Pedigree analysis and inbreeding effects on early growth traits and greasy fleece weight in Markhoz goat

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ABSTRACT

The aims of this study were the analysis of pedigree information and evaluation of inbreeding effects on birth weight (BW), average daily gain from birth to weaning (ADG), weaning weight (WW) and yearling greasy fleece weight (GFW) in Markhoz kids. Mean of inbreeding coefficients in whole and inbred populations were estimated to be 2.73% and 5.25%, respectively. Pedigree information over a 23-year period (from 1990 to 2013) was used. Kids born from 2010 to 2013 were considered as reference population. Taking the reference population into account an average inbreeding coefficient of 4.20% was obtained. Average coancestry in the reference population was estimated as 1.93%. Mean of generation interval, computed from four pathways, was 3.55 years, with a longer interval from dam-progeny pathways relative to sire-progeny ones. Average equivalent complete generation, as a measure of pedigree completeness, in the reference population was 5.84. Realized effective population size was estimated from the individual rate in coancestry and from the individual increase in inbreeding (ΔF_i) as 84 and 69, respectively. The effective numbers of founders, ancestors, founder genomes (founder genome equivalents) and non-founder genomes for reference population were estimated at 49, 37, 26 and 56, respectively. Approximately, 75% of total genetic variation was explained by the 28 most influential ancestors, with a maximum individual contribution of 6.97%. Inbreeding depressions were estimated for studied traits by fitting ΔF_i of kids as linear covariates under univariate animal models. Significant individual inbreeding depression was found only for GFW ($P < 0.01$) as -3.1 g per 1% increase of ΔF_i and not found for other traits ($P > 0.05$). The effects of inbreeding on estimation of variance components and ranking of animals based on predicted breeding values were not significant ($P > 0.05$). The obtained results revealed the evidences on loss of genetic diversity and bottlenecks in the population, mainly because of unbalanced contribution of breeding animals to gene pool of population.

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1. Introduction

Selection under animal models brings genetic gain accompanied with the loss of genetic variation (Mrode, 2005). Therefore, for some of economic traits under selection, inbreeding depression may be happened. Inbreeding has long been a serious concern in animal breeding due to its detrimental effect on genetic variability (Falconer, 1996). Maintenance of genetic variation at an acceptable level by control of inbreeding is of crucial importance so that it will ensure that animals in the future can reply to the changes caused by selection (van Wyk et al., 2009). Setting

up an efficient genetic improvement program requires the knowledge of genetic variation and genealogical structure of population (Gutierrez et al., 2003). Genetic variation is referred as the variety of alleles and genotypes that exist in a population; such diversity may be expressed through morphological, physiological and behavioral differences in the levels of individuals and populations (Frankham et al., 2002). The accuracy of demographic parameters estimated using pedigree analysis may be influenced by several factors; level of pedigree completeness as a main factor (Boichard et al., 1997). Therefore, for overcoming partly such inadequacies fundamental concepts such as effective number of founders (Lacy, 1989), ancestors (Boichard et al., 1997), founder genome equivalents and non-founder genomes (Caballero and Toro, 2000) have been proposed.

Markhoz goat breed is one of the most important native goat breeds in Iran mainly raised in a wide range of forest mountain habitats in the region of Kurdistan, north-west of Iran. These goats are small-sized with a wide range in brown, white and black coat color. The range of coat color characters is a unique between goats in the world. Markhoz goats had a considerable cultural role in Kurdistan since the mohair obtained from these animals is being used as a raw material for making national clothes. Like other developing countries, official recording and pedigree registration on Markhoz goat is mainly limited to a performance testing station which may act as an integral part of a nucleus-based breeding scheme for genetically improvement of this breed, dissemination of superior bucks into local flocks and thereby promotion of production efficiency. Assessment of genetic diversity and possible effects of inbreeding on economical traits in Markhoz goat are of great importance to set up a nucleus-based breeding scheme. Application of pedigree information for studying the genetic variation is a thriftily and efficient approach and reveals useful information concerning managerial decisions practiced in historical background of a population through the past years.

There are limited reports regarding the study of genetic variation using pedigree analysis (Portolano et al., 2004) and inbreeding effects on growth traits (Sajjad Khan et al., 2007) of goat breeds. Therefore, the aims of the present study were assessing the genetic variability by using pedigree analysis method and the evaluation of inbreeding effects on pre-weaning growth traits and yearling greasy fleece weight in Markhoz goats.

2. Materials and methods

2.1. Data collection and management

The data set and pedigree information used in this study were collected at Markhoz Goat Station located in Sanandaj, Kurdistan province, north-western part of Iran. Goats raised under semi-intensive managerial conditions which were similar to prevalent condition on pastoral flocks. This station may act as a main part of a nucleus-based breeding scheme for genetically improvement of Markhoz goat breed, dissemination of superior bucks into native flocks and thereby enhancement of production efficiency. Mating was from October to November with February to March kidding. Does were first exposed to the bucks at about 18 months of age. Annually 20–30 bucks were randomly allocated to mate with about 10 or 15 does in breeding pens and sire identification recorded. Some of sires were used for two or three mating seasons. Newborn kids were weighed

and ear-tagged after birth time and allowed to remain with their dam for a week. One week after birth the kids were separated from their dams and suckled twice a day until 3–4 months of age (Rashidi et al., 2011).

2.2. Pedigree analysis

Pedigree records collected during a 23-year period (1990–2013) were analyzed and the kids born from 2010 to 2013 were considered as reference population. The inbreeding coefficient of individuals (F) for each animal implies the probability that two alleles at any locus are identical by descent was computed using algorithm of Meuwissen and Luo (1992). Coancestry coefficient (f) of each animal is defined as the probability that any two alleles, sampled at random one from each individual, were identical copies of an ancestral allele.

2.3. Generation interval

The generation interval was defined as the average age of the parents at the birth time of their progeny kept for reproduction. It was computed across four genetic pathways, sire to son (L_{ss}), sire to daughter (L_{sd}), dam to son (L_{ds}), and dam to daughter (L_{dd}). The average generation interval ($G.I.$) was computed as follows:

$$G.I. = \frac{L_{ss} + L_{sd} + L_{ds} + L_{dd}}{4}$$

2.4. Equivalent complete generations

Completeness of pedigree was assessed by equivalent complete generations. Individual equivalent complete generation for individual i ($E_q G_i$) were computed according to Maignel et al. (1996) as follows:

$$E_q G_i = \sum \left(\frac{1}{2}\right)^n$$

where, n is the number of generations separating the individual from each known ancestor. Average equivalent complete generations for whole and reference population were computed simply by averaging individual equivalent complete generations.

2.5. Realized effective population size

The effective population size is the size of an ideal population, characterized by equal sex ratio, absence of mutation, migration and selection, which has the same inbreeding rate as the real population under consideration. The realized effective population size (Ne) was estimated by two methods for a comparison to see if the rotational mating was being effective.

The first method for estimating realized effective population size was based on individual increase in inbreeding. The coefficients of individual increases in inbreeding (ΔF_i) were computed according to the method described by Gutierrez et al. (2008) and modified by Gutierrez et al. (2009) using the following formula:

$$\Delta F_i = 1 - {}^{E_q G_i - 1}\sqrt{1 - F_i}$$

where F_i and $E_q G_i$ are the coefficient of inbreeding and the equivalent complete generation for individual i, respectively. The coefficients of individual increase in inbreeding were averaged and realized effective population size was estimated as:

$$NeF = \frac{1}{2\overline{\Delta F}}$$

The second method was proposed by Cervantes et al. (2011) using the rate of coancestry for all pairs of individual j and k (ΔC_{jk}) in a reference population as:

$$\Delta C_{jk} = 1 - {}^{((g_j + g_k)/2)}\sqrt{1 - C_{jk}}$$

where, C_{jk} is the inbreeding coefficient of a progeny from individuals j and k, and g_j and g_k are the equivalent complete generation of individuals j and

k, respectively. Realized effective population size in a reference population was estimated by averaging in rate of coancestry for all pairs of the individuals as the follows:

$$NeC = \frac{1}{2\Delta C}$$

NeF and NeC are theoretically equivalent under random mating. Therefore its comparison must provide a measure of the structure of the population (if NeF is higher) or of the mating efficiency avoiding relatedness (if NeF is lower). The number of equivalent subpopulations was computed as NeC/NeF according to Cervantes et al. (2008).

2.6. Measures on the probabilities of gene origin

Considering the reference population four measures on probability of gene origin including the effective number of founders, ancestors, founder genomes and non-founder genomes were estimated. Effective number of founders (f_e) denotes the numbers of equally contributing founders that would result to the same level of genetic diversity in the current population and was estimated according to Lacy (1989):

$$f_e = \frac{1}{\sum_{k=1}^{m} q_k^2}$$

where, q_k is the expected proportional genetic contribution of founder k; computed by the average relationship of the respective founder to each animal in the population and m is the total number of founders.

Effective number of ancestors (f_a) measure is the minimum number of ancestors, not necessarily founders, explaining the complete genetic diversity of the current population and was computed according to Boichard et al. (1997):

$$f_a = \frac{1}{\sum_{k=1}^{n} p_k^2}$$

where, p_k is the marginal contribution of each ancestor; the contribution made by an ancestor not explained by a previously chosen ancestor and n is the total number of ancestors. Effective number of founder genomes or founder genome equivalents f_g indicates that how many founders would be required to produce the same genetic diversity that found in the population if all founders contributing equally and no founder alleles were lost under random mating (Caballero and Toro, 2000). This parameter was computed as the inverse of twice average coancestry of the individuals defined in a reference sub-population:

$$f_g = \frac{1}{2\bar{f}}$$

Relying upon to this fact that f_g accounts for all of the factors affecting gene loss during segregation, it is always lower than both, f_a and f_e. Effective number of non-founder genomes (f_{ne}) considers only the effect of genetic drift in non-founder generations and was estimated as follow (Caballero and Toro, 2000).

$$\frac{1}{f_{ne}} = \frac{1}{f_g} + \frac{1}{f_e}$$

2.7. Inbreeding depression

The effect of inbreeding on growth traits including birth weight (BW), average daily gain from birth to weaning (ADG), weaning weight (WW) that recorded at 4 months of age and on greasy fleece weight at yearling age (GFW) were studied. Inbreeding depression was estimated as the linear regression of performance on the coefficients of individual increase in inbreeding of kids, fitting an animal model (Mokhtari et al., 2014). The coefficient of individual increase in inbreeding, unlike inbreeding coefficient, is a measure of inbreeding which is not dependent on the pedigree depth. Unlike to inbreeding coefficient, the relation of individual increase in inbreeding with the performance is linear because inbreeding coefficient has an exponential growth regarding pedigree knowledge (Gonzalez-Recio et al., 2007). Furthermore, individual increase in inbreeding does not present co-linearity with the effect of year.

Common fixed effects included in the models for BW, ADG, WW and GFW were sex of kids in 2 classes, dam age at lambing in 6 classes (2–7 years old) and birth type in 3 classes (single, twin and triplet). For the studied growth traits, birth year was in 23 classes (1990–2013). For GFW, data covered a period from 1990 to 2009 and therefore birth year was in 19 classes. Age of kids at weaning and at shearing (in days) was considered as a linear covariate for WW and GFW, respectively.

Restricted maximum likelihood (REML) procedure under a derivative free algorithm was used to estimate the (co) variance components and corresponding genetic parameters. Tested models (in matrix notation) are as below:

$y = Xb + Z_a a + e$		Model 1
$y = Xb + Z_a a + Z_{pe} pe + e$		Model 2
$y = Xb + Z_a a + Z_m m + e$	Cov (a,m) = 0	Model 3
$y = Xb + Z_a a + Z_m m + e$	Cov (a,m) = $A\sigma_{am}$	Model 4
$y = Xb + Z_a a + Z_m m + Z_{pe} pe + e$	Cov (a,m) = 0	Model 5
$y = Xb + Z_a a + Z_m m + Z_{pe} pe + e$	Cov (a,m) = $A\sigma_{am}$	Model 6
$y = Xb + Z_a a + Z_l l + e$		Model 7
$y = Xb + Z_a a + Z_{pe} pe + Z_l l + e$		Model 8
$y = Xb + Z_a a + Z_m m + Z_{pe} pe + Z_l l + e$	Cov (a,m) = 0	Model 9
$y = Xb + Z_a a + Z_m m + Z_{pe} pe + Z_l l + e$	Cov (a,m) = $A\sigma_{am}$	Model 10

where, y is a vector of records for studied traits; b, a, m, pe, l and e are vectors of fixed, direct genetic, maternal genetic, maternal permanent environmental, maternal temporary environmental (common litter effects) and the residual effects, respectively. X, Z_a, Z_m, Z_{pe} and Z_l are design matrices associating corresponding effects to vector of y. Also, A is the numerator relationship matrix and σ_{am} denotes covariance between direct and maternal effects.

The Akaike's Information Criterion (AIC) was applied for the determination of the most appropriate model among tested models (Akaike, 1974):

$$AIC_i = -2 \log L_i + 2P_i$$

where $\log L_i$ is the maximized log likelihood and p_i is the parameters fitted for model i. In each case, the model with the lowest AIC is considered as the best model.

Considered univariate models were fitted including and/or excluding the coefficient of individual increase rate in inbreeding of kids (ΔF_i) as linear covariate using ASReml program (Gilmour et al., 2002) to investigate the effect of ΔF_i on genetic parameters and breeding values. Pearson and Spearman rank correlation coefficients between the predicted breeding values of animals for each trait were also computed under two models. The ENDOG v4.8 program of Gutierrez and Goyache (2005) was used for genealogical analysis.

3. Results and discussion

3.1. Generation interval and pedigree completeness

The generation intervals obtained from four pathways included sire-son sire-daughter dam-son and dam-daughter were 3.16 ± 0.05, 3.27 ± 0.06, 3.93 ± 0.04 and 3.83 ± 0.04 years, respectively. The mean generation interval from four pathways was obtained 3.55 years. The generation interval in sire-progeny pathways was shorter than dam-progeny pathways. The estimated generation interval in the present study was higher than those of 2.5 years reported by Portolano et al. (2004) in Girgentana goat breed. Higher generation interval obtained for Markhoz goat may be ascribed partly to use of a few breeding animals within the flock. The higher interval of the does-progeny pathways relative to buck-progeny pathways reflects that breeding dams have usually been employed for more years to produce offspring than the sires. Pedigree completeness level has sizable effect on the estimation of inbreeding coefficient due to the fact that chance of finding common ancestors increases along with level of pedigree completeness (Gutierrez et al., 2003). Average equivalent complete generation of kids in the reference and whole populations
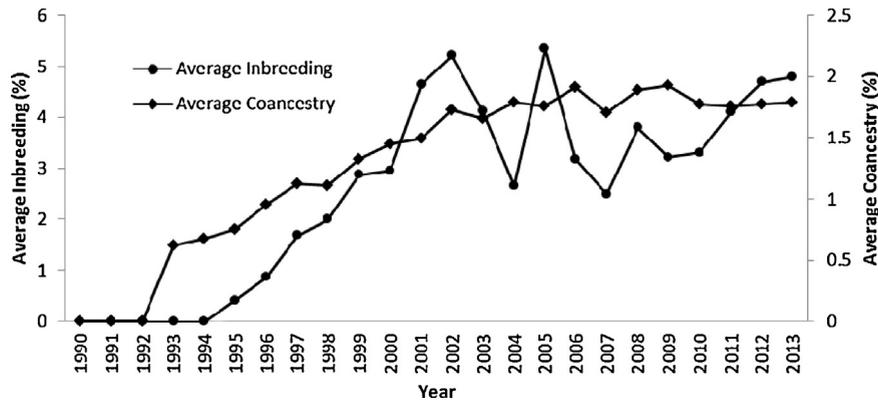
Fig. 1. Evolution of average inbreeding and coancestry through the studied period.

were 5.84 and 3.36, respectively. Which are comparable with average equivalent complete generations of 3.15 in Zandi sheep (Ghafouri-Kesbi, 2010) and 5.47 in Baluchi sheep (Tahmoorespur and Sheikhloo, 2011).

3.2. Trends in inbreeding and coancestry

Approximately 45% of kids were male and 55% were female. A relatively high proportion of kids born were inbred; about 48% of total kids (47% of male and 53% of female kids). Means of inbreeding coefficients in whole animals and inbred kids were 2.73% and 5.25%, respectively.

Evolution of average inbreeding coefficients and average coancestry of kids across birth years during the study period are shown in Fig. 1. Means of inbreeding coefficients were increased steadily from 1994 to 2002 but several fluctuations were observed afterwards. Average coancestry in the reference population was computed as 1.93%. The rate of ΔF_i during the studied period is shown in Fig. 2. The inbreeding rate during a certain period may be considered as a more efficient tool in genetic management of population than the corresponding mean inbreeding coefficient (Falconer, 1996). Portolano et al. (2004) reported an inbreeding rate of 0.13% per generation in the Girgentana goats breed. In a population, the average coancestry of animals forecasts the average of inbreeding coefficient in the next generation. The results of pedigree analysis are

Table 1
Summary statistics of the pedigree analysis.

Item	Value
Whole population	
No. of animals with progeny	1580
No. of animals without progeny	3216
No. of animals with both known parents	4456
No. of animals with both unknown parents	340
No. of animals with one unknown parent	0
Reference population	
No. of animals	792
Mean of inbreeding coefficient (%)	4.20
Average coancestry (%)	1.93
Average No. of equivalent complete generations	5.84
No. of founders	348
No. of ancestors	159
Effective population size[a]	84
Effective population size[b]	69
Effective No. of founders (f_e)	49
Effective No. of ancestors (f_a)	37
Founder genome equivalent (f_g)	26
Effective No. of non-founder genomes (f_{ne})	56
No. of ancestors explaining 75% of genetic variation	28

[a] Estimated based on individual increase in coancestry.
[b] Estimated based on individual increase in inbreeding.

presented in Table 1. Kids with both parents known and with both parents unknown constituted 92.91% and 7.09% of total kids, respectively. There were no animals with only one parent known. Considering reference population an average inbreeding coefficient of 4.20% was obtained.
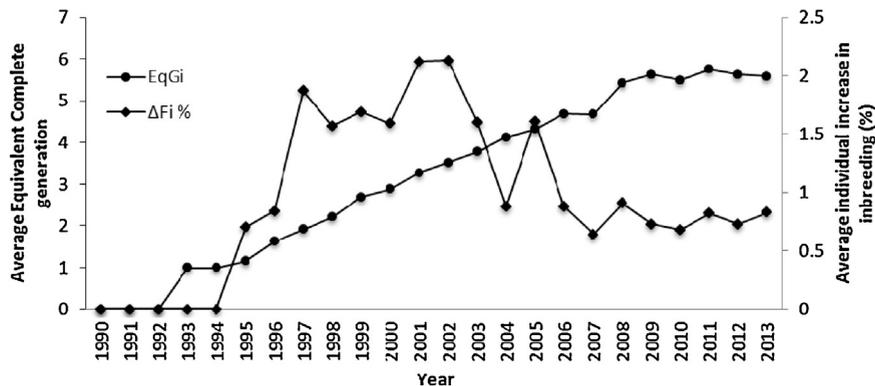

Fig. 2. Average equivalent complete generation (E_qG_i) and average individual increase in inbreeding (ΔF_i) in percentage through the studied period.

3.3. Realized effective population size

Increase in coancestry is slightly affected by population structure (Gutierrez et al., 2008) and the effective population size can be estimated from increase in coancestry instead of increase in inbreeding when dealing with structured population (Caballero, 1994). As shown in Table 1 the realized effective population size estimates based on individual increase in coancestry and on individual increase in inbreeding were 84 and 69, respectively. Efficient implementation of management strategies for genetic conservation is required quantifying the contributions made to diversity. Subdivision in a population resulted in increase of inbreeding higher than those expected considering population size. The number of equivalent subpopulations was calculated as 1.217. Santana Jr et al. (2014) obtained a value of 1.76 for the number of equivalent subpopulations in Brazilian Gir cattle. The effective population size based on individual increase in coancestry was higher than that obtained based on individual increase in inbreeding. Furthermore, as shown in Fig. 1, the averages of inbreeding in the studied population through the years have fluctuations from 2002 to 2010 with a general increase from beginning of the studied period. Therefore, it can be concluded that designed rotational mating in Markhoz goat was not implemented efficiently for preventing inbreeding. The effective population size is an important parameter in population genetics and indicates the genetic viability of populations (Frankham et al., 2002).

The determination of a strict critical level for effective population size is not straightforward and effective population size should be interpreted considering factors such as the method applied, animal species and the structure of population studied (Leroy et al., 2013).

3.4. Probability of gene origin measures

The measures of probability of gene origin including f_e, f_a, f_g and f_{ne} were estimated as, 49, 37, 26 and 56, respectively. The number of founders contributed in the reference population and the effective number of founders were 348 and 49, respectively; indicating the excessive use of some animals as parents. Portolano et al. (2004) reported total number of founders and effective number of founders in Girgentana goat breed as 93 and 22.94, respectively. The ratio between effective number of founders to the total number of founders was approximately 0.14; indicating disequilibrium among founder contributions in the studied population of Markhoz goat. A corresponding ratio of 0.25 was obtained by Portolano et al. (2004) in Girgentana goat breed. Unequal contribution of founders in a population has been taken into account by using effective number of founders (Lacy, 1989). When a bottleneck imposed on a population, f_e is over estimated due to ignoring the possible bottleneck effects. Therefore, estimation of effective number of ancestors (f_a) as more important measure of genetic diversity is of crucial.

Boichard et al. (1997) pointed out that the f_a complements the information offered by the effective number of founders taking the losses of genetic variation into account; caused by the unbalanced use of breeding animals

producing bottleneck. The effective number of ancestors (f_a) and the total number of ancestors contributed in the reference population were estimated to be 37 and 159, respectively. Such unbalanced contribution of breeding animals is evident.

The founder genome equivalents f_g was estimated to be 26 and as it was expected lower than both f_e and f_a. The parameter f_g dealing with the loss in variability and is directly associated with genetic diversity but it does not take mutation and/or migration into account (Ghafouri-Kesbi, 2012). The lower f_g in a reference population denotes the existence of lower proportions of the founders' genes.

Boichard et al. (1997) stated that evaluation of the loss in genetic diversity that exist in the founders because of the bottleneck between the base and the reference population can be studied applying a ratio of f_e/f_a; the ratio of effective number of founders to effective number of ancestors. The importance of bottleneck in the population under consideration can be evaluated applying this ratio; the greater the f_e/f_a ratio, the more stringent the bottlenecks. In the present study, the ratio of f_e/f_a was obtained 1.32.

The f_{ne} takes the effect of genetic drift in non-founder generations into account and provides indication on the relative importance of random genetic drift accumulated in non-founder generations and unequal contribution of founders regarding the loss of genetic diversity. Estimated value for f_{ne} in the present study was 56. If the f_e to be higher than f_{ne} it can be concluded that the reduction in genetic variability is more attributable to genetic drift accumulated in non-founder generation. Where f_e to be lower than f_{ne}, as observed in the current study, the unequal contribution of founders would be considered as the main factor affecting the loss of genetic diversity.

The estimated values of f_g, f_a and f_e are lower than the estimated values for realized effective population size. It suggests that the population has been increasing in size from the foundation. The most influential ancestor explained 6.97% of the genetic diversity in the reference population.

3.5. Effects of inbreeding on the studied traits

A detailed statistics on the studied traits with distribution of inbreeding classes (the classes were chosen arbitrarily) is presented in Table 2. Among the inbred animals the kids with inbreeding coefficients of lower than or equal to 6.25% were the largest and animals had to inbreeding coefficient class more than 25% are lower than that of 0.6% total animals in each trait.

Estimates of inbreeding depressions for all the studied traits are presented in Table 3. Only GFW was significantly ($P < 0.01$) affected by inbreeding (-3.1 g per 1% individual increase in inbreeding). No significant inbreeding depression due to individual increase in inbreeding of kids on the other traits was evident ($P > 0.05$).

Transforming the inbreeding depression estimated based on individual increase in inbreeding to an increase in inbreeding basis considering the formula which explains the relation between ΔF_i, F_i and EqG_i may be interesting. The average numbers of equivalent complete generations

Table 2
Descriptive statistics of the studied traits.

Item	Traits[a]			
	BW (kg)	ADG(g/d)	WW (kg)	GFW (g)
No. of records	4456	3729	3729	2528
Mean	2.50	111.09	15.40	408.19
S.D.	0.48	37.05	4.44	197.70
C.V. (%)	19.20	31.49	28.83	48.78
Min.	1.10	17.35	3.80	50.00
Max.	4.50	290.63	31.00	2900.00
No. of sires	209	203	203	147
No. of dams	1370	1283	1283	951
$F_i = 0$[b]	1961	1755	1755	1320
$0 < F_i \leq 6.25$	1710	1347	1347	805
$6.25 < F_i \leq 12.5$	473	380	380	273
$12.5 < F_i \leq 25$	284	227	227	122
$F_i > 25$	28	20	20	8

[a] BW: birth weight; ADG: average daily gain from birth to weaning; WW: weaning weight; GFW: yearling greasy fleece weight.
[b] Range of inbreeding coefficients for animals (F_i) in a percentage basis.

Table 3
Estimates of the linear regressions trait on individual increase in inbreeding for the studied traits.

Traits[a]	Linear regression[b]	S.E.
BW (kg)	−0.0031[ns]	0.0024
ADG (g/d)	−0.1705[ns]	0.1754
WW (kg)	−0.0165[ns]	0.0204
GFW (g)	−3.1000[**]	0.0012

[a] BW: birth weight; ADG: average daily gain from birth to weaning; WW: weaning weight; GFW: yearling greasy fleece weight.
[b] Linear regression coefficient on individual increase in inbreeding of kids.
[**] $P < 0.01$.
[ns] $P > 0.05$.

of the animals with records was obtained 3.06. Therefore, one percent of ΔF_i is corresponded to a 2.05% F_i and the estimated value for inbreeding depression of GFW was −1.51 g per 1% increase in inbreeding. The inbreeding depression as the regression of performance on inbreeding coefficient were −0.150 kg, −0.083 g/d and -0.800 kg per 1% increase in F_i, respectively.

Sajjad Khan et al. (2007) studied the effect of inbreeding on growth and reproduction traits of Beetal goats applying a regression analysis. Contrary to our results, significant effects of inbreeding on birth weight, weaning weight, pre- and post-weaning average daily gain were observed

($P < 0.05$). Marete et al. (2011) studied the effect of inbreeding on birth weight and weaning weight of Kenya Alpine dairy goat. They found a significant improvement in birth weight and weaning weight of inbred kids. Sheep and goat as small ruminants mainly kept under similar managerial conditions and comparison of results from inbreeding depression studies in sheep breeds may be interesting here. Pedrosa et al. (2010) studied the effect of inbreeding depression on birth weight, body weight at 60 days and weight at 180 days of Santa Inês sheep breed. They found a significant depressive effect of the inbreeding for all traits.

3.6. Genetic analysis under different models

The AIC values for the studied traits under the considered animal models are presented in Table 4. The model included direct additive, maternal additive, maternal permanent and maternal temporary environmental effects with correlation between direct and maternal additive effects was determined as the most appropriate one for BW and ADG while the model included direct additive, maternal additive and maternal permanent environmental effects as random ones without considering the correlation between direct additive and maternal additive effect was the best model for WW. Maternal effects had no significant influences on GFW. Therefore, the simplest model which

Table 4
AIC[a] values obtained by each model with the best model in bold face.

Model	Traits[b]			
	BW	ADG	WW	GFW
1	−3141.56	22,534.98	10,132.75	**5,782,661.75**
2	−3154.76	22,533.76	10,134.29	7,306,312.39
3	−3155.83	22,534.37	10,136.64	7,265,786.66
4	−3156.76	22,531.04	10,144.35	6,512,972.53
5	−3211.65	22,530.35	**10,134.38**	6,250,222.04
6	−3196.34	22,525.12	10,134.57	6,550,403.34
7	−3356.84	22,538.14	10,162.38	7,118,606.27
8	−3345.32	22,529.38	10,169.43	7,653,385.90
9	−3370.59	22,527.06	10,141.55	6,197,907.45
10	**−3372.54**	**22,520.43**	10,041.56	6,847,592.42

[a] AIC: Akaike's Information Criterion.
[b] BW: birth weight; ADG: average daily gain from birth to weaning; WW: weaning weight; GFW: yearling greasy fleece weight.

Table 5

Estimates of variance components for the studied traits under two univariate animal model.

Variance components[a]	Model[b]	Traits[c]			
		BW (kg)	ADG (g/d)	WW (kg)	GFW (kg)
σ_P^2	1	0.168	889.342	11.569	13.652
	2	0.166	888.734	11.645	13.562
σ_a^2	1	0.039	168.086	1.747	2.880
	2	0.038	155.528	1.735	2.860
σ_m^2	1	0.012	22.233	0.301	–
	2	0.011	21.330	0.303	–
σ_{Pe}^2	1	0.012	24.901	0.590	–
	2	0.011	22.218	0.570	–
σ_l^2	1	0.098	34.684	–	–
	2	0.093	37.327	–	–
σ_{am}	1	−0.010	17.545	–	–
	2	−0.009	16.530	–	–

[a] σ_P^2: phenotypic variance; σ_a^2: direct additive genetic variance; σ_m^2: maternal additive genetic variance; σ_{Pe}^2: variance due to maternal permanent environmental effects; σ_l^2: variance due to maternal temporary environmental effects or litter effects; σ_{am}: direct-maternal genetic covariance.

[b] Model 1: Excluded individual increase in inbreeding of kids as linear covariate. Model 2: Included individual increase in inbreeding of kids as linear covariate.

[c] BW: birth weight; ADG: average daily gain from birth to weaning; WW: weaning weight; GFW: yearling greasy fleece weight.

contained only the direct additive effects was determined as the most suitable model for this trait.

Estimates of variance components under two univariate animal models, including and excluding ΔF_i of kids, are presented in Table 5. There were also no significant differences in the variance components estimated for all the studied traits. Direct heritability estimates for BW, ADG, WW and GFW were 0.23, 0.18, 0.15 and 0.21, respectively. While, maternal heritability estimates were 0.07, 0.02 and 0.03 for BW, ADG and WW, respectively. The ratios of maternal permanent environmental variance to phenotypic variance for BW (0.07), ADG (0.03) and WW (0.05) were low but the ratio of litter variance to phenotypic variance was 0.58 for BW and 0.04 for ADG. A value of −0.46 was estimated for correlation between direct and maternal effects of BW and corresponding value for ADG was 0.28. The Obtained results were in general agreement with Rashidi et al. Rashidi et al. (2008, 2011). van Wyk et al. (2009) found no difference between estimates of variance components and variance ratios for production and reproduction traits in the Elsenburg Dormer sheep stud which is in general accordance with the corresponding results obtained in the present study.

Ranking of kids based on predicted of breeding value (PBVs) were compared under two models (inclusion and

exclusion of individual increase in inbreeding coefficients of kids as linear covariates) by trait is presented in Table 6. The obtained results showed the existence of high and significant correlation coefficients. Therefore, no significant changes in the ranking of PBV's of the animals should occur when ΔF_i is included in the models for genetic evaluation of Markhoz goat, in accordance with the findings of Gonzalez-Recio et al. (2007) for the Spanish Holstein population and of Santana et al. (2012) for the Brazilian Marchigiana and Bonsmara cattle breeds.

4. Conclusions

Demographic characterization of Markhoz goat applying pedigree analysis revealed some appropriate indications regarding changes in population structure through years. The average rate in inbreeding and the other parameters estimated, revealed that the genetic variability of this breed has been decreased mainly due to unbalanced contribution and excessive use of some breeding animals. The results revealed that the genetic variability in Markhoz goat was influenced by both gene losses during segregation and bottlenecks. A significant increase in inbreeding rate was observed. Although, estimated inbreeding rate per generation was not critical but it should be noted that careful management of mating decisions is of crucial aiming reduction of inbreeding. The current investigation confirmed the unfavorable effects of inbreeding on GFW, but not significant effect on pre-weaning growth traits. The results obtained from this study revealed the levels of inbreeding had not changed variance component and ranking of breeding value of animals.

Table 6

Correlation between PBVs of animals (inclusion or exclusion of inbreeding coefficient as covariate).

Traits[a]	r_p	r_s
BW (kg)	1.000	1.000
ADG (g/d)	0.921	0.920
WW (kg)	1.000	1.000
GFW (kg)	0.999	0.998

r_p = Pearson correlation coefficient; r_s = Spearman rank correlation coefficient.

[a] BW: birth weight; ADG: average daily gain from birth to weaning; WW: weaning weight; GFW: yearling greasy fleece weight.

Conflicts of interest

The authors declare that there are no conflicts of interest.

Acknowledgments

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