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Characterization of population structure and genetic diversity of Adani goats

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Abstract Characterization of population structure and genetic diversity of Adani goats of Iran was assessed through pedigree analysis by using the pedigree data on 2535 kids (offspring of 748 does and 106 bucks), collected for a period of 12 years (2003 through 2014). The kids born during 2011 to 2014 were considered as the reference population. A small proportion of kids (4.10%) were inbred with mean inbreeding coefficients of 0.31 and 7.68 % for the whole and inbred populations, respectively. The mean of generation interval, computed from four gametic pathways including sire-son, sire-daughter, dam-son and dam-daughter, was 2.87 years, with a longer interval from dam-progeny pathway relative to the sire-progeny ones. The effective population size estimated from the individual rate in inbreeding was 45.6. Probability of gene origin measures including the effective numbers of founders (f_e), ancestors (f_a), founder genomes (f_g) and non-founder genomes (f_{ng}) were 26, 25, 18 and 70, respectively. Approximately, 50% and 75 % of the total genetic variations were explained by the first 11 and 37 influential ancestors, with a maximum individual contribution of 11.8%. The ratio of f_e to f_a, as a measure of bottleneck, was 1.04. The average values for genetic conservation index (GCI) in whole, male and female individuals were 2.57, 2.85 and 2.36, respectively. The results revealed that although 3% of the total heterozygosity had been lost from the population, a considerable genetic variability still existed in the population of Adani goats.

Keywords: Adani goats, pedigree, inbreeding, ancestral contribution, genetic diversity

Introduction

Small ruminants play an important role in the livelihood of a significant portion of human population in the developing countries including Iran. These species mainly reared under low-input production systems by nomadic pastoralists are well adapted to the dry and harsh climatic conditions in the tropics (Kosgey and Okeyo, 2007). The Adani goat, one of the most important dairy native goat breeds, is generally kept by local farmers for milk production under low input systems in Boushehr province, south-western Iran. Moreover, the breed is regarded as a valuable source for the export market in the Persian Gulf states (Yazdanshenas et al., 2013). In any livestock enterprise, maintenance of genetic variability is a primary objective in the management of animal populations. Beside, setting up an efficient genetic improvement program for any breed requires the knowledge of genetic variation and genealogical structure of the population (Gutierrez et al., 2003). Maintenance of genetic variation at an acceptable level, by controlled inbreeding, is of great importance and will ensure that animals in the future can respond to changes caused by selection (van Wyk et al., 2009). Generally, local and/or regional climatic conditions, e.g., temperature, humidity, and precipitation, influence the spatial distribution of phenotypic and genetic variations in livestock species. Genetic diversity within gene pools determines the fitness/robustness (Goddard, 2009; Bijlsma and Loeschcke, 2012) and ultimately the adaptability of animals to the prevailing production environment. Genetic variability of population can be monitored by analyzing the pedigree information by evaluating the inbreeding level, effective population size, generation interval, genetic diversity, and several other important population parameters (Joezy-Shekalgorabi et al., 2017). Vozzi et al. (2007) pointed out that one of the undesirable consequence of genetic improvement programs is the loss of genetic diversity mainly due to increased inbreeding and loss of founder alleles through genetic selection and drift. Published reports are available on the genetic diversity of different Iranian native goat breeds using pedigree analysis (Rashidi et al., 2015; Joezy-Shekalgorabi et al., 2016; Mokhtari et al., 2017), but the detailed assessment of population structure and genetic variability of Iranian Adani breed is scanty. Therefore, the present study was conducted to assess the genetic variability and population structure of an experimental population of Adani goats, as one of the native goat breed for tropical region of Iran, through pedigree analysis.

Material and methods

Data collection

The pedigree information on 2535 Adani goats, maintained at the Adani Goats Breeding Center located in Agriculture-Jahad Organization of Bushehr, Tangestan city, Bushehr province, south-west of Iran, was collected from 2003 to 2014. The station is located in a hot and humid climate with an average annual rainfall of about 100 mm (Sadeghi et al., 2020). Animals were raised under the semi-intensive feeding conditions in their habitat, and allowed to graze for 6-7 hours per day and penned at night.

Genealogical parameters

Pedigree analysis was carried out on the whole population or a reference population using the program ENDOG v4.8 (Gutierrez and Goyache, 2005) to estimate the parameters such as the inbreeding coefficients, effective population size, effective number of founders, effective number of ancestors and effective number of founder genomes, etc. for describing the genetic diversity of the population. Kids born from 2011 to 2014 were considered as the reference population.

The individual inbreeding coefficients (F) were computed using the algorithm of Meuwissen and Luo (1992). Completeness of pedigree was evaluated by two measures, including the pedigree completeness index (PCI) and equivalent complete generations (EqG). The PCI was computed following the MacCluer et al. (1983) algorithm by EVA software (Berg et al., 2007). This procedure summarized the proportion of known ancestors in each ascending generation. The following equations (MacCluer et al., 1983) were used:

$$PCI=\frac{4C_{sire}C_{dam}}{C_{sire}+C_{dam}}$$

and

$$C=\frac{1}{d}\sum_{i=1}^{d} a_i$$

where, C_{sire} and C_{dam} are the proportions for contribution of sire and maternal lines, respectively. Furthermore, a_i represents the number of ancestors for each animal in the i^{th} generation and d is the number of generations.

Equivalent complete generation for individual i (EqG_i) was computed according to Maignel et al. (1996) as:

$$EqG_i=\sum(\frac{1}{2})^{n}$$

where, n denotes the number of generations separating the individual i from each known ancestor. The mean equivalent complete generations for the whole and reference populations were computed simply by averaging the individual equivalent complete generations.

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

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

Effective population size

The effective population size is the size of an ideal population, characterized by equal sex ratio, and absence of mutation, migration and selection, which has the same inbreeding rate as the real population under consideration (Menezes et al., 2015). The effective population size (N_e) was estimated based on the individual increases in inbreeding. The coefficients of individual increase 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:

$$\Delta F_i = 1 - \sqrt[EqG_i - 1]{1 - F_i}$$

where, the components of F_i and E_qG_i are the coefficient of inbreeding and the equivalent complete generation for individual *i*, respectively. The coefficients of individual increase in inbreeding are averaged and effective population size were estimated as (Falconer and Mackay, 1996):

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

Furthermore, effective population size was also estimated by regressing the individual inbreeding coefficients on the complete generations traced, maximum generations traced and equivalent complete generations (Maignel et al., 1996).

Probability of gene origin measures

Effective number of founders (f_e) denotes the numbers of equally contributing founders that would result in the same level of genetic diversity in the current population and was computed 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) 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):

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

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.

The effective numbers of founder genomes or founder genome equivalents (f_g) indicate that how many founders would be required to produce the same genetic diversity found in the population if all founders were contributing equally and no founder alleles were lost by the drift 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 population as follows:

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

The effective number of non-founder genomes (f_{ng}) considers only the effect of genetic drift in non-founder generations and was computed as follows (Caballero and Toro, 2000):

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

The degree of genetic diversity (G.D.) in the reference population in comparison to that existed in the base population was approximated as follows, where the genetic diversity is expressed as the expected heterozygosity (Lacy, 1989):

$$G.D. = 1 - \frac{1}{2f_g}$$

Genetic diversity in the base population was computed as:

$$G.D.^{*} = 1 - \frac{1}{2f_e}$$

The difference between genetic diversity in the base and reference populations was computed as (Caballero and Toro, 2000):

$$G.D.^{*} - G.D. = \frac{1}{2f_{ng}}$$

Genetic conservation index (GCI; Alderson, 1992) was computed from the genetic contributions of all the identified founders as:

$$GCI = \frac{1}{\sum p_i^2}$$

where, p_i is the proportion of genes of founder *i* in the pedigree of an animal. GCI is based on the assumption that the purpose of a conservation program is to maintain the full range of alleles possessed by the base population. The ideal individual would receive equal contributions from all the founder ancestors in the population and, consequently, the higher the GCI value the higher the value of an animal for conservation (Alderson, 1992).

Results and discussion

General considerations

The distribution of recorded animals per birth year is shown in Figure 1. The number of kids born in different years varied considerably, increasing from 2003-2007 and decreasing thereafter except in 2011. The mean age at first breeding was 2.38 and 2.88 years for Adani bucks and does, respectively. Summary statistics of the pedigree analysis is shown in Table 1. Overall, 43.55% of the kids were males and 55.45% females. Among the kids born with both parents known, 40.6 and 37.9 % were sired by 1-2 and 2-3 years old bucks, respectively. On the other hand, 37.2 % and 24.7% kids were progeny of of 1-2 and 2-3 years-old does, respectively.

Among registered animals, the percentage of kids

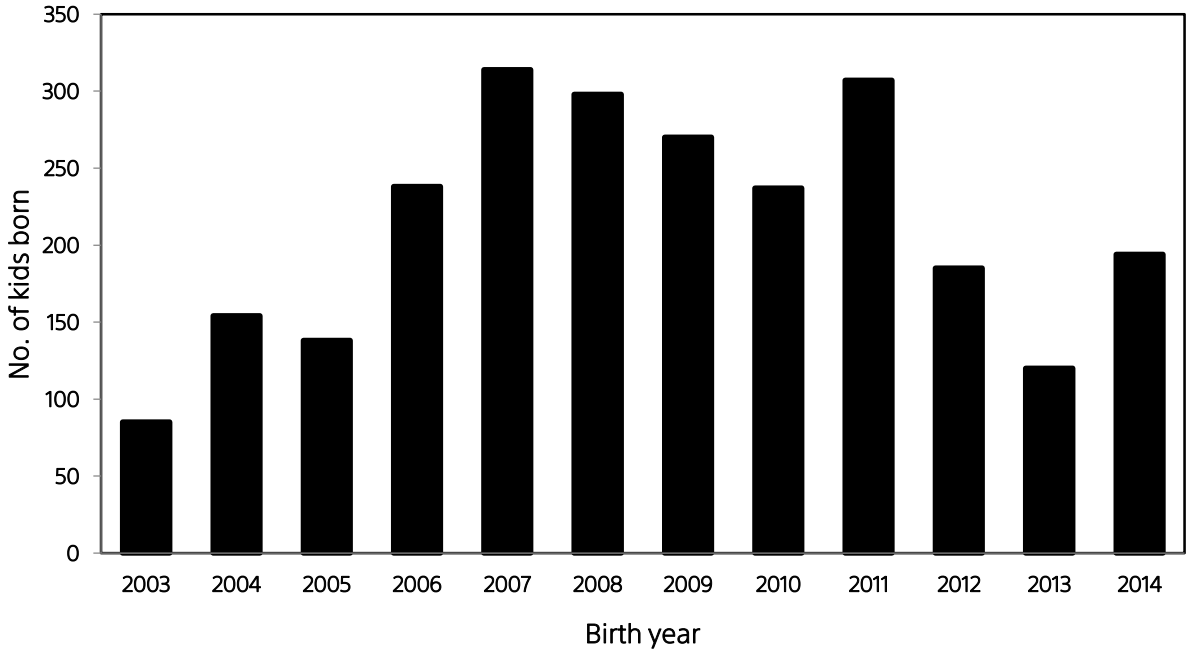

Figure 1. Number of Adani goats recorded per birth year

Table 1. Summary statistics of the pedigree analysis in Adani goats

Item	Whole	Male	Female
Total no. of animals	2535	1104	1431
No. of inbred animals	104	53	51
No. of non-inbred animals	2431	1051	1380
No. of animals with both parents unknown (founders; *f*)	471	46	425
No. of animals with one unknown parent	136	61	75
No. of animals with both parents known (non-founders)	1928	997	931
No. of animals with progeny	854	106	748
No. of animals without progeny	1681	998	683
Average number of discrete generation equivalents	1.22	1.06	1.43
Maximum number of discrete generation equivalents	3.47	3.28	3.47

with both parents unknown, one parent unknown and both parents known were 18.58, 5.36 and 76.06%, respectively. Animals with and without progeny constituted 33.68% (12.4% of male & 87.6% of female kids) and 66.32% (59.4% of male and 40.6% of female kids) of the registered kids. The mean number of kids per buck was 23.91. The offspring of 46% of bucks (49 out of 106 bucks) had no opportunity for breeding. On the other hand, 8 bucks had more than 10 kids with frequent use for breeding in the subsequent generations; which implies an unequal contribution of animals for breeding. The offspring of 68.77 % of does (512 out of 748 does) had no opportunity for breeding. Amongst the does, 19.03 %, 7.91 %, 2.82 % and 1.47 % had one, two, three and four kids selected for breeding, respectively.

Pedigree completeness index, equivalent complete generation and generation interval

The completeness, quality and depth of the pedigree affect the estimates of inbreeding coefficients, relationships among animals, and, to a lesser extent, generation intervals and effective numbers of founders and ancestors. In the present study, the average values for PCI for the whole and reference populations were 6.54% and 22.89%, respectively. Similarly, low PCI value (11%) was obtained by Oravcová (2013) in White Shorthaired goat. Oliveira et al. (2016) and Mokhtari et al. (2017) reported that the pedigree completeness was zero after fifth generation in Murciano-Granadina and Raeini Cashmere goats, respectively. Further pedigree integrity impacts accuracy of estimation of population parameters and genetic diversity in a population and may be assessed using the equivalent number of complete generations (Maignel et al., 1996). The evolution of equivalent complete generation throughout the study period is presented in Figure 2. In the present study, averages for equivalent complete generations in the whole population and reference population were obtained as 1.22 and 2.27, respectively. However, Oliveira et al. (2016) observed the lower (0.64) estimate for equivalent complete generation in Spanish Murciano-Granadina goat. Higher estimates than the present findings were reported by Rashidi et al. (2015) in Markhoz goat (5.84) and Danchin-Burge et al. (2012) in French goat breeds (5.5 to 7.8). The low PCI value for Adani goat population in our study is reflected by the low average equivalent generation of 1.22 in the whole population, showing a shallow structure for the studied pedigree of Adani goats.

In the present study, the mean generation interval of 2.87 years was well comparable with the reports of Portolano et al. (2004) in Girgentana goat (2.5 years), Lima et al. (2007) in Canindé and Graúna goats (2.75 and 2.87 years, respectively), León et al. (2005) in Granadina goat (2.88 years) and Oliveira et al. (2016) in Spanish Murciano-Granadina goat (2.77 years). In the current study, the higher mean generation interval of the dam-progeny pathways (dam-son = 3.28 and dam-daughter = 3.16 years), than the sire-progeny pathways (sire-son = 2.48 and sire-daughter = 2.56 years), maybe due to the

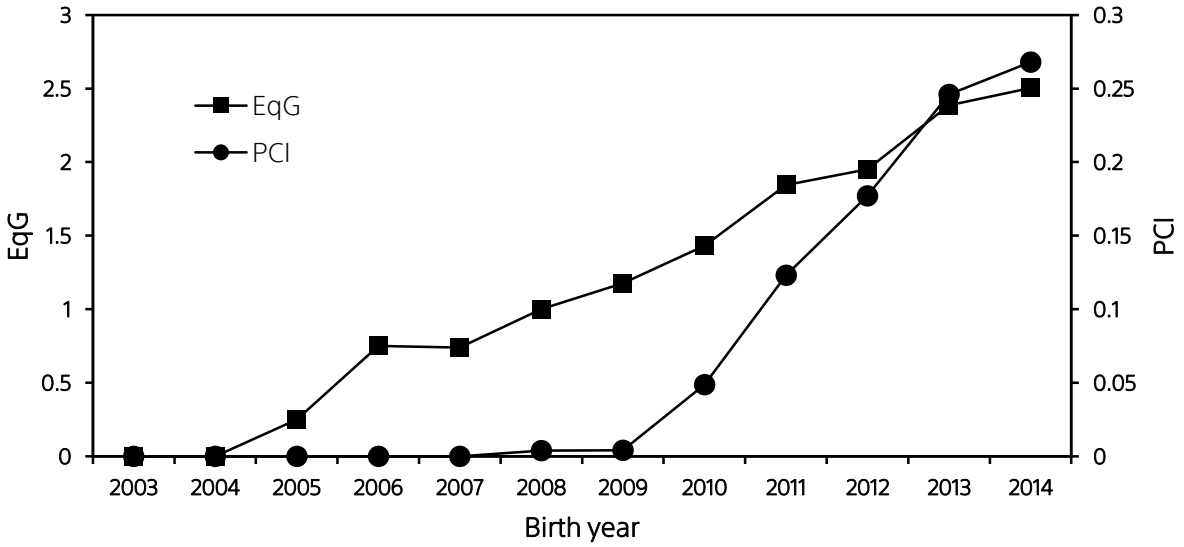

Figure 2. Evolution of the equivalent complete generation (EqG) and pedigree completeness index (PCI) for Adani goats

fact that breeding does are usually kept for more years to produce offspring than the sires. Similar findings were also observed by Rashidi et al. (2015) in Markhoz and Mokhtari et al. (2017) in Raeini Cashmere goats.

Inbreeding and average relatedness

Summary of the descriptive statistics on inbreeding coefficients in the studied population is shown in Table 2. In the studied population, a small proportion of kids (4.10%) were inbred with approximately equal sex ratio. The average inbreeding coefficients for all animals and inbred kids in the whole population were 0.31 and 7.68%, respectively, whereas the corresponding values for the reference population were 1.30 and 7.20%, respectively (Table 2). Similar estimate of the inbreeding coefficient (0.42%) in Iranian Adani goats was previously reported by Joezy-Shekalgorabi et al. (2016) who used multiple flock's data for this breed. However, estimates (ranging from 0.04 - 0.18%) smaller than our study were reported by several researchers (Joezy-Shekalgorabi et al., 2016; Mokhtari et al., 2017; Oliveira et al.,2016) in different goat breeds. In the present study, the low inbreeding level for the whole population may be due to lack of pedigree information rather than the absence of inbreeding because unknown relatives are presumed to be unrelated when calculating the inbreeding coefficients.

The evolution of average inbreeding coefficients and average relatedness of kids across the study period is shown in Figure 3, in which the inbreeding level of animals, which was practically nil from 2003 to 2007, gradually increased afterwards until 2012 and abruptly decreased in 2013 with a sharp increase in 2014. Such fluctuations may be ascribed to the introduction of unrelated sires from other flocks, as well the low quality of pedigree and/or mating policy planned for avoiding mating between related individuals. The average relatedness, inversely associated with the genetic diversity of a population, is a useful measure to manage the genetic diversity (Oliveira et al., 2016). In the present study, the mean average relatedness of all individuals and those in the reference population was 1.52% and 5.05%, respectively. The evolution of average relatedness of animals was similar to that of the average inbreeding coefficient of animals throughout the study period (Figure 1). Similar trends were observed in Brazilian Boer (Menezes et al., 2015) and Spanish Murciano-Granadina (Oliveira et al., 2016) goats. However, Joezy-Shekalgorabi

Table 2. Average inbreeding coefficients (%) for the whole and inbred populations of Adani goats by sex

	Whole population				Reference population			
	All animals		Inbred animals		All animals		Inbred animals	
	Mean ± SE	Range (%)	Mean ± SE	Range (%)	Mean ± SE	Range (%)	Mean ± SE	Range (%)
Both sexes	0.31±0.03	0-25	7.677±0.411	1.563-25	1.3±0.14	0-12.5	7.205±0.396	1.563-12.5
Male	0.37±0.06	0-12.5	7.665±0.53	3.125-12.5	1.5±0.23	0-12.5	7.745±0.573	3.125-12.5
Female	0.27±0.04	0-25	7.69±0.637	1.563-25	1.12±0.18	0-12.5	6.641±0.538	1.563-12.5

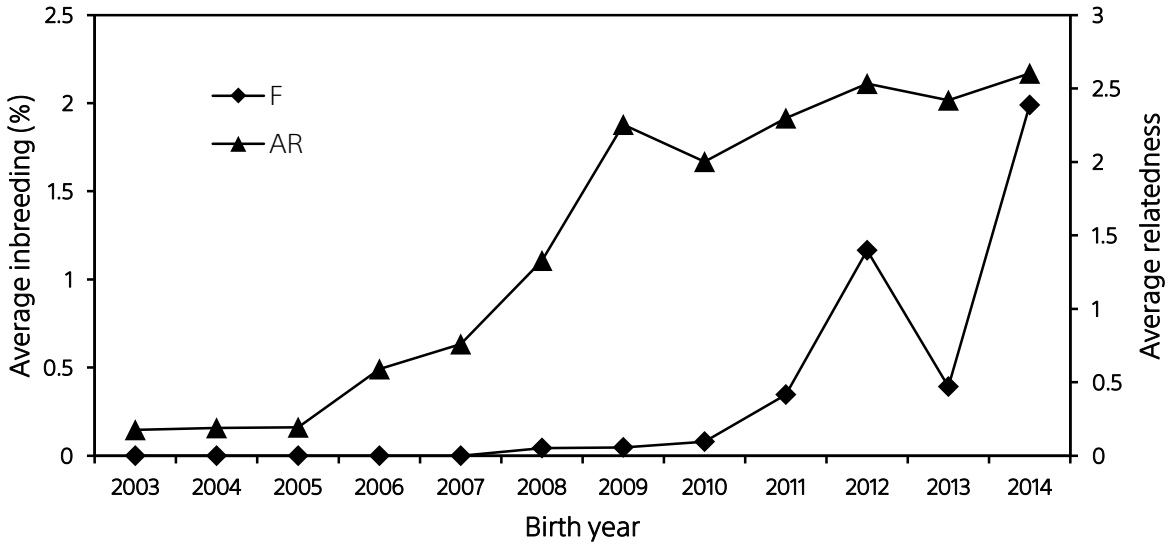

Figure 3. Evolution of the average inbreeding (F) and average relatedness (AR) for Adani goats

et al. (2016) obtained higher average relatedness value (2.36%) in Iranian Cashmere goat.

Effective population size

Estimating the effective population size, an important parameter in population genetics, is essential to assess the genetic viability of populations (Frankham et al., 2002). The effective population size denotes the number of breeding animals that would contribute to the observed rate of inbreeding in the recent generation under ideal conditions (Falconer and Mackay, 1996). In the present study, the estimated realized effective population size (*Ne*) based on individual increases in inbreeding was 45.6. Compared to the present findings, higher estimates for the effective population size via individual rate of inbreeding were reported by Oravcová (2013) in White Shorthaired goats (182); Menezes et al. (2015) in Boer goats (173.5) and Rashidi et al. (2015) in Markhoz goats (69). Danchin-Burge et al. (2012) also estimated the effective population size in Alpine (149), Saanen (129) and Angora goats (76) via individual increase in inbreeding, which was higher than our estimate. However, Baldursdottir et al. (2012) reported lower effective population size of 5.1 in Icelandic goats using the population data. In this study, differences in *Ne* resulted when inbreeding coefficients were regressed on the number of complete generations, maximum generations and equivalent complete generations, yielding *Ne* values of 75.3, 143.22 and 88.36, respectively. Published literature on the estimation of *Ne* by different methods using pedigree information in various domestic species showed that assessing the critical level for *Ne* is not straightforward and it should be discussed considering the factors like method used, species, and population structure (Leroy et al., 2013). Furthermore, it should be kept in mind that estimates of *Ne* may vary with the changes in inbreeding level of the population across generations.

Probability of gene origin measures

In the present study, the total number of founders (*f*) contributed to the reference population and the effective number of founders (f_e) were 184 and 26, respectively (Table 3); indicating the excessive use of some animals as the parents. However, Joezy-Shekalgorabi et al. (2016) obtained higher total number of founders and effective number of founders in Cashmere goat breed of South Khorasan. Portolano et al. (2004) reported the 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 and the total number of founders was approximately 0.14; indicating disequilibrium among founder contributions in Adani goats. Similarly, low ratios of effective number of founder to total number of founders were observed by Portolano et al. (2004) in Italian Girgentana (0.25), Rashidi et al. (2015) in Markhoz (0.14) and Mokhtari et al. (2017) in Raeini Cashmere goats (0.17). Unequal contribution of founders in a population was taken into account by using the effective number of founders (Lacy, 1989). Whenever a bottleneck is imposed on a population, f_e will be overestimated due to ignoring the possible effects of bottleneck (Boichard et al., 1997). Fur-

Table 3. Parameters characterizing the probability of gene origin in Adani goats

Item	N
Total no. of animals in the population	2535
No. of animals in the reference population	499
No. of founders contributing to the reference population	184
Effective no. of founders for the reference population (f_e)	26
No. of ancestors contributing to the reference population	178
Effective no. of ancestors in the reference population (f_a)	25
No. of ancestors explaining:	
50% of the gene pool	11
75% of the gene pool	37
100% of the gene pool	178
Contribution of the main ancestor (%)	11.80
Expected inbreeding (%) due to unequal founder contributions (%)	0.7
Effective no. of founder genomes for the reference population (f_g)	19
Effective no. of non-founder genomes for the reference population (f_{ng})	70
Genetic conservation index (GCI) for whole population	2.57
GCI for males	2.85
GCI for females	2.36

ther, Boichard et al. (1997) pointed out that f_a complements the information provided by the f_e taking the losses of genetic variation into account; caused by the unbalanced use of breeding animals producing bottleneck. Table 3 showed the large differences between total (178) and effective number of ancestors (25), indicating unequal ancestor contributions in the studied population of Adani goats. The ratio between effective number of ancestors and the total number of ancestors was approximately 0.14 in this study was well comparable with the estimates of 0.12 in Raeini Cashmere goats (Mokhtari et al., 2017). Estimate of the effective number of ancestors (f_a) in our study (25) was lower than the estimates of Oravcová (2013) in White Shorthaired goats (45), Menezes et al. (2015) in Boer goats (56), Oliveira et al. (2016) in Murciano-Granadina goats (965), Joezy-Shekalgorabi et al. (2016) in Cashmere goat (60) and Mokhtari et al. (2017) in Raeini Cashmere goats (137).

Boichard et al. (1997) stated that evaluation of the loss in genetic diversity that exists in the founders because of the bottleneck between the base and reference population can be studied by applying the ratio of f_e/f_a; the ratio of effective number of founders to effective number of ancestors. The greater the f_e/f_a ratio, the more stringent the bottlenecks. If all founders contribute their genes to the next generations, the maintenance of the original genetic diversity is ensured and, in such situation, the f_e will be equal to f_a (Oliveira et al., 2016). Anyhow, it should be noted that the parameters estimated for describing genetic diversity of population based on probabilities of gene origin are less sensitive to pedigree completeness as compared to parameters based on identity-by-descent of genes (Boichard et al., 1997). In this technique, genetic diversity in a given population is assessed by measuring the genetic contributions of the founder animals. Since knowledge of the total number of founders is insufficient to ascertain the genetic basis of the population, owing to unknown pedigrees and the unequal contribution of founders to the genetic composition of the following generation, Lacy (1989) proposed the concept of effective number of founders, thereby accounting for the unequal contribution of founders and the idea of founder genome equivalents as well as bottlenecks and random loss of alleles due to genetic drift. When accurate records have been kept, then the information on the genetic size of a population can be obtained by analyzing the pedigree information. Pedigree analysis allows the population manager to assess the genetic structure of the population and to plan appropriate breeding strategies aimed at making a balance between the genetic response and loss of genetic diversity (Ghafouri-Kesbi, 2010).

In the present study, the ratio of f_e/ f_a was 1.04, near the ideal value of 1, for the Adani goat population. Oliveira et al. (2016) obtained an ideal value of 1 for the ratio of f_e/ f_a in Spanish Murciano-Granadina goats. However, higher ratios were observed by Oravcová (2013) in White Shorthaired goats (1.6), Rashidi et al. (2015) in Markhoz goats (1.32), Menezes et al. (2015) in Boer goats (2.38) and Mokhtari et al. (2017) in Raeini Cashmere goats (1.76). Compared to present findings, smaller ratios of f_e/ f_a ranging from 0.22-0.41 were reported by Danchin-Burge et al. (2012) in Alpine, Saanen and Agora goat breeds. The obtained f_e/ f_a ratio in this study (1.04) for Adani goat indicated the population was stable in terms of effective contribution of ancestors, and showed the bottleneck has not played any significant role in the population.

In the present study, out of 178 ancestors, only 11 and 37 ancestors contributed 50% and 75% of the genetic diversity in the reference population, respectively. The most influential ancestor explained 11.8% of the genetic diversity in the reference population. Oravcová (2013) estimated that 15 ancestors accounted for 50% of the genetic variability in White Shorthaired goat population.

The founder genome equivalents (f_g), which deals with the loss in variability, is directly associated with genetic diversity but it does not take mutation and/or migration into account (Ghafouri-Kesbi, 2010). In the current study, the estimated f_g value of 19.08 was close to the value of 26 in Markhoz goats (Rashidi et al., 2015). The lower f_g value in the present study denotes the existence of lower proportions of the founders' genes. The f_g/f_a ratio indicated that 79.2% of the ancestral genetic diversity was still present in the reference population. Estimated values of f_e, f_a, and f_g (Table 3) were smaller than estimates of the realized effective population size (45.6), suggesting the Adani goat population was increasing in effective size.

The effective number of non-founder genome (f_{ng}) takes the effect of genetic drift in non-founder generations into account and provides information on the relative importance of random genetic drift accumulated in non-founder generations and unequal contribution of founders regarding the loss of genetic diversity. The estimated value for f_{ng} in the present study was 70.19 (Table 3), which was close to the estimates of Joezy-Shekalgorabi et al. (2016) in Cashmere goat (68.7) and Rashidi et al. (2015) in Markhoz goat (56). However, Joezy-shekalgorabi et al. (2017) obtained smaller values for Ira-

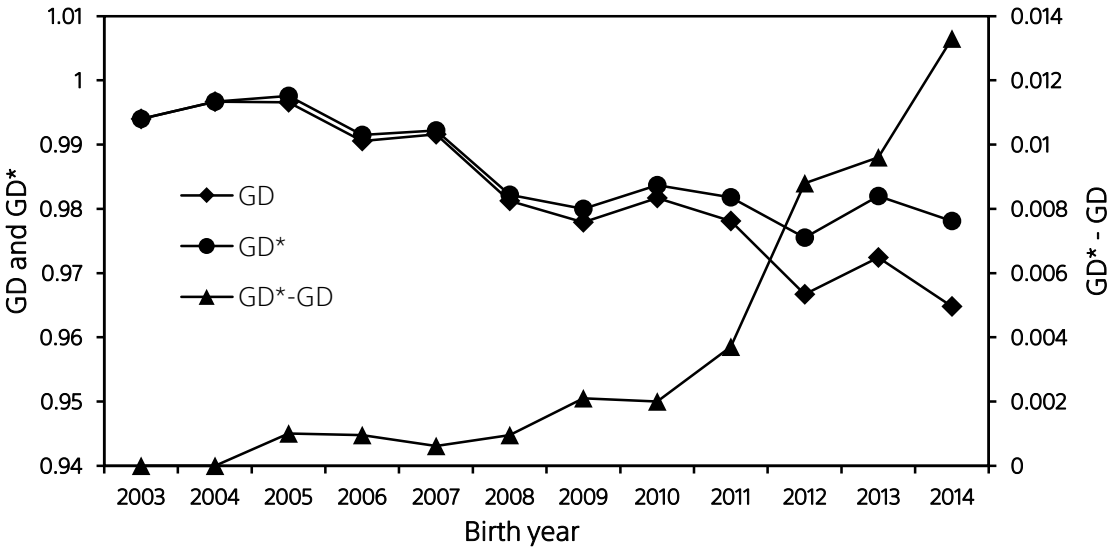

Figure 4. Evolution of genetic diversity in the reference population (GD), base population (GD*) and their difference (GD*-GD) in Adani goats

nian Adani goat (53.09). When the f_e is higher than f_{ng}, as observed in the current study, it can be concluded that the reduction in genetic variability is more due to the genetic drift accumulated in the non-founder generation.

The coefficient of genetic diversity considers the impact on heterozygosity of unequal contribution of founder genes and genetic drift (Lacy 1989). Evolution of genetic diversity in the reference population (GD), base population (GD*), and their difference (GD*-GD) during the study period is shown in Figure 4. The estimated value for GD was 0.97, indicating that about 3% of the genetic diversity existed in the base population was lost during the studied period.

The genetic conservation index (GCI) which can be used at an individual-animal level to monitor intra-population genetic diversity, was 2.57 for the whole population, and the GCI values for male and female individuals were 2.85 and 2.36, respectively (Table 3). Smaller GCI value (1.64) was obtained by Oliveira et al. (2016) in Spanish Murciano-Granadina goats. However, larger value of 7.35 was reported in Brazilian Boer goat (Menezes et al., 2015). The small GCI value in Adani goat may partly be due to shallow pedigree and low contribution of founders in the population.

Conclusions

The level of inbreeding was low in the studied population of Adani goats. The animals with unknown parents (one or both ones) constituted about 24% of all animals; therefore, the inbreeding coefficient of animals might have been underestimated. For developing any breeding and / or conservation program in Adani goats, accurate registration of pedigree information is crucial. Estimates of the effective numbers of founders, ancestors, founder genomes, and non-founder genomes indicated that unequal contributions of founders and bottleneck had not played any significant role in the population. Approximately, 3% of the total heterozygosity was lost from the population, but considerable genetic variability existed in the population. Because of the low quality pedigree available, the genealogical parameters should be interpreted with cautious in the light of factors such as pedigree completeness.

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