



DIFFERENT BREEDING SCENARIOS OF CLOSED NUCLEUS STRATEGY IN IRANIAN BUFFALOES USING COMPUTER SIMULATION

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ABSTRACT

The aim of this study was to compare genetic gain, aggregate genotype values and inbreeding coefficients in different breeding scenarios of closed nucleus using a computer simulation and to introduce suitable scenarios of closed nucleus for Iranian native buffaloes breeding schemes. Four traits including milk production (MP) milk fat production (MF), age at first calving (AFC) and interval between first and second calving (CI) data were obtained from 9278 milk and 8050 milk fat percentage test day records of Iranian native buffaloes and were included in selection index and breeding goal. Computer simulation program was written with R software. Superior males and females were selected from base population and then distributed in to commercial herds under 18 different scenarios, including three levels of herd size and herd number and two levels of transfer rate of sires from nucleus to herds. Results represented that genetic gain in all of closed nucleus scenarios were increasing as aggregate genotype value and inbreeding for 10 generation of selection. The highest value for aggregate genotype (H) was 898.34 that represented in scenario 18 by herd size, herd number and transfer rate of 50, 50 and 1, respectively. Cumulative genetic gain in closed nucleus after 10 generations of selection was 1056.85 kg, 26.07 kg, -12.42 months and -17.93 days for milk yield, milk fat, AFC and CI, respectively. Also average inbreeding coefficient was 0.04 percentages in the scenario lower than other scenarios that represent it's more suitable than other scenarios.

Keywords: breeding strategy, closed nucleus, buffalo, computer simulation.

INTRODUCTION

The buffalo is a very quiet and intelligent animal. It can be found in many countries worldwide. Remarkable characteristics of buffalo are high milk fat and growth rate, ability of using low quality feed, resistance to some diseases and having specific dairy products like Mozzarella. According to recent report of (Food and Agriculture Organization (FAO), there are about half a million buffaloes in Iran. This number had been up to 1.5 million in 1930's (FAO, 2005). Some of the main reasons for this decline maybe according to industrialization, the increasing demand for buffalo meat but a lack of replacement of the slaughtered animals and farming diversification and income. Official neglect and pro-Holstein propaganda have caused a significant decrease in buffalo numbers. The trend of decreasing buffalo numbers inverted in recent years through the demand for particular products obtained only from buffalo milk and another reason is that buffalo has changed from a rustic triple purpose animal to a dairy purpose animal. Iranian buffaloes are Azeri and Khuzestani breeds (FAO, 2005). Most of the animals live in south and North West of Iran. All of Iranian buffaloes are in category of river breeds (Naserian and Saremi, 2007). In the process of formulating breeding programs for genetic improvement, the structure of the herd has a special role to play (JAMES, 1977). Group Nucleus Breeding Structures were originally widely used in New Zealand and Australia in their sheep genetic improvement schemes. According to reports of FAO, Iran in comparison to other countries like India, that has about 10% of the world's population by

itself, has recorded lower genetic progress in the productivity of local buffaloes. One of the main reasons is lack of a suitable breeding strategy for genetic improvement of buffalo breeds in Iran. During the recent years; some researchers have characterized Iranian rural buffalo's production and genetic parameters. Results of these studies can be used as inputs for designing suitable breeding schemes especially for closed and open nucleus strategies. The main goal of this study is to compare genetic gain, aggregate genotype and inbreeding rate under closed nucleus strategy using stochastic computer simulation and to introduce a suitable scenario for Iranian native buffalo breeding plans.

MATERIALS AND METHODS

Breeding estimation of genetic parameters for productive and reproductive traits of Iranian native buffaloes, including Milk production (MP) milk fat production (MF), age at first calving (AFC) and interval between first and second calving (CI), were conducted using data from 9278 milk and 8050 milk fat percentage test day records of Iranian native buffaloes from 1990 to 2009 (Madad, 2011). Parameters were consisted of trait Means, heritability coefficients and genetic and permanent environmental correlations. The parameters were estimated by using multi-trait animal model (Table-1). The economic values of traits used in this study separate research (Taheri, 2012) (Table-1). For simulation phenotypic values, it was supposed that those have been selected from a non-inbred and non-related population, randomly.



Economic weights

In this research, relative economic weights were 0.56, 8.25, -0.28, -4.9 and for MP, MF, AFC and CI, respectively.

Simulation of breeding values and phenotypic observations

In order to simulate multivariate additive genetic (V_g) and environmental effects (V_e), (co)variance matrices having same dimensions as the number of traits, were established. Using a Cholsky decomposition, lower triangular matrices (L_g) and (L_e) under the condition $L_e L_e' = V_e$ and $L_g L_g' = V_g$ were calculated. In the next step a vector of random numbers (w) driven from a normal distribution was made and as a result of multiplying lower triangular genetic and environmental matrices to w vector, vectors having additive genetic and environmental values for each animal were obtained. For any animal, the effects of herds for given traits were simulated and after adding them to additive genetic and environmental values, the phenotypes of those animals were made.

For animals in the base population a vector of breeding values (bvi) were calculated as:

$$bvi = L' * r_1 \quad (1)$$

For base population for a vector of observations ($obsi$) for the simulated traits for each animal were calculated as:

$$obsi = bvi + C' * r_2 \quad (2)$$

Where r_1 and r_2 were vectors of random numbers from a standardized normal distribution

Also selection criteria (I) and aggregate genotype (H) equations were:

$$I = b1P_{MP} + b2P_{MF} + b3P_{AFC} + b4P_{CI} \quad (3)$$

$$H = v1a_{MP} + v2a_{MF} + v3a_{AFC} + v4a_{CI} \quad (4)$$

Breeding values for offspring were calculated as follow:

$$BV = 0.5 (BV_s + BV_d) + \{0.5 (1-0.5(F_s + F_d))\} 0.5 (L'g w) \quad (5)$$

Where, BV , F , L_g and w are breeding values, coefficient of inbreeding, genetic lower triangular matrix and vector of standard normal numbers, respectively. Subscripts of s and d are used to represent progeny, sire and dam, respectively.

Simulated breeding scenarios

Since simulation of breeding strategies using this program is very computing intensive only a few breeding schemes have been investigated until now. In the present investigation three factors have been varied, and each factor had three levels. All combinations were investigated (Table-2).

Genetic gain, aggregate genotype and inbreeding coefficients under all scenarios of nucleus strategy were calculated for 10 years of selection.

After genetic evaluation of base population, selection indices were used for selecting the parents.

Superior males and females were selected as nucleus animals under given criterions. Dimension of nucleus was three times bigger than herd sizes. Thus residual superior animals were distributed into commercial herds under 18 different scenarios, including three levels of herd size and herd number and two levels of transfer rate of sires from nucleus to herds.

Table-1. Means, genetic (co) variance components of Milk production (MP) milk fat production (MF), age at first calving (AFC) and interval between first and second calving (CI) (Madad, 2013).

Traits	Means	Genetic (co) variance components				$h^2 \pm SE$	Economic values
		(MP)	(MF)	(AFC)	(CI)		
(MP)	1731.22 kg	34009	-	-	-	0.46± 0.01	0.56
(MF)	114.87 kg	0.51	141.22	-	-	0.27± 0.17	8.25
(AFC)	54.31 months	0.05	0.07	41.62	-	0.21± 0.21	-0.28
(CI)	506.03 days	0.05	0.05	-0.09	286.15	0.01± 0.29	-4.9

RESULTS AND DISCUSSIONS

Genetic gains were positive for productive traits including milk yield and milk fat in all of scenarios in closed nucleus strategies. Conversely, for traits of age at first calving (AFC) and interval between first and second calving (CI) genetic trends were negative because of their

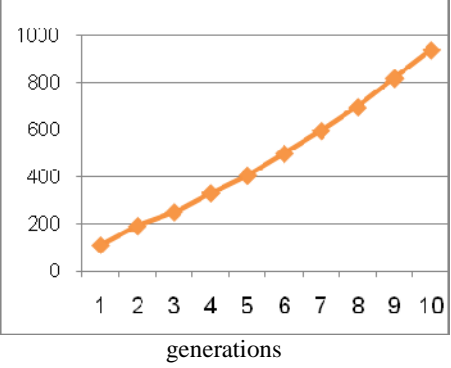
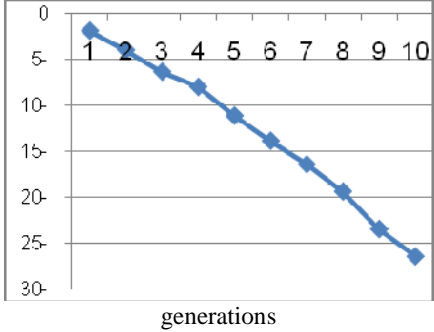
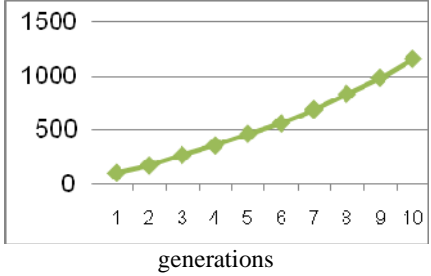
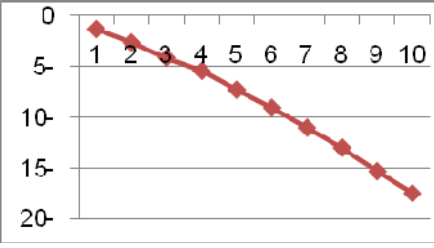
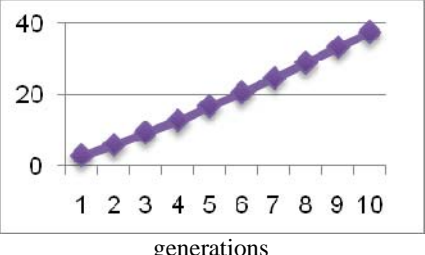
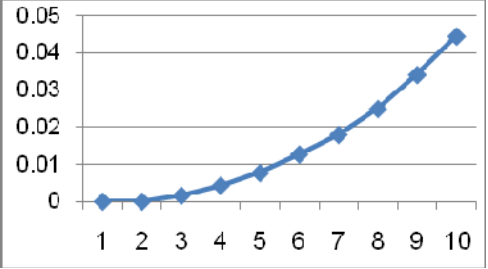
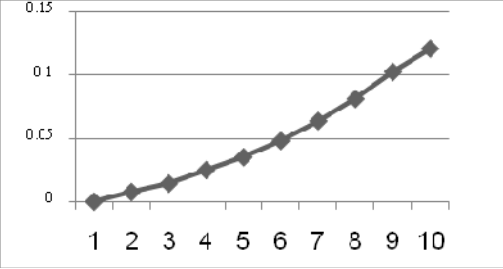
negative economic values. The highest value for aggregate genotype (H) was represented in scenario 18 by value of 898.34 (Table-2) (Figure-1). Cumulative genetic gain in closed nucleus after 10 generations of selection was 496.57 kg, 23.15kg, -11.19 months and -19.49 days for milk yield, milk fat, AFC and CI, respectively.



Table-2. Amounts of genetic progress in traits of milk production (MP) milk fat production (MF), age at first calving (AFC) and interval between first and second calving (CI), aggregate genotype and inbreeding after 10 generations of selection under different scenarios of closed nucleus strategy.

	Scenarios			R				F (%)	H
	NH	SH	Transfer Rate of sires from nucleus to herds	MP (kg)	MF(kg)	(AFC) months	(CI) days		
1	10	10	0.5	496.57	23.15	-11.19	-19.49	0.11	567.71
2	10	10	1	457.65	20.02	-5.42	-6.28	0.09	453.74
3	10	20	0.5	477.83	21.34	-10.64	-17.53	0.11	532.50
4	10	20	1	682.99	31.01	-14.19	-21.02	0.12	745.31
5	10	50	0.5	779.82	34.60	-16.08	-24.40	0.09	846.22
6	10	50	1	796.55	29.36	-13.43	-21.52	0.06	797.50
7	20	10	0.5	514.64	22.77	-10.53	-15.79	0.11	556.37
8	20	10	1	443.50	13.98	-8.72	-13.55	0.09	432.54
9	20	20	0.5	642.13	27.34	-14.19	-20.67	0.12	690.39
10	20	20	1	666.17	25.21	-11.44	-17.67	0.09	670.82
11	20	50	0.5	696.11	31.40	-14.05	-21.12	0.09	756.35
12	20	50	1	815.42	30.47	-14.90	-23.32	0.05	826.47
13	50	10	0.5	522.53	24.57	-11.29	-18.08	0.12	587.11
14	50	10	1	662.34	17.50	-5.88	-8.27	0.09	557.49
15	50	20	0.5	602.83	29.91	-13.34	-22.58	0.11	698.69
16	50	20	1	848.89	20.65	-9.16	-15.30	0.08	723.24
17	50	50	0.5	710.91	32.27	-14.96	-22.48	0.08	778.69
18	50	50	1	1056.85	26.08	-12.42	-17.94	0.04	898.34



<p style="writing-mode: vertical-rl; transform: rotate(180deg);">Aggregate genotype value</p>	 <p>Figure-1. Trend of aggregate genotype values in scenario 18 after 10 generations.</p>	<p style="writing-mode: vertical-rl; transform: rotate(180deg);">Breeding Values</p>  <p>Figure-3. Trend of breeding value coefficients for CI in scenario 5 after 10 generations</p>
<p style="writing-mode: vertical-rl; transform: rotate(180deg);">Breeding Values</p>	 <p>Figure-2. Trend of breeding value coefficients for milk yield scenario 18 after 10 generations.</p>	 <p>Figure-4. Trend of breeding value coefficients for AFC in scenario 5 after 10 generations.</p>
<p style="writing-mode: vertical-rl; transform: rotate(180deg);">Breeding Values</p>	 <p>Figure-5. Trend of breeding value coefficients for milk fat in Scenario 5 after 10 generations.</p>	
<p style="writing-mode: vertical-rl; transform: rotate(180deg);">inbreeding</p>	 <p>Figure-6. Trend of inbreeding coefficients in Scenario 5 after 10 generations selection</p>	<p style="writing-mode: vertical-rl; transform: rotate(180deg);">inbreeding F</p>  <p>Figure-7. Trend of inbreeding coefficients in Scenario 18 after 10 generations selection</p>

Average inbreeding coefficient was ascending across generations and its value was between 0.04 to 0.12 following 10 years of selection for all scenarios of closed nucleus strategies. Scenario of 18 has highest (Figure-6) average inbreeding coefficient. Also lowest Inbreeding coefficient was for Scenario of 5 (Figure-7) Results of different simulated scenarios is shown in Table-2. Genetic

gains and inbreeding were affected by transfer rate of sires from nucleus to commercial herds, Herd sizes and herd's numbers. Results are shown that herds by size of 50, for all of including scenarios, had highest Genetic gains. But different transfer rates were not effective enough on Genetic gains and inbreeding amounts. Genetic gain and inbreeding is affected by the number of traits in the



selection index, (co) variance components, economic weights, selection intensity, selection methods, population size and number of dams per sire (Sorensen, 1999; Nimbkar and Wrary, 1991). Therefore, comparison of simulation study results should be carried out with respect to these factors. Several studies have shown that breeding schemes resulting in high genetic gain generally also result in large increases in inbreeding (Quinton *et al.*, 1992; De Boer and Van Arendonk, 1994; Brisbane and Gibson, 1995). Results of this research confirmed those reports. Genetic gains in closed and open nucleus strategies were compared based on the number of traits in selection index and two daughter group sizes by Sorensen (1999). They recommended daughter group sizes around 160. After that in most cases total genetic gain increased. This study showed that genetic gain and inbreeding coefficient in highest herd size, herd number and transfer rate in closed nucleus was higher than other scenarios.

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