

Contents lists available at [SciVerse ScienceDirect](http://SciVerse.ScienceDirect.com)

## Small Ruminant Research

journal homepage: [www.elsevier.com/locate/smallrumres](http://www.elsevier.com/locate/smallrumres)

Short communication

### Genetic diversity in Kermani sheep assessed from pedigree analysis



M.S. Mokhtari <sup>a,b,\*</sup>, M. Moradi Shahrabak <sup>b</sup>, A.K. Esmailzadeh <sup>c</sup>,  
R. Abdollahi-Arpanahi <sup>b</sup>, J.P. Gutierrez <sup>d</sup>

<sup>a</sup> Department of Animal Science, Faculty of Agriculture, University of Jiroft, P.O. Box 364, Jiroft, Iran

<sup>b</sup> Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran, P.O. Box 31587-77871, Karadj, Iran

<sup>c</sup> Department of Animal Science, Faculty of Agriculture, Shahid Bahonar University of Kerman, P.O. Box 76169-133, Kerman, Iran

<sup>d</sup> Departamento de Produccion Animal, Facultad de Veterinaria, Avda. Puerta de Hierro s/n, E-28040 Madrid, Spain

#### ARTICLE INFO

##### Article history:

Received 18 March 2013

Received in revised form 29 June 2013

Accepted 2 July 2013

Available online 22 July 2013

##### Keywords:

Pedigree

Genetic diversity

Genealogical parameters

Kermani sheep

#### 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.

© 2013 Elsevier B.V. All rights reserved.

#### 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

\* Corresponding author at: Department of Animal Science, Faculty of Agriculture, University of Jiroft, P.O. Box 364, Jiroft, Iran.  
Tel.: +98 2632248082; fax: +98 2632246752.

E-mail address: [msmokhtari@ut.ac.ir](mailto:msmokhtari@ut.ac.ir) (M.S. Mokhtari).

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 Sheikhlou, 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 Shahrehabak, 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 (Gutiérrez 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

**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 <sup>a</sup>                         | 100   |
| Effective population size <sup>b</sup>                         | 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    |

<sup>a</sup> Estimated based on individual increase in coancestry.

<sup>b</sup> Estimated based on individual increase in inbreeding.

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

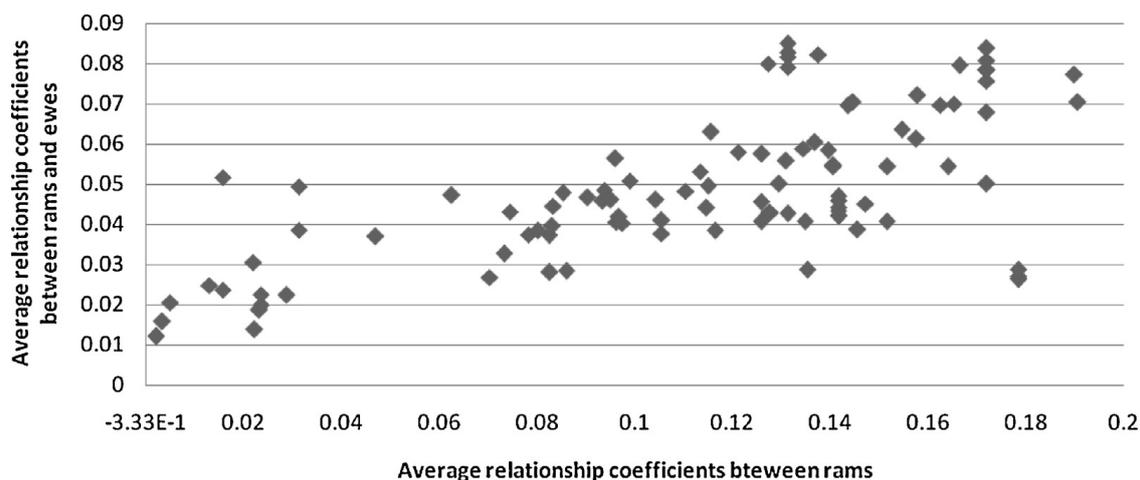


Fig. 1. Average relationship coefficient among rams against average relationship between rams and ewes in breeding animals born during 2008–2011.

that obtained based on individual increase in inbreeding. Therefore, it can be concluded that rotational mating was effective for avoiding inbreeding. The estimated values of  $N_e$  suggest an acceptable level of effective population size. Nevertheless, it should be noted that estimates of  $N_e$  may vary following changes in inbreeding level of the population across generations. In the present study, average equivalent complete generation, as a measure of pedigree completeness level, was low (2.22) for the reference population. Higher average equivalent complete generation has been reported by Tahmoorespour and Sheikhlou (2011) in Baluchi sheep (5.47). A value of 149 was estimated for the effective numbers of founders ( $f_e$ ) while the numbers of founders contributed in the reference population was 420 indicating the excessive use of some animals as parents. Ghafouri-Kesbi (2010) reported an estimate of 86 for  $f_e$  in Zandi sheep with a total of 615 individuals in the reference population. In our study, the ratio of the effective numbers of founders to the total numbers of founders was computed as 0.35 indicating unbalance in contribution of founders to the reference population. Lower corresponding ratio of 0.24 was reported by Goyache et al. (2003) in Xalda and Zandi sheep. The estimation of the effective numbers of ancestors ( $f_a$ ) is of paramount importance. The  $f_a$  and the total numbers of ancestors contributed in the reference population were obtained as 72 and 289, respectively. Estimated value for  $f_a$  in the present study was in agreement with the value computed by Ghafouri-Kesbi (2010) in Zandi sheep (74). Boichard et al. (1997) stated that evaluation of the loss in genetic diversity that exists in the founders due to the bottleneck between the base and the reference populations can be accomplished using a ratio of the effective numbers of founders to the effective numbers of ancestors ( $f_e/f_a$ ). The importance of bottleneck in the population under consideration can be assessed applying the above-mentioned ratio; the greater the  $f_e/f_a$  ratio, the more stringent the bottlenecks. The ideal value for this ratio would be one. In the present study a value of 2.07 was computed for the  $f_e/f_a$  ratio in the reference population implying that unbalancing between ancestors and founders resulted in reduction of genetic variability. The founder genome equivalents ( $f_g$ ) were estimated as 48. The lower  $f_g$  in a reference

population suggests the presence of lower proportions of the genes of founders. The  $f_g$  parameter accounts for the total loss in diversity and is directly associated with genetic diversity but it does not consider mutation. Comparisons between the three parameters of  $f_e$  (149),  $f_a$  (72) and  $f_g$  (48) and  $N_e$  allow concluding if the population can be considered as increasing or decreasing in the genetic variability. In the foundation, there was 149, but then decreased due to bottlenecks (72) and other causes (48), being actually reproducing as more (100), probably because an increase in the census and a correct use of mating design.

The effective number of non-founder genome ( $f_{ne}$ ) was 71. It considers the effect of genetic drift in non-founder generations 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. If  $f_e > f_{ne}$ , the reduction in genetic diversity would be more attributable to genetic drift accumulated in non-founder generation and where  $f_e < f_{ne}$  the unequal contribution of founders would be considered as the main influencing factor affecting the loss of genetic diversity. Among all ancestors contributed in the reference population 50% of genetic diversity was explained by 33 ancestors with maximum individual contribution of 4.8%. The scatter plot of average relationship coefficients between ram lambs and other rams (breeding rams from 2008 to 2011) against those between ram lambs and ewes is shown in Fig. 1. Average corresponding relationship coefficients were 0.11 and 0.05, respectively. The aim of this analysis was to identify rams with a low relationship coefficient with the rams and ewes that exists in the current population of Kermani sheep. This would be of crucial importance for conserving genetic diversity in this population. A total of 37 rams among 102 rams were identified as having average relationship coefficients less than 0.10, with other rams and ewes. The remaining 65 rams had minimum and maximum average relationship coefficients of 0.10 and 0.19 with other rams, respectively. The corresponding minimum and maximum relationship coefficients of the rams with ewes were 0.03 and 0.09, respectively.

In general, analysis of pedigree related to Kermani sheep revealed evidence for changes in population structure and demographic parameters. It can be concluded that the mating strategies to minimize inbreeding in the flock were appropriate. Analysis of relationships between rams born during 2008–2011 and other rams revealed a higher average relationship than that obtained between recently born rams and ewes. Therefore, minimization of genetic relationships between breeding animals is of high importance for long-term maintenance of genetic diversity.

## References

- Boichard, D., Maignel, L., Verrier, E., 1997. The value of using probabilities of gene origin to measure genetic variability in a population. *Genet. Select. Evol.* 29, 5–23.
- Caballero, A., Toro, M.A., 2000. Interrelations between effective population size and other pedigree tools for the management of conserved populations. *Genet. Res.* 75, 331–343.
- Cervantes, I., Goyache, F., Molina, A., Valera, M., Gutiérrez, J.P., 2011. Estimation of effective population size from the rate of coancestry in pedigreed populations. *J. Anim. Breed. Genet.* 128, 56–63.
- Fernandez, J., Villanueva, B., Pong-Wong, R., Toro, M.A., 2005. Efficiency of the use of pedigree and molecular marker information in conservation programs. *Genet. Select. Evol.* 170, 1313–1321.
- Food Agriculture Organization, 1998. Secondary Guidelines for Development of National Farm Animal Genetic Resources Management Plans. Page 63 in Management of Small Populations at Risk. Food Agric. Org. United Nations, Rome, Italy.
- Ghafouri-Kesbi, F., 2010. Analysis of genetic diversity in a close population of Zandi sheep using genealogical information. *J. Genet.* 89, 479–483.
- Ghafouri-Kesbi, F., 2012. Using pedigree information to study genetic diversity and reevaluating a selection program in an experimental flock of Afshari sheep. *Arch. Tierz.* 55, 375–384.
- Goyache, F., Gutierrez, J.P., Fernandez, I., Gomez, E., Alvarez, I., Diez, J., Royo, L.J., 2003. Using pedigree information to monitor genetic variability of endangered populations: the Xalda sheep breed of Asturias as an example. *J. Anim. Breed. Genet.* 120, 95–103.
- Gutierrez, J.P., Goyache, F., 2005. A note on ENDOG: a computer program for analysing pedigree information. *J. Anim. Breed. Genet.* 122, 357–360.
- Gutiérrez, J.P., Cervantes, I., Goyache, F., 2009. Improving the estimation of realized effective population sizes in farm animals. *J. Anim. Breed. Genet.* 126, 327–332.
- Lacy, R.C., 1989. Analysis of founder representation in pedigrees: founder equivalents and founder genome equivalents. *Zoo Biol.* 8, 111–123.
- Leroy, G., Mary-Huard, T., Verrier, E., Danvy, S., Charvolin, E., Danchin-Burge, C., 2013. Methods to estimate effective population size using pedigree data: examples in dog, sheep, cattle and horse. *Genet. Select. Evol.* 45, 1.
- Maignel, L., Boichard, D., Verrier, E., 1996. Genetic variability of French dairy breeds estimated from pedigree information. *Interbull Bull.* 14, 49–54.
- Malécot, G., 1948. *Les Mathématiques de l'Hérédité*. Massonet Cie, Paris, 80 pp.
- Meuwissen, T.H.E., Luo, Z., 1992. Computing inbreeding coefficients in large populations. *Genet. Select. Evol.* 24, 305–313.
- Mokhtari, M.S., Rashidi, A., Esmailzadeh, A.K., 2010. Estimates of phenotypic and genetic parameters for reproductive traits in Kermani sheep. *Small Rumin. Res.* 88, 27–31.
- Tahmoorespour, M., Sheikhlou, M., 2011. Pedigree analysis of the closed nucleus of Iranian Baluchisheep. *Small Rumin. Res.* 99, 1–6.
- Vozzi, P.A., Marcondes, C.R., Bezerra, L.A.F., Lobo, R.B., 2007. Pedigree analyses in the breeding program for Nellore cattle. *Genet. Mol. Res.* 29, 482–485.