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Short communication

Genetic diversity in Kermani sheep assessed from pedigree analysis

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ABSTRACT

Genetic diversity in Kermani sheep was assessed using the pedigree records by quantifying demographic parameters under pedigree analysis via studbook information collected from 1990 to 2011 in the breeding station of Kermani sheep, Sharebabak, south-east of Iran. Lambs born during 2008–2011 were considered as reference population. The mean generation interval from four pathways was 4.48 years. The generation interval in sire-progeny pathway was longer than dam-progeny. Mean inbreeding and average coancestry for reference population were computed as 0.51% and 1.04%, respectively. Average equivalent complete generation, as a measure of pedigree completeness, was 2.22. Effective population size was estimated to be 100 from the individual rate in coancestry and 120 from the individual increase in inbreeding. Genealogical parameters estimated based on probabilities of gene origin including the effective number of founders, the effective number of ancestors, the effective number of founder genomes (founder genome equivalents) and the effective number of non-founder genomes for reference population were estimated as 149, 72, 48 and 71, respectively. Approximately, 50% of total genetic variation was explained by the 33 most influential ancestors, with a maximum individual contribution of 4.8%. The average relationship coefficient among active rams and the average relationship coefficient between active rams and ewes during the last 4 years (2008–2011) were 0.11 and 0.05, respectively. The results indicated that although some evidences on bottlenecks and genetic drift during recent years were identified in the studied population, a relatively considerable genetic variability exists in this population.

1. Introduction

An undesirable consequence of genetic improvement programs is loss of genetic diversity mainly because of the increased inbreeding and loss of founder alleles through genetic selection and drift (Vozzi et al., 2007). Maintaining genetic diversity at a high level and at the same time inbreeding at a low level is a primary goal in the management of animal populations (Fernandez et al., 2005). Monitoring genetic diversity using pedigree information is an efficient and cost-effective approach. Kermani sheep is one of the most important Iranian native sheep breeds and well adapted to harsh environmental conditions of south-eastern part of country, here dry and hot weather

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is prevalent and pastures are of low quality and quantity. The breeding station of Kermani sheep may act as a main part of nucleus-based breeding schemes for genetically improvement of this breed, dissemination of superior animals into local flocks and thereby enhancement of production efficiency. Given that pedigree recording is exception in Iran, there are rare reports concerning pedigree analysis of Iranian native sheep breeds and mainly limited to recently published papers (Ghafouri-Kesbi, 2010, 2012; Tahmoorespour and Sheikhloo, 2011). The aim of the present study was to study demographic parameters and the status of genetic diversity in Kermani sheep using pedigree analysis.

2. Materials and methods

Pedigree records used in the present study were collected during 21 years period (1990–2011) derived from the breeding station of Kermani sheep situated in Shahrebabak, Kerman Province, south-east of Iran. The lambs born from 2008 to 2011 were considered as reference population. In the breeding station performance records of animals were collected and superior animals were disseminated into pastoral flocks. Lambs were weighed and ear-tagged at birth and their sex, birth type, dam age and identifications of their sire and dam were recorded. A detailed description on flock management has been reported by Mokhtari et al. (2010). The coefficient of inbreeding (F) for each individual was computed using an algorithm from Meuwissen and Luo (1992). The coancestry coefficients (f) of animals were also calculated (Malécot, 1948). The mean additive relationship coefficients of each male lamb born during 2008–2011 with other animals in the flock were calculated. Then, the scatter diagram of the mean additive relationship coefficients of the male lambs born with active rams and ewes was plotted to identify the newborn rams which have low relationship coefficients to the current active rams and ewes.

The generation interval was calculated as the average age of the parents at the birth time of their progeny kept for reproduction and was computed by averaging the four genetic pathways, sire to son (L_{ss}), sire to daughter (L_{sd}), dam to son (L_{ds}) and dam to daughter (L_{dd}). Completeness of pedigree was assessed by the proportion of lambs in the whole file with both parents known and by addressing the equivalent complete generations. Individual equivalent complete generations were calculated according to Maignel et al. (1996). Average equivalent complete generations for whole and reference population was computed simply by averaging individual equivalent complete generations. The effective population size (N_e) was obtained by two approaches for a comparison to see if the rotational mating is being effective. The first was computed following the approach proposed by Cervantes et al. (2011) using the rate of coancestry for all pairs of individual in a reference population. The second approach was proposed by Gutiérrez et al. (2009) and based on individual increase in inbreeding. Four measures based on probability of gene origin included the effective numbers of founders (f_e) that denote the numbers of equally contributing founders that would result to the same level of genetic diversity in the current population (Lacy, 1989), the effective numbers of ancestors (f_a) as the minimum numbers of ancestors, not necessarily founders, explaining the complete genetic diversity of the current population (Boichard et al., 1997), the effective numbers of founder genomes or founder genome equivalents (f_g) indicating 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 by drift under random mating and the effective numbers of non-founder genomes (f_{ne}) that considers only the effect of genetic drift in non-founder generations (Caballero and Toro, 2000). Genealogical parameters were estimated using the ENDOG v4.8 program (Gutierrez and Goyache, 2005).

3. Results and discussion

The results of pedigree analysis are shown in Table 1. A low proportion (about 3.7% of the total lambs) of the recorded lambs were inbred. Mean inbreeding coefficients of 0.51% and 4.87% were obtained in the total and inbred individuals, respectively. Ghafouri-Kesbi (2010) estimated a value of 1.46% for mean inbreeding in Zandi sheep. The difference in mean of inbreeding could be ascribed to the population size structure and different number of equivalent generations. The mean generation interval was 4.48 years. The generation intervals across four pathways were as L_{ss} = 4.73 years, L_{sd} = 4.72 years, L_{ds} = 4.57 years and L_{dd} = 4.22 years. The generation interval in sire-progeny pathways was slightly longer than the dam-progeny pathways. Relatively high generation interval obtained may be explained partly by intensive use of a few breeding animals within the flock. Higher generation interval for ram-progeny pathways would be attributable to the fact that breeding rams had usually been employed longer to produce offspring than the ewes. Average coancestry in the reference population was 1.04%. The average coancestry of the animals in a population forecasts the average of inbreeding coefficient in the subsequent generations. The realized effective population size estimates based on individual increase in coancestry and on individual increase in inbreeding were 100 and 120, respectively. An effective population size of 50 was determined by FAO (1998) as a critical level for an animal population. The results of a recently published paper on estimation of effective population size using pedigree data under different methods across several domestic species shown that the determination of a strict critical level for effective population size is not straightforward and estimated effective population size should be interpreted in the light of factors such as method used, species and population structure (Leroy et al., 2013). In this study, the effective population size based on individual increase in coancestry was lower than

Table 1
Summary statistics of the pedigree analysis in Kermani sheep.

Item	Value
No. of animals in whole population	3562
No. of animals with progeny	1299
No. of animals without progeny	2263
No. of animals with both known parents	2069
No. of animals with both unknown parents	422
No. of animals with one unknown parent	1071
No. of animals in reference population	292
Mean inbreeding in reference population (%)	0.51
Average coancestry in reference population (%)	1.04
No. of equivalent complete generations in reference population	2.22
No. of founders	420
No. of ancestors	289
Effective population size[a]	100
Effective population size[b]	120
Effective no. of founders (f_e)	149
Effective no. of ancestors (f_a)	72
Founder genome equivalent (f_g)	48
Effective no. of non-founder genomes (f_{ne})	71
No. of ancestors explaining 50% of genetic variation	33

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