by selection of sires and dams of the next generations. Mating ratio (male: females) were designed to differ from 1:25 to 1:100 in natural mating (NM) and from 1:1000 to 1:5000 in artificial insemination (AI). Genetic gain per generation and annual genetic gain were calculated.

Genetic gain increased significantly ($P<0.05$) with increase in generation number (G) being 282, 389, 457 and 488 kg milk per generation for G_1 , G_2 , G_3 and G_4 , respectively. The annual genetic gain ranged from 64 kg/yr for $z=10000$ to 73 kg/yr for $z=100000$. Increasing nucleus size (p) from 0.05 to 0.10 increased genetic gain significantly ($P<0.05$) from 390 to 418 kg milk. Non-significant differences in genetic gain among different proportions of males born used as sires (a) were observed.

Annual genetic gain ranged from 50 to 66 kg milk/yr in NM and from 80 to 82 kg milk/yr in AI. Applying open nucleus breeding scheme (ONBS) for many generations of selection could accelerate the rate of genetic gain of milk production in Egyptian buffalo and increased the average milk yield from 15% in G_1 to 26% in G_4 .

Keywords: Open nucleus breeding scheme, genetic gain, simulation, Egyptian buffalo.

1.0 Introduction

According to FAOSTAT (2009) the Egyptian buffalo contributes about 2.7% and 8.4% to the world buffalo's milk and meat, respectively. The proportion of Egyptian buffaloes to the world buffalo's milk production decreases year after year. The increase of total milk production of Egyptian buffaloes was due only to increasing buffalo population size. Lack of effective sustainable breeding programs for local breeds in developing countries is a reason that such breeds lose their competitive advantage, especially where production systems or external conditions are subjected to change (Hiemstra *et al.*, 2007).

Livestock production in developing regions is generally characterized by small herd-size (particularly in mixed crop/livestock systems), communally shared grazing, uncontrolled mating, and the absence of pedigree and performance recording. These characteristics limit the implementation of effective genetic improvement programs. To overcome these problems, nucleus breeding schemes have been suggested, in which genetic improvement is centrally organized in a population maintained in research institutes or government farms (Galal, 1986; Terrill, 1986 and Solomon *et al.*, 2009). The open nucleus breeding scheme offers a simpler procedure for producing and disseminating breeding stock of known value (Cunningham, 1979 and 1987; Hanks, 1978 and Jasirowski, 1991). Bondoc and Smith (1993) recommended the establishment of two-tier open nucleus breeding system to maximize genetic improvement, reduce inbreeding rate and reduce the total cost of recording in smallholder system. Several studies indicated the significance of using open nucleus breeding scheme to improve milk production of buffalo and increase the rate of genetic gain (Dixit and Sadana, 1999, Abdel-Salam *et al.*, 2004 and Nigm *et al.*, 2005).

The purpose of this paper was to use the simulation technique to study the expected genetic gain by changing migration rates and male selection intensity in four generations of applying two-tier open

nucleus breeding scheme to improve milk production of Egyptian buffaloes using different nucleus and population sizes.

2.0 Material and methods

2.1 Basic parameters

Simulation technique was used to generate population of buffaloes with one milk record for each buffalo. A total number of 3526 lactation records of 2179 buffaloes recorded by Cattle Information Systems/Egypt (CISE, 2007) of the Faculty of Agriculture, Cairo University during the period from 1990 to 2006 were used to estimate various parameters (Table 1) which were used to generate simulated populations.

Table 1. The estimates used in generating the simulated populations.

Parameter	Estimate	Reference
Average total milk yield (TMY)	1884, kg	CISE, 2007
Phenotypic variance for TMY	191845, kg ²	CISE, 2007
Phenotypic standard deviation for TMY	438, kg	CISE, 2007
Average generation interval	5.78, yr	Mourad, 1990
Heritability estimate	0.17	CISE, 2007

CISE: Cattle Information Systems/Egypt

2.2 Generation of the simulated population of buffaloes

Populations were generated using stochastic Monte Carlo simulation procedure of SAS (2004) with assumed mean (0) and variance (1). Simulation was replicated four times to generate four different sizes of populations: 10000, 25000, 50000 and 100000 animals. Four generations were generated by selection of progenies with the highest breeding values for milk production to be sires and dams of the next generation. Selected bulls and heifers were mated at random. Figure (1) shows the structure of designed open nucleus breeding scheme and gene migration from nucleus to base and vice versa.

Genetic gain per generation was estimated as the average genetic selection differentials of animals used in nucleus and base (James, 1977). The rate of progress as response to selection is modified by migration of genes between parts of the population with different mean breeding values, i.e. from the nucleus to the base and vice versa. The best selected males are kept for breeding in the nucleus while other selected males are given to the base herds for breeding. The best selected females are maintained in the nucleus while females disseminated to the base herds are surplus to the nucleus replacement. By this means, improvements are quickly spread throughout the population. The nucleus remains open to animals from the base herds, the best selected females in the base transfer to the nucleus. Thus, the ultimate genetic gain was estimated by a weighted average of the genetic selection differentials in the nucleus and base, the weights being the gene migration rates from each part of the population to the other. Both additive genetic and residual effects were assumed to be distributed normally. This procedure was carried out for four generations. It was assumed that all buffalo females were mated naturally or artificially to bulls coming from the nucleus or base (Figure 1). Mating ratio (male: females) were 1:25, 1:50 and 1:100 in natural mating (NM), and 1:1000, 1:2500 and 1:5000 in artificial insemination (AI). The objective of using different mating ratios was to compare between different selection intensities in males.

The genotypes of animals were simulated by the following formula (1) according to (Meuwissen, 1991):

$$g_i = \frac{1}{2}g_s + \frac{1}{2}g_d + a_i \sqrt{0.5h^2\sigma_p^2} \quad (1)$$

Where g_i , g_s , and g_d are the additive genetic values of individual i , its sire (s) and its dam (d), respectively, h^2 is the heritability in population ($h^2 = 0.17$), σ_p^2 is the phenotypic variance, a_i is the

random number from the distribution $N(0,1)$ and $\sqrt{0.5h^2\sigma_p^2}$ is the Mendelian sampling term.

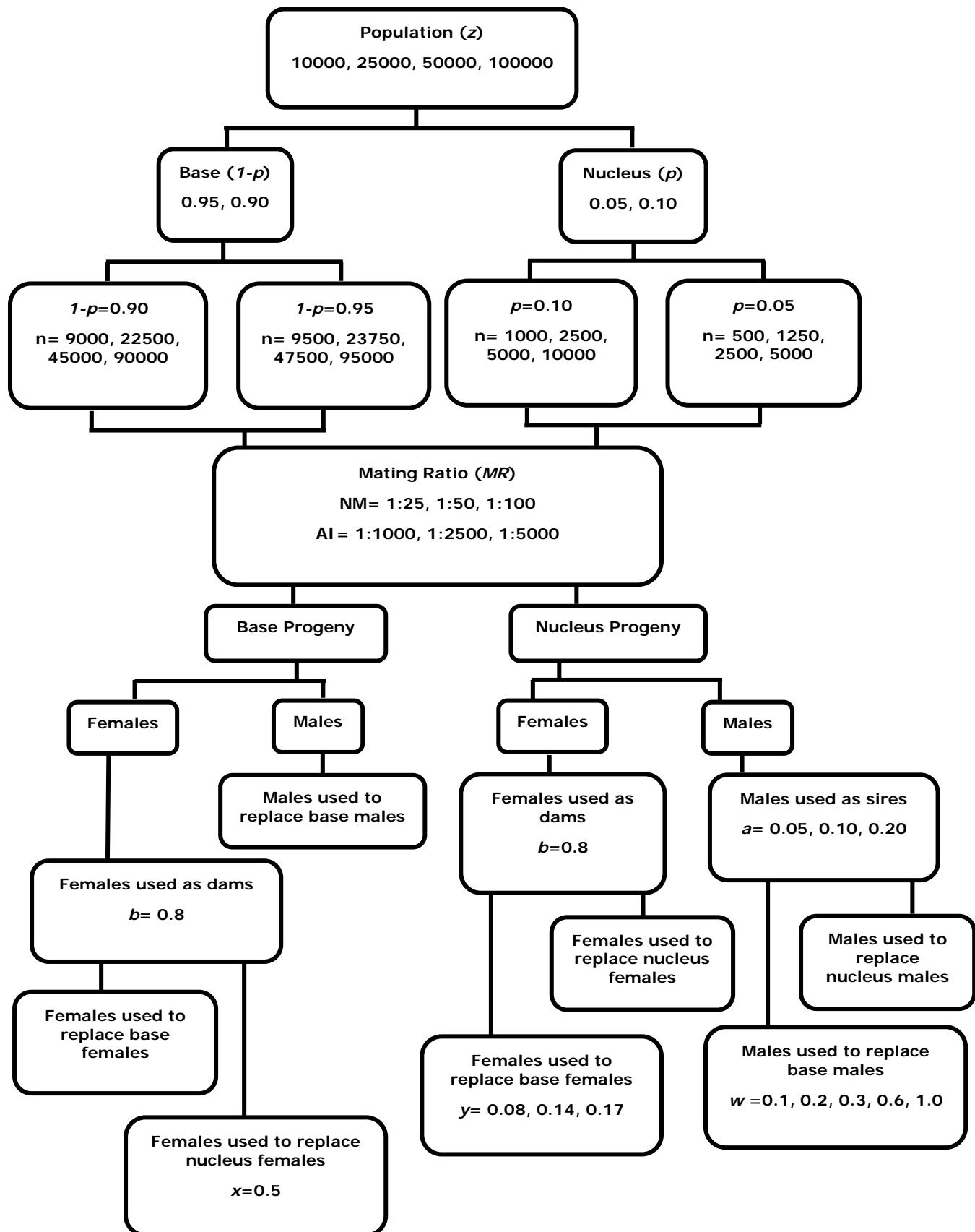


Figure 1. Structure of breeding scheme and gene migration.

The record of buffalo i was simulated by the following formula (2) according to (Meuwissen, 1991):

$$Y_i = \mu + g_i + E_i \quad (2)$$

Where Y_i is the lactation of the i^{th} buffalo, μ is the mean total milk yield, g_i is the additive genetic value of individual i , E_i is the environmental effect of the i^{th} buffalo and assumed to equal $\sigma_e a_i$, σ_e is the square root of the error variance and a_i is the random number from the distribution $N(0,1)$.

2.3 Estimation of breeding values

Breeding values were estimated using the Derivative – Free Restricted Maximum Likelihood (DF-REML) procedure (Meyer, 1998).

The linear animal model (3) used for analyzing simulated records was as follows:

$$Y = X\beta + Z_a a + e \quad (3)$$

Where Y is the vector of observations, X is the incidence matrix for assumed fixed effect required by software to run distributed to the data at random, β is vector of an overall mean and fixed effect (2 levels) distributed to the data at random, Z is the incidence matrix for random effects, a is the vector of direct genetic effects of buffalo and e is vector of random errors normally and independently distributed with zero mean and variance $I\sigma^2_e$.

2.4 Calculation of the expected genetic gain in milk yield

Seven schematic variables, namely, number of generations (G), population size (z), nucleus size (p), mating ratio (male: females) (MR), proportion of males born used as sires (a), fraction of base sires born in nucleus (w) and fraction of base dams born in nucleus (y) were studied.

The parameters assumed for estimating the genetic gain of the simulated open nucleus breeding scheme and levels of variables are shown in table 2. Genetic gain per generation and annual genetic gain were calculated according to James (1977).

Table 2. Input variables for calculating genetic gain.

Item Description	Symbol	Value
Heritability estimate	h^2	0.17
Replacement rate	r	0.20
Fraction of total population in nucleus	p	0.05, 0.10
Fraction of nucleus dams born in base	x	0.50
Fraction of base dams born in nucleus	y	0.08, 0.14, 0.17
Fraction of nucleus sires born in base	v	0.00
Fraction of base sires born in nucleus	w	0.10, 0.20, 0.30, 0.60, 1.00
Proportion of all males born used as sires	a	0.05, 0.10, 0.20
Proportion of all females born used as dams	b	0.80
Simulated population size (number of breedable females)	z	10000, 25000, 50000, 100000
Generations	G	1, 2, 3, 4

The effects of the different variables on genetic gain were analyzed according to the following model (4):

$$GG_{ijklmno} = \mu + G_i + z_j + p_k + a_l + MR_m + w_n + y_o + e_{ijklmno} \quad (4)$$

where GG is the genetic gain, μ is the average genetic gain, G_i is the number of generation (4 level), z_j is the population size (4 level), p_k is the fraction of total population in nucleus (2 levels), a_l is the proportion of all males born used as sires (3 levels), MR_m is the mating ratio (6 levels), w_n is the fraction of base sires born in nucleus (5 levels), y_o is the fraction of base dams born in nucleus (3 levels) and $e_{ijklmno}$ is the residual term.

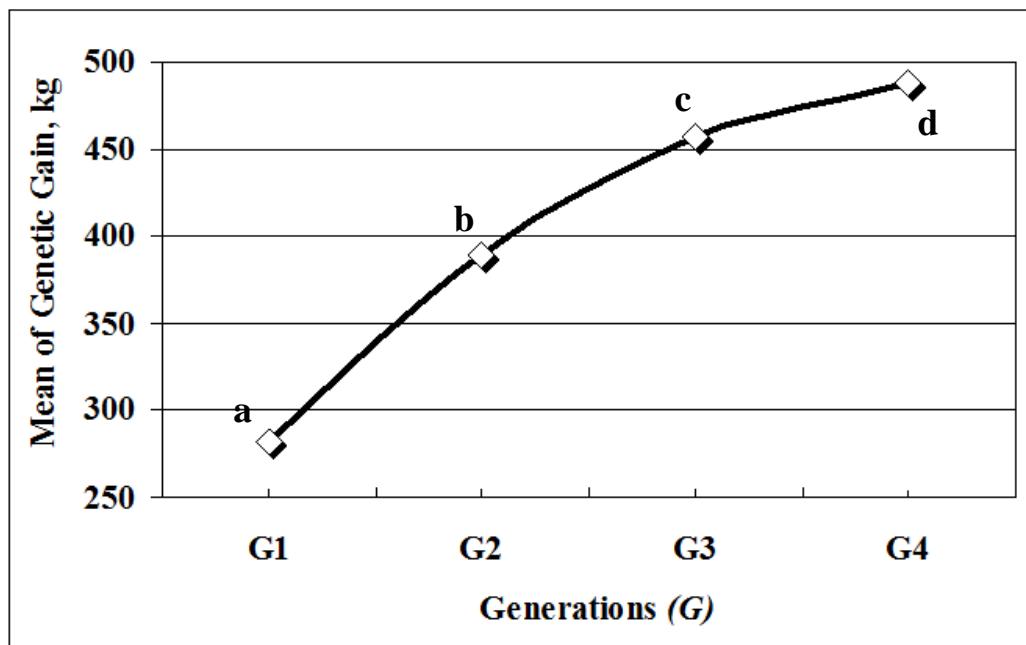
Significance of differences among means of genetic gain resulting from applying different input variables was tested using Duncan Test procedure (SAS, 2004).

3.0 Results and discussion

3.1 Number of generations (G)

Genetic gain increased significantly ($P<0.05$) by increasing generation number as shown in figure 2. The genetic gains by generation were 282, 389, 457 and 488 kg of milk for G1, G2, G3 and G4, respectively. The average annual genetic gain ranged from 48 kg for G1 to 83 kg for G4.

The rate of increase of genetic gains decreased by increasing the generation number (Figure 2). The highest rate of increasing genetic gain (38%) was observed between G1 and G2 and the lowest (7%) was observed between G3 and G4. The reason for decreasing rate of genetic gain by increasing the generation number was due to reducing genetic lag between nucleus and base, by advancing generation, which means that the genetic selection differential between nucleus and base decreased by increasing generation of selection.



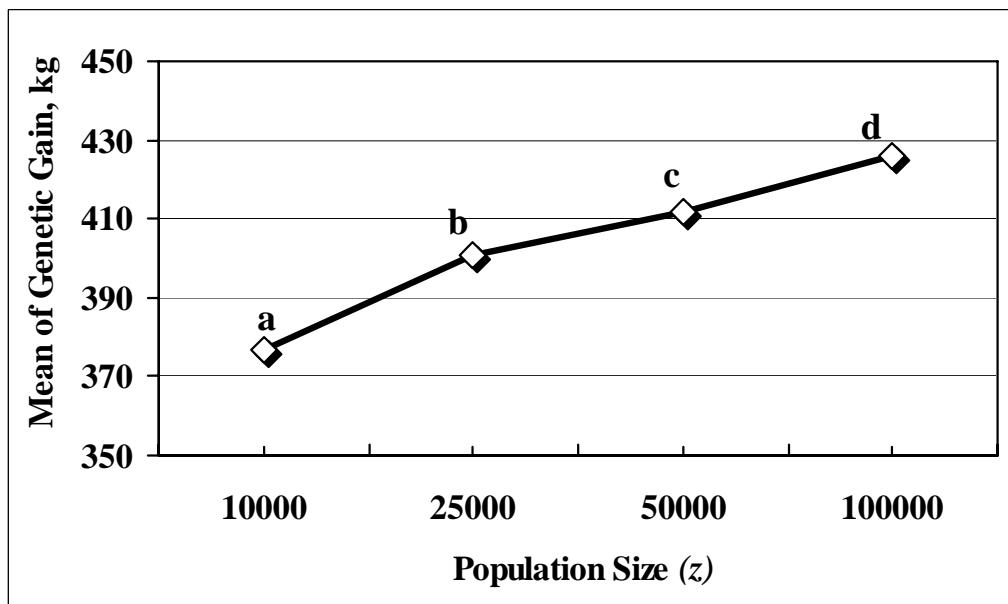
^{a,b,c,d}Means with different letters differ significantly ($P<0.05$).

Figure 2. Change of genetic gain means by generation number.

This result is in agreement with the findings of Mueller and James (1983). They reported that the cumulated gain after 10 generations of selection, in a likely sheep or cattle system, would be overestimated by about 20%. This may be important in economic evaluations of nucleus schemes.

3.2 Population size (z)

Genetic gain increased significantly ($P<0.05$) by increasing population size (z) (Figure 3) due to increasing migration rates in the large populations. Increasing z from 100 00 to 2 5000 resulted in an increase of 6% in genetic gain. The rate of increase in the genetic gain increased to 27% and 34% when the population size increased from 25000 to 50000 and from 50000 to 100000, respectively. There were significant differences ($P<0.05$) among all means. The average annual genetic gain ranged from 64 kg for $z=10000$ to 73 kg for $z=100000$. These results are comparable with the results observed by Abdel-Salam *et al.* (2004) and Nigm *et al.* (2005).



^{a,b,c,d}Means with different letters differ significantly ($P<0.05$).

Figure 3. Change of genetic gain means by changing population size (z).

The large population needs large numbers of animals in the nucleus and this situation is difficult in practical application. For avoiding this obstacle it is suggested that the required nucleus size is divided into more than one nucleus (sub-nucleus) working as big nucleus and that depends on the prevailing production systems and population structure.

3.3 Nucleus size (p)

Table 3 shows the change in genetic gain by changing the fraction of total population in nucleus from 0.05 to 0.10. Increasing p from 0.05 to 0.10 increased genetic gain significantly (4.5%, $P<0.05$) from 397 to 415 kg milk per generation.

Abdel-Salam *et al.* (2004), however, showed that increasing p from 0.05 to 0.10 resulted in a non-significant increase of only 0.3% in the genetic gain of milk yield in buffalo for one generation of selection.

The increase of genetic gain by increasing p was due to increasing migration (fraction of base dams born in nucleus, y , and fraction of base sires born in nucleus, w) rates from nucleus to base in large nucleus size and that led to acceleration genetic change by genetic improvement at both levels of nucleus and base.

Table 3. Least squares mean and standard errors (SE) of genetic gain of milk yield (kg) in simulated buffalo populations of different nucleus sizes (p).

P	Mean	SE
0.05	397 ^a	7
0.10	415 ^b	6

^{a,b}Means with different letters differ significantly ($P<0.05$).

Phillips (2001) reported that the most important decision in establishing a nucleus breeding operation is to determine its size. There are several tradeoffs. With increasing nucleus size, greater selection pressure can be applied to potential breeding stock resulting in more rapid genetic gains. However, increasing the nucleus size also increases the cost of maintaining it. If replacement females for the nucleus are selected

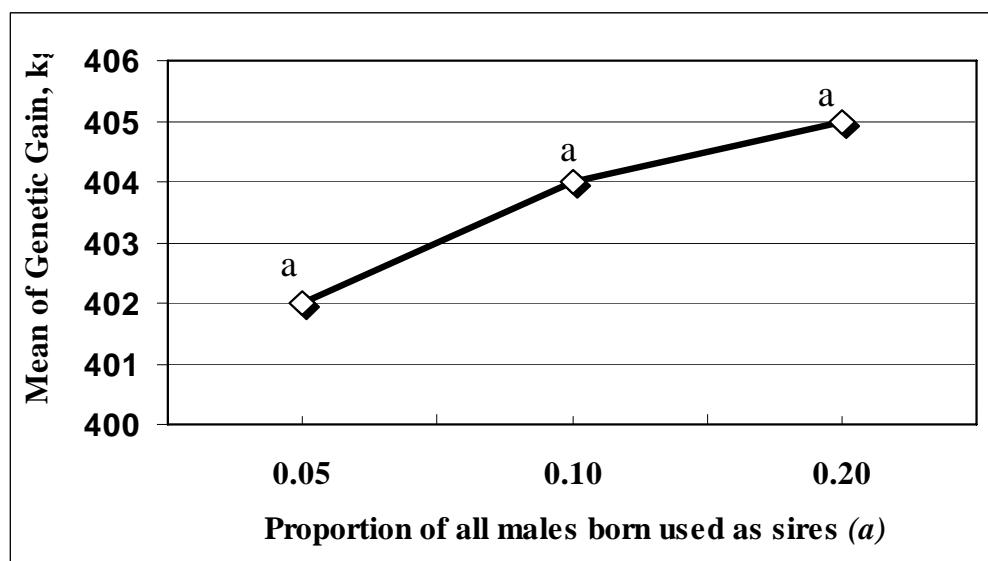
from the nucleus and the commercial herd, larger nucleus herds are less elite when compared to the commercial herd.

3.4 Proportion of all males born used as sires (a)

Figure (4) shows change of genetic gain by changing proportions of males born used as sires (a). Non-significant differences in genetic gain means among different proportions of all males born used as sires were observed. The expected annual genetic gain increased 1.5% by increasing a from 0.05 to 0.10. Further increase of annual genetic gain (1.5%) by increasing a from 0.10 to 0.20. The reason of increasing the genetic gain with increasing a is mainly due to increasing fraction of base sires born in nucleus (w) with increasing a . However, by increasing a all replacement sires in the base came from the nucleus (w). It was clear that, the genetic improvement of the designed ONBS in the present study depended mainly on migration rate of sires from nucleus to base.

This result is contrary to the result found by Abdel-Salam *et al.* (2004) applying open nucleus breeding scheme for one generation and using different nucleus size (0.01, 0.05 and 0.20), who reported a significant decrease in genetic gain with increasing proportion of selected males (a). Decreasing a from 0.20 to 0.10 resulted in an increase of 1.6% in genetic gain. The increase was enlarged to 3.3% when a decreased from 0.10 to 0.05.

Often the base is managed for commercial production and the nucleus to breed superior sires. Hopkins (1978) emphasized that using more efficient selection strategies and short generation lengths in the nucleus would increase rates of gain.



^aMeans with same letters do not differ significantly ($P>0.05$).

Figure 4. Change of genetic gain means by changing proportion of all males born used as sires (a).

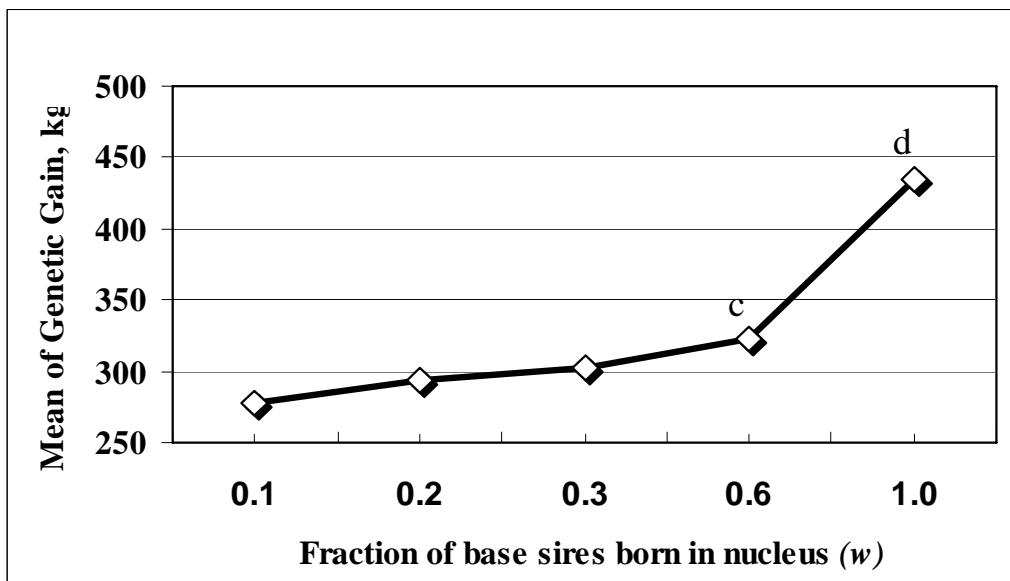
3.5 Fraction of base sires born in nucleus (w)

The genetic gain ranged from 278 to 435 kg of milk (Figure 5) and the annual genetic gain ranged from 49 to 74 kg of milk at different levels of w . Genetic gain increased non-significantly by increasing w from 0.1 to 0.20 and from 0.20 to 0.30. Differences between w levels were significant ($P<0.05$) when $w=0.60$ and all sires used in base ($w=1$) came from the sires born in nucleus.

The results of this study indicate that the main variables affecting the fraction of base sires born in nucleus were z , p and a . The direct relationship was observed between z , p and a on one hand and w on the other hand. However, this relationship is not absolute but depends on the different combinations of population size, nucleus size, and selection intensity in males.

The increase of w led to decreasing genetic lag between nucleus and base. For applying ONBS, it is recommended that all sires used in the base are introduced from sires born in nucleus.

This result is not in line with the result showed by Abdel-Salam *et al.* (2004) who observed that the genetic gain decreased significantly by increasing w from 0.05 to 0.10 or 0.20 and differences were significant between 0.05 on one hand and 0.10 and 0.20 on the other hand which was applying for one generation and different nucleus size. James (1977) reported that it is, however, of interest to note that the value of w depends on the nucleus size (p) as w increases with any increase in p . Also, w depends on the proportion of males born and used as sires (a).



^{a,b,c,d}Means with different letters differ significantly ($P<0.05$).

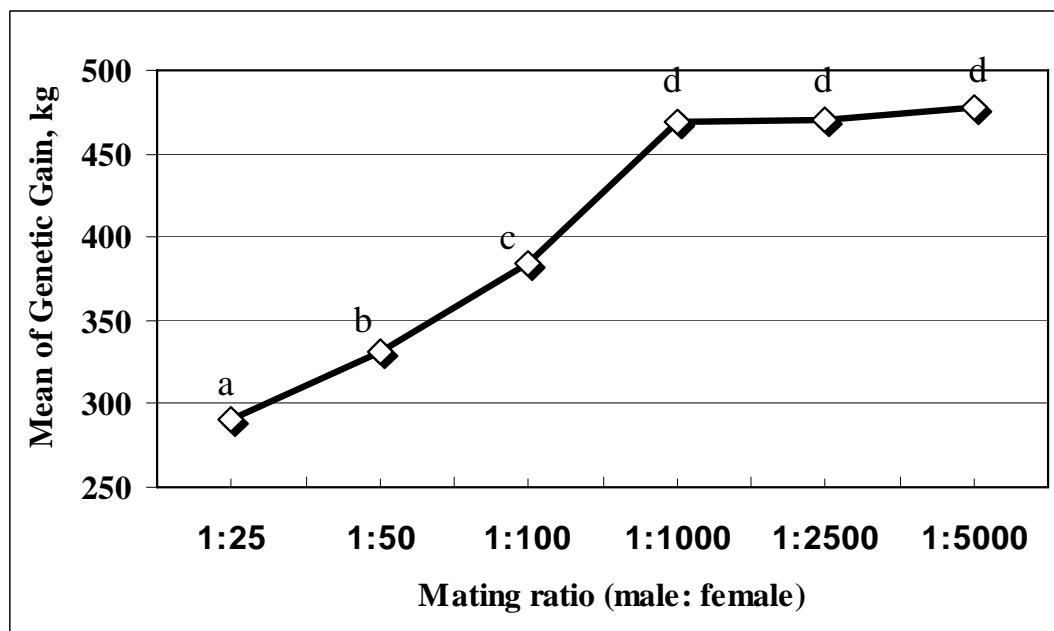
Figure 5. Change of genetic gain means by changing fraction of base sires born in nucleus (w).

3.6 Mating ratios, MR, (male: females)

Figure (6) shows the change of genetic gain with mating ratios in natural mating and artificial insemination. Significant differences ($P<0.05$) were observed between MR within natural mating (NM), and between MR in natural mating and artificial insemination (AI). No significant differences were shown between mating ratios within AI.

Using NM, 14% increase of genetic gain was observed by increasing MR from (1:25) to (1:50) and 16% by increasing MR from (1:50) to (1:100). Increasing MR from (1:100) to (1:1000) by using AI was accompanied with an increase in genetic gain of 22%. Further increase in genetic gain was shown (0.2%) with increasing MR from (1:1000) to (1:2500) and by 1.7% with increasing MR from (1:2500) to (1:5000).

It was concluded that increasing genetic gain by increasing MR is mainly due to increasing the selection intensity in males used as sires and that was clear when comparison between NM and AI. Using small number of males led to reduction in the proportions of males born used as sires (a) and increase the fraction of base sires born in nucleus (w).



^{a,b,c,d}Means with different letters differ significantly ($P<0.05$).

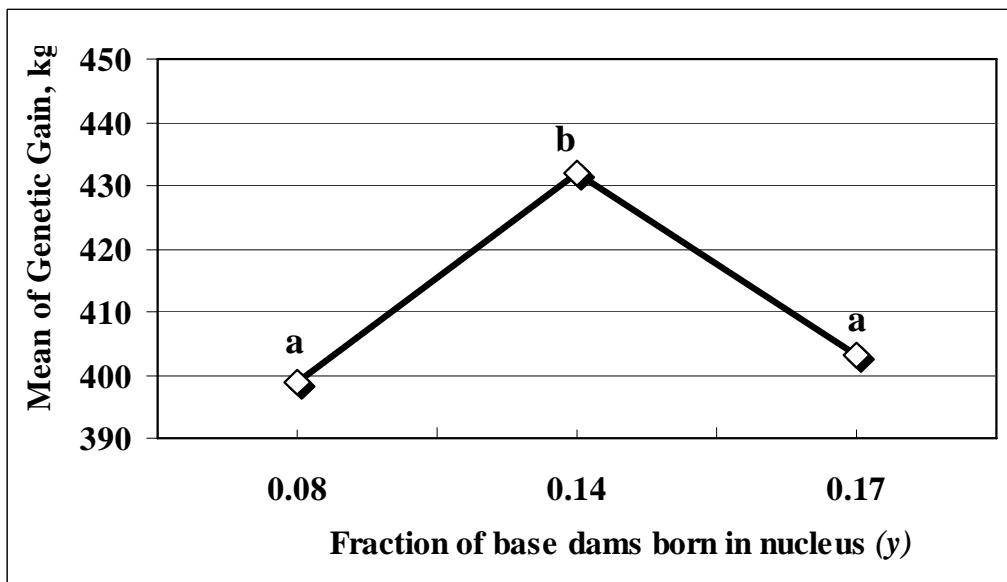
Figure 6. Change of genetic gain means by changing different mating ratios (MR).

The results agree with those of Ni gm *et al.* (2005) who concluded that the observed increase in genetic gain is mainly due to the higher selection intensity of males used as sires in AI. Also, AI will enable higher selection intensity even in small nucleus size of small populations. From the practical point of view, large number of breedable females could be inseminated by a smaller number of bulls with higher breeding values. In addition, it is recommended to concern about increasing rate of inbreeding and decreasing genetic variation in the population.

3.7 Fraction of base dams born in nucleus (y)

Genetic gain of milk yield change by changing fraction of base dams born in nucleus (y) is shown in figure (7). Significant differences ($P<0.05$) are shown by increasing y from 0.08 to 0.14 and from 0.14 to 0.17. However, no non-significant differences ($P < 0.05$) were observed by increasing y from 0.08 to 0.17. Increasing y from 0.08 to 0.14 increased the genetic gain by 8%. Slight increase of y from 0.14 to 0.17 resulted in a significant ($P<0.05$) decrease of 6.7% in genetic gain.

The results presented in this study indicated that increasing the migration rate of females born in nucleus (y) to the base led to lower selection intensity of females selected in nucleus to transfer to the base. This result agreed with the result reported by Abdel-Salam *et al.* (2004) for applying ONBS for one generation to improve milk production in buffalo. James (1977) reported that the low value of y is caused by the fact that only a small proportion of needed base-breeding females can be supplied from the nucleus. In sheep and cattle then, only a light culling of nucleus-born females would be recommended.



^{a,b}Means with different letters differ significantly ($P<0.05$).

Figure 7. Change of genetic gain means by changing fraction of base dams born in nucleus (y).

4.0 Conclusion

The open nucleus breeding scheme offers a suitable practical procedure for producing and disseminating buffalo bulls of known breeding values. Applying ONBS for many generations of selection could accelerate the rate of genetic gain of milk production in buffalo and increase the average milk yield by 15% in G_1 to 26% in G_4 . It is recommended to take into account mating ratios when applying ONBS with the combinations of z and p which affect a and w .

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