

GENETIC VARIABILITY OF IRANIAN ADANI GOAT BREED USING PEDIGREE ANALYSIS

S. Joezy-Shekalgorabi^{1*}, A. Maghsoudi², A. Taheri-Yeganeh³ and B. Rajabi-Marand⁴

¹Young Researchers and Elites club, Shahr-e-Qods Branch, Islamic Azad University, Tehran, Iran

²Department of Animal Science, Faculty of Agriculture, and Center of Agricultural Biotechnology, University of Zabol, Zabol, Iran; ³Animal Breeding and Milk Improvement Center, Ministry of Jihad Agriculture, Karaj, Iran

⁴Department of Animal Science, College of Agriculture and Natural Resources, University of Tehran, Karaj, Iran

*Corresponding Author email: s_joezy@qodsiau.ac.ir ; joezy5949@gmail.com

ABSTRACT

In the current research, genetic diversity of Iranian Adani dairy goat was assessed utilizing pedigree analysis. Pedigree records from a total of 2985 animals during 1999-2013 were analysed. A total of 96 animals were inbred. The average inbreeding coefficients in the whole, the inbred and the reference population (living reproductive animals born from 2009 to 2013) were found 0.24, 7.33 and 0.56 %, respectively. The low inbreeding coefficient obtained for Adani dairy goat was mainly related to the lack of sire registration in a large number of animals (about 44.4% missing sire information). Low ratio of the effective number of founders (fe) to the total number of founders (f) ($fe/f=0.13$) for Adani goat breed represents unbalanced contribution of founders to the reference population. Effective number of ancestors (fa) was equal to 39. The Ratio of fe to fa was 1.44 which could be a result of occurring genetic bottleneck in the population and the use of a limited number of parents across generations. Low equivalent generation obtained for the Adani dairy goat indicates low pedigree depth in the studied breed and the need for using molecular based methods to overcome the problem of pedigree incompleteness in this breed.

Keywords: Adani dairy goat, Inbreeding, Iran, Pedigree analysis.

INTRODUCTION

The increased extinction of farm animal biodiversity has increased the necessity for preserving rare livestock breeds (Scherf, 2000). Genetic adaptability of a breed to different environmental conditions depends significantly on the breed genetic biodiversity (Baldursdottir, 2010). Intense genetic selection, inbreeding and drift are the main reasons for loss of genetic biodiversity of a population (Hammami *et al.*, 2007; Vozzi *et al.*, 2007).

The national goat population of Iran amounts to more than 25 million heads (FAO, 1998; Ansari-Renani *et al.*, 2013). The Adani dairy goat is one of the most important indigenous goat breeds of Iran and is reared in the coastal area of the Persian Gulf in Boushehr province. The province is located in South-western region of Iran. In spite of high average temperatures, humidity and low quality and quantity pastures, the breed has been well adapted to the harsh environmental conditions. At the same time, the breed has been regarded as a valuable source for the export market in Persian Gulf region countries (Yazdanshenas *et al.*, 2013). The official breed registry on Adani goat was established in the year 1999. A few flocks of this breed are included in performance records. Currently, the recorded population involves 800-900 animals.

Monitoring the genetic diversity within a population needs the regular evaluation of average relationship and inbreeding coefficient as well as effective population size (Groeneveld *et al.*, 2010). Pedigree analysis is considered as an appropriate method for evaluation of the genetic diversity. With the use of pedigree analysis, changes of genetic diversity could be traced by monitoring inbreeding coefficient of a population. Utilizing parameters based on probability of gene origin (such as effective number of founders and founder genome equivalent) could help with a more accurate prediction of the genetic biodiversity (Solkner *et al.*, 1998; Honda *et al.*, 2004). The population structure, as a characteristic of the underlying pedigree, is considered as a key factor in applying genetic association studies. Pedigree analysis has been performed in various livestock species including pig (Melka and Schenkel, 2010; Veroneze *et al.*, 2014; Szabó *et al.*, 2015), sheep (Li *et al.*, 2009; Mokhtari *et al.*, 2014), cattle (Vozzi *et al.*, 2006; Mc Parland *et al.*, 2007; Oliveira *et al.*, 2012; Pienaar *et al.*, 2015), buffalo (Marcondes *et al.*, 2014), horse (Hasler *et al.*, 2011), donkey (Gutierrez *et al.*, 2005; Cecchi *et al.*, 2006) and in pet animals (Leory *et al.*, 2009; Cecchi *et al.*, 2013). Genetic diversity of some goat breeds have also been evaluated through this method (Portolano *et al.*, 2004; Mucha and Windig, 2009; Baldursdottir, *et al.*, 2012; Oravcova, 2013). In some recent published studies, pedigree analysis has been

performed in Iranian Markhoz goat breed as well as in Cashmere goat breed of South Khorasan (Rashidi *et al.*, 2015; Joezy-Shekalgorabi *et al.*, 2016). Considering the importance of conservation of indigenous breeds adapted to harsh environmental conditions and with regard to the valuable parameters obtained by pedigree analysis, the objective of the current study was to demonstrate demographic characteristics of Adani dairy goat breed through analysing the collected genealogical data.

MATERIALS AND METHODS

Genealogical information of 2985 Adani goat collected during 14 years period (from 1999 to 2013) was evaluated in this study. Data were provided by Animal Breeding and Milk Improvement Centre (ABMIC), Karaj, Iran. Animals were reared under semi-intensive and extensive management system at Bushehr province, in the south of Iran. The province is located in arid regions of Iran with a hot and dry climate. The average temperature and the annual precipitation is estimated about 24.4°C and 212 mm, respectively. The flock feeding is based on pasture grazing with 1 to 2 months hand feeding at winter. Mating season starts from early autumn and kidding occurs at early spring.

The pedigree was edited for inconsistencies in dam and sire registration, birth date and sex registration. Founders were defined as individuals with one or both unknown parents. A four years' time path was used for defining the reference population because this time duration represent an approximate generation interval in goat. Inbreeding coefficient and the coancestry coefficient were estimated by the algorithms proposed by Meuwissen and Luo (1992) and Malecot (1948), respectively. The absolute and the effective number of founders and ancestors, the number of full traced generation, the equivalent complete generation, the maximum number of generation traced, effective population size and inbreeding rate considering various generation definition, etc., were also obtained (Lacy, 1989; Maignel *et al.*, 1996; Biochard *et al.*, 1997; Gutierrez *et al.*, 2009; Cervantes *et al.*, 2011). These parameters could help in providing insights into the genetic history of the breed.

The programs CFC 1.0 (Sargolzaei *et al.*, 2006) and Endog 4.8 (Gutierrez and Goyache, 2005) were used for performing pedigree analysis. Of the total 2985 animals, about 28.2 % were considered to be founders (with both unknown dam and sire), and about 69.4% of animals did not have any progeny.

RESULTS AND DISCUSSION

Main demographic characteristics derived from genealogical data of 6 flocks of Adani goat breed are

summarized in Table 1. Among the studied population, 2.9% and 27.7% were presented as sires and dams in the pedigree, respectively. Of the total 2985 animals, about 28.2% were considered to be founders (with both unknown dam and sire), and about 69.4% of animals did not have any progeny. Timeline trend of founders and animals with no progeny in various years is presented in Fig. 1. Present results indicated that from 1999 to 2003, all the animals in the pedigree were founder. There did not exist a regular trend for the rate of founders in population, from 2004 to 2010. However, from 2011 afterward no founder was found in the population.

The structure of population across flocks and year are presented in Figures 2 and 3. Among the studied flocks, flocks numbered 6 and 3 had the most and the least registered population, respectively. In addition about 21.1 and 100% of the registered population, in flocks 6 and 3, were considered as a founder. The number of registered animals showed a descending trend over the last decade of evaluation. No inbred animal was found till 2007. An overall increasing trend did exist in the inbreeding coefficient for Adani dairy goat, since 2008. Inbred animals reached to 25% of the registered animals by 2013. The distribution of the inbreeding coefficient among of Adani goat breed is presented in table 2. A total of 96 animals were inbred. About 52.1% of inbred animals had inbreeding lower than 5%. The inbreeding coefficient ranged from 0.03% to 25%. The average inbreeding value and the mean average relatedness in the whole studied population were 0.24 and 0.91%, respectively. The average inbreeding in the inbred individuals was 7.33%.

The average inbreeding coefficients in the whole and the inbred population are illustrated in Figure 4. Evolution of the inbreeding coefficient per year of birth revealed that the occurrence of inbreeding was mainly due to the recent generations indicating that the historical knowledge of the pedigree is lacking (Gutierrez *et al.*, 2003). The extensive production system used in Adani dairy goat contributed toward loss of much of fatherhood information data from past generation. Investigation of inbred individuals in various flocks indicated that all the inbred animals were found in flock 6. No relatedness was found between animals in various flocks.

The average inbreeding and coancestry in the reference population were 0.07 and 1.56%, respectively. Similar inbreeding coefficient was reported by Joezy-Shekalgorabi *et al.* (2016) for the Cashmere goat breed of South Khorasan in Iran. Investigation of the pedigree structure in German Hanoverian horse breed during 1920 to 2000 indicated that the average inbreeding coefficients were 1.33, 1.19, and 1.29 % for the reference population, stallions, and breeding mares, respectively (Hamann and Distl, 2008). They argued that such limited inbreeding coefficient was due to the breeding of Hanoverian with other German horse breeds across generations. The

average relatedness of individuals within the reference population was about 3.12%. The probabilities of gene origin parameters in the studied breed is presented in Table 3. Of the total 1007 animals in the reference population, there did exist a number of 528 males and 479 females, respectively. The ratio of the effective number of founders (f_e) to the total number of founders (f) in the studied population was 0.13 indicating unbalanced contribution of founders as parents in the population. A greater f_e/f ratio was recorded for the Slovak White Shorthaired, Italian Girgentana and Iranian Markhoz goat breeds (Portolano *et al.*, 2004; Oravcova, 2013; Rashidi *et al.*, 2015) indicating more equivalent contribution of founders to the reference population on these breed. The number of ancestors contributing to the reference population of Adani goat was about 94% of founders, which is a sign of lack of pedigree depth and short time distance among founder and young living population (Gutierrez *et al.*, 2003; Oravcova, 2013). Effective number of ancestor was about 39, which could be a result of occurring genetic bottleneck and loss of genetic diversity in the studied breed. The ratio of the effective number of founders to the effective number of ancestors (f_e/f_a) was about 1.44 which was similar to the result reported for the White Shorthaired breed (1.6) and Markhoz breed (1.32). Large f_e/f_a ratio (greater than one) indicates a more intense bottleneck effect and the use of a limited number of parents across generations (Fair *et al.*, 2012; Oliveira *et al.*, 2012). Smaller value of effective number of founder flocks compared with the actual number of flocks refers the unbalanced contribution of various flocks in gene pool of the population and emphasizes that some flocks behave as nucleus flocks providing genetic material for other flocks (Gutierrez *et al.*, 2003).

Mean maximum generation, mean complete generation and mean equivalent generation was 1.33, 0.67 and 0.93 respectively. Figure 5 represents the mean value of equivalent generation over the studied period. Low value obtained for the equivalent generation in this study indicates pedigree incompleteness and low depth of the pedigree. In the study of Hamann and Distl (2008) on a horse breed the mean complete generation equivalent was 8.43 for the reference population. The mean complete generation equivalent of the female reference population in Iranian Baluchi sheep was 5.47 (Tahmoorespur and Sheikhlou, 2011). The mean complete generation equivalent, the effective population size and inbreeding rate considering the generation type is summarized in Table 4. Loss of genetic diversity is expected in population with small effective population size. According to the FAO (1998) guideline on preserving animal genetic resources, effective population size less than 50 affects the fitness of the breed under consideration. Estimate of effective population size for Adani dairy goat was above the critical level which

ensures low inbreeding rate and consequently, stable development of population without concerning about high relatedness of animals. The inbreeding rate obtained in this study was similar to the results obtained for Saanen (Gipson, 2002) and clearly lower than the FAO limit for breeds classified as threatened with extinction (FAO, 1998). However, missing pedigree information could be the main reason for obtaining low inbreeding value (Biochard *et al.* 1997) and it have to be taken into account when interpreting the results for the Adani goat breed.

Table 1. Pedigree structure of Adani dairy goat.

Item	N
Individuals in total	2985
Males	1212
Females	1773
Sires in total	86
Dams in total	826
Base population ^a	1325
Individuals with known sire	1660
Individuals with known dam	1776
Individuals with both unknown parent	843
Individuals with both known parent	1660
Individuals with no progeny	2073

^aone or more unknown parents

Table 2. Distribution of inbreeding coefficient in Adani goat breed.

Level Of Inbreeding (%)	Number Of Animals
$0 < F \leq 0.05$	50
$0.05 < F \leq 0.10$	14
$0.10 < F \leq 0.15$	27
$0.15 < F \leq 0.20$	0
$0.20 < F \leq 0.25$	5

Table 3. Parameters of probability of gene origin for the reference population in Adani goat.

Item	Value
Number of animals in the reference population	666
Number of ancestors contributing to the reference population	403
Total number of founder animals in the reference population	428
Effective number of founders	167.29
Effective number of founders for the reference population	56
Effective number of ancestors for the reference population	39
Number of founder herds	5
Effective number of founder herds for the reference population	1.6

Founder equivalent for the reference population	80.66
Founder genome equivalent for the reference population	32.01
Effective number of non-founders	53.09
Number of ancestors explaining 50% of gene pool	26
Number of ancestors explaining 75% of gene pool	97
Number of ancestors explaining 100% of gene pool	403

Table 4. Effective population size and inbreeding rate considering various generation type in Adani goat.

Generation Type	Effective Population Size	Inbreeding Rate (%)
Maximum generation	158.49	0.32
Complete generation	85.75	0.58
Equivalent generation	98.61	0.51

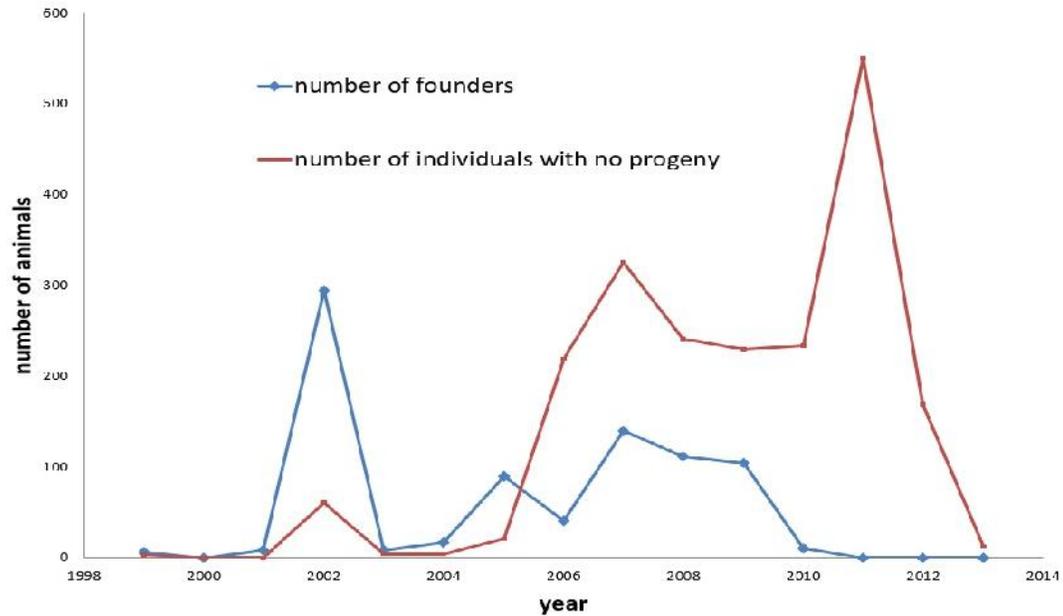


Fig1. Number of founders and number of animals across years in Adani goat

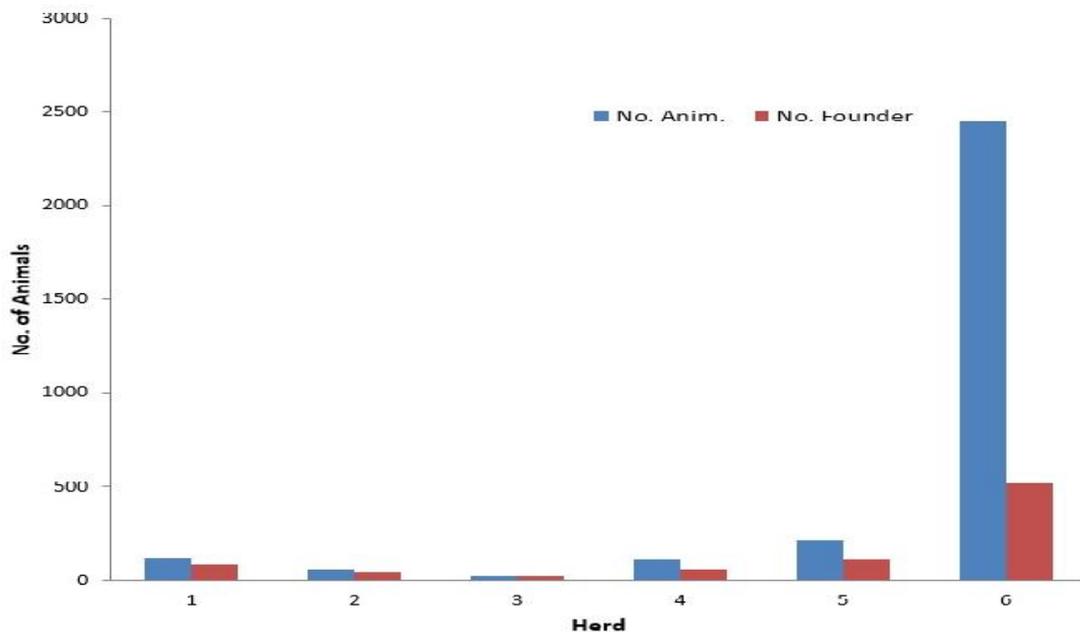


Fig 2. The number of animals and the number of founders in various flocks of Adani dairy goat

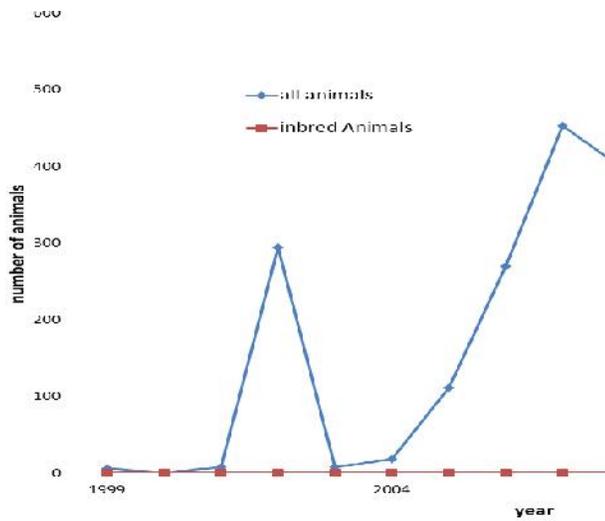


Fig 3. Registered and inbred individuals of Adani dairy goat during the studied period

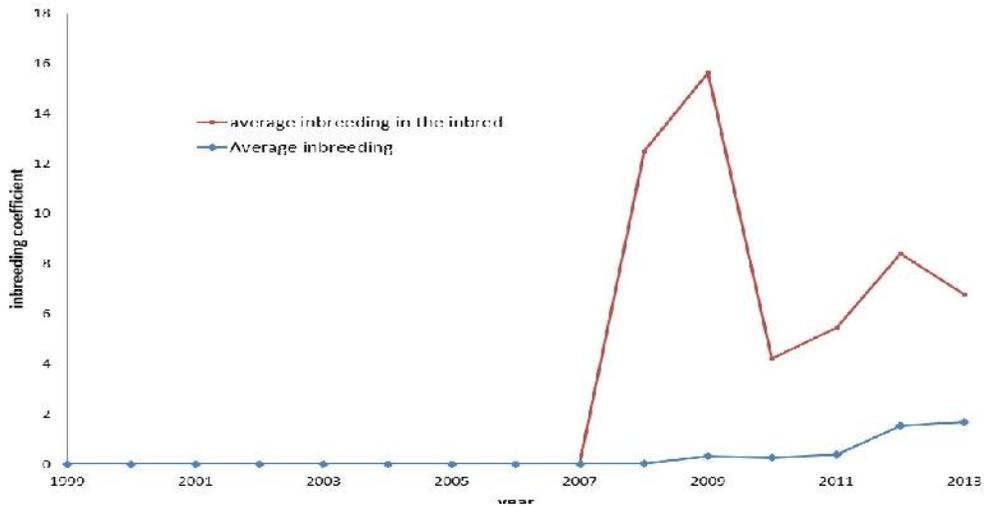


Fig 4. Evolution per birth year of average inbreeding coefficient in registered and inbred individuals in Adani goat

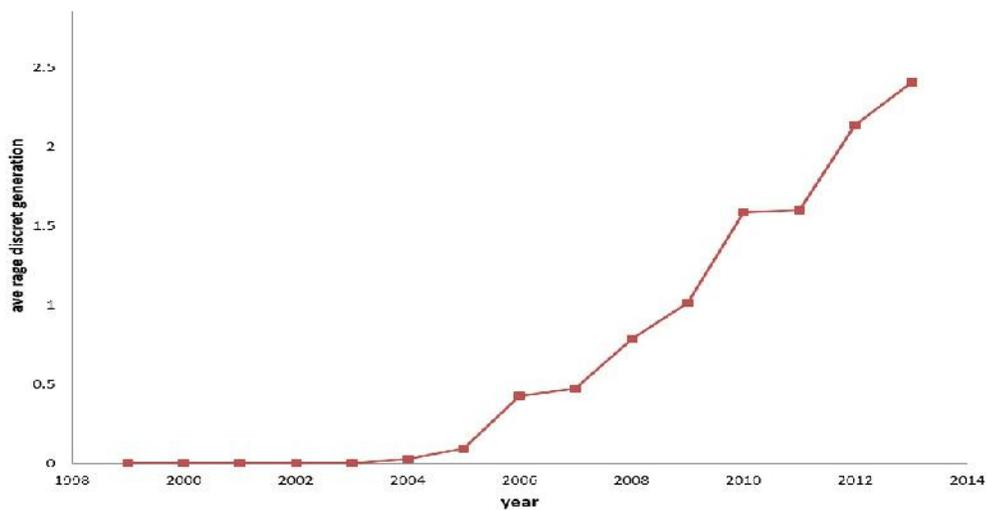


Fig 5. Average number of discrete generation equivalent in Adani dairy goat across various studied years

Conclusion: Population structure across years and flocks in Adani goat breed was documented in this study. Results indicated to unbalance contribution of founders in the population. Generally, animals with unknown parents are assumed to have no inbreeding. However, in reality, they quite often are related to each other leading to underestimation of the inbreeding coefficient. For including the studied breed in the conservation program, solving the problem of pedigree completeness is necessary. Utilizing various DNA analysis methods could practically help with the estimation of relationship between animals and overcome the problem of pedigree incompleteness in the studied breed.

Acknowledgments: The authors of the article would like to send their sincere gratitude to Young Researchers and Elites Club, Shahr-e-Qods Branch, Islamic Azad University, for their financial support. This paper is part of the research project entitled "Pedigree analysis in some Iranian goat breeds". Additionally, the authors would like to thank the Animal Breeding and Milk Improvement Center of Iran is for providing the necessary data for completing this study.

REFERENCES

- Ansari-Renani, H.R., J.P. Mueller, B. Rischkowsky and S.Moradi (2013). Cashmere in Iran. ICARDA-ASRI, 4-5.
- Baldursdottir, B.K. (2010). Genetic variation within the Icelandic goat breed. Assessment using population data and DNA analysis. MSc Thesis, 51 p.
- Baldursdottir, B.K., T. Kristjansson and J.H. Hallsson (2012). Diversity of the Icelandic goat breed assessed using population data. *Acta Agric. Scandinavica*, Section A-Anim. Sci. 62(2): 53-65.
- Biochard, D., L. Maignel and E. Verrier (1997). The value of using probabilities of gene origin to measure genetic variability in a population. *Gen. Sel. Evol.* 29: 5-23.
- Cecchi, F., R. Ciampolini, E. Ciani, B. Matteoli, E. Mazzanti, M. Tancredi and S. Presciuttini (2006). Demographic genetics of the endangered Amiata donkey breed. *Ital. J. Anim. Sci.* 5(4): 387-391.
- Cecchi, F., G. Paci, A. Spaterna and R. Ciampolini (2013). Genetic variability in Bracco Italiano dog breed assessed by pedigree data. *Ital. J. Anim. Sci.* 12(3): 348-352.
- Cervantes, I., F. Goyache, A. Molina, M. Valera and J.P. Gutiérrez (2011). Estimation of effective population size from the rate of coancestry in pedigreed populations. *Genet. Res.* 75: 331-343.
- Fair, M.D., J.B. Van Wyk, and S.W. Cloete (2012). Pedigree analysis of an ostrich breeding flock. *SA. J. Anim. Sci.* 42(2):114-22.
- FAO (1998). Secondary Guidelines for the National Farm Animal Genetic Resources
- Gipson, T.A. (2002). Preliminary observations: inbreeding in dairy goats and its effects on milk production. Institute for Goat Research Langston University, Langston, OK.
- Groeneveld, L.F., J.A. Lenstra, H. Eding, M.A. Toro, B. Scherf, D. Pilling, R. Negrini, E.K. Finlay, H. Jianlin, E. Groeneveld, S. Weigend and G.C. The (2010). Genetic diversity in farm animals – a review. *Anim. Genet.* 41: 6-31.
- Gutiérrez, J.P., J. Altarriba, C. Díaz, R. Quintanilla, J. Cañón and J. Piedrafita (2003). Pedigree analysis of eight Spanish beef cattle breeds. *Genet. Sel. Evol.* 35(1):43-64.
- Gutiérrez, J.P. and F. Goyache (2005). A note on ENDOG: a computer program for analyzing pedigree information. *J. Anim. Breed. Genet.* 122(3): 172-176.
- Gutiérrez, J.P., J.Marmi, F. Goyache and J. Jordana (2005). Pedigree information reveals moderate to high levels of inbreeding and a weak population structure in the endangered Catalanian donkey breed. *J. Anim. Breed. Genet.* 122(6): 378-386.
- Gutiérrez, J.P., I. Cervantes and F. Goyache (2009). Improving the estimation of realized effective population size in farm animals. *J. Anim. Breed. Genet.* 126: 327-332.
- Hamann, H., and O. Distl (2008). Genetic variability in Hanoverian warmblood horses using pedigree analysis. *J. Anim. Sci.* 86: 1503-1513.
- Hammami, H., C. Croquet, J. Stoll, B. Rekik and N. Gengler (2007). Genetic diversity and joint-pedigree analysis of two importing Holstein populations. *J. Dairy Sci.* 90(7): 3530-3541.
- Hasler, H., C. Flury, S. Menet, B. Haase, T. Leeb, H. Simianer, P.A. Poncet and S. Rieder (2011). Genetic diversity in an indigenous horse breed – implications for mating strategies and the control of future inbreeding. *J. Anim. Breed. Genet.* 128(5): 394-406.
- Honda, T., T. Nomura, Y. Yamaguchi and F. Mukai (2004). Monitoring of genetic diversity in the Japanese Black cattle population by the use of pedigree information. *J. Anim. Breed. Genet.* 121(4): 242-252.
- Joezy-Shekalgorabi, S., A. Maghsoudi, A. Taheri Yeganeh and B. RajabiMarand. (2016). Pedigree analysis of Cashmere goat breed of South Khorasan. *Ital. J. of Animal Science.* 15(4): 590-594.

- Lacy, R.C. (1989). Analysis of founder representation in pedigrees: founder equivalents and founder genome equivalents. *Zoo. Biol.* 8: 111-123.
- Leroy, G., E. Verrier, J.C. Meriaux and X. Rognon (2009). Genetic diversity of dog breeds: within-breed diversity comparing genealogical and molecular data. *Anim. Genet.* 40(3): 323-332.
- Li, M.H., I. Strandén and J. Kantanen (2009). Genetic diversity and pedigree analysis of the Finnsheep breed. *J. Anim. Sci.* 87(5): 1598-1605
- Maignel, L., D. Boichard and E. Verrier (1996). Genetic variability of French dairy breeds estimated from pedigree information. *Interbull Bull.* 14: 49-54.
- Malecot, G. (1948). *Les mathématiques de l'hérédité*. MassonetCie, Paris. 80 pp.
- Marcondes, C.R., L.C. Marques, P.A. Vozzi, J.F. Aguiar, R.N.C. Camargo Junior, S.R.R. Duarte and J.R.F. Marques (2014). Pedigree analysis applied to an endangered buffalo population: possible management strategy. *Livest. Res. Rural Develop.* 26(2): Article #22. Retrieved March 14, 2016, from <http://www.lrrd.org/lrrd26/2/marc26022.htm>
- Mc Parland, S., J.F. Kearney, M. Rath and D.P. Berry (2007). Inbreeding trends and pedigree analysis of Irish dairy and beef cattle populations. *J. Anim. Sci.* 85: 322-331.
- Melka, M.G. and F. Schenkel (2010). Analysis of genetic diversity in four Canadian swine breeds using pedigree data. *Canad. J. Anim. Sci.* 90(3): 331-340.
- Meuwissen, T.H.E. and Z. Luo (1992). Computing inbreeding coefficients in large populations. *Genet. Sel. Evol.* 24: 305-313.
- Mokhtari, M.S., M.M. Shahrabak, A.K. Esmailzadeh, H.M. Shahrabak and J.P. Gutierrez (2014). Pedigree analysis of Iran-Black sheep and inbreeding effects on growth and reproduction traits. *Small Rum. Res.* 116(1): 14-20.
- Mucha, S. and J.J. Windig (2009). Effects of incomplete pedigree on genetic management of the Dutch Landrace goat. *J. Anim. Breed. Genet.* 126(3): 250-256.
- Oliveira, A. P., C. H. Malhado, P. L. Carneiro, R. Martins Filho, É. S. Silveira, L.D. Souza, L. M. Muniz and D. M. Azevêdo (2012). Pedigree analysis on the population of Gir cattle in Northeast Brazil. *Revista Brasileira de Zootecnia.* 41(5):1153-7.
- Oravcová, M. (2013). Pedigree analysis in White Shorthaired goat: First results. *Arch. Tierz.* 56: 547-554.
- Pienaar, L., F.W.C. Naser, J.P. Grobler, M.M. Scholtz and M.D. MacNeil (2015). Pedigree analysis of the Afrikaner cattle breed. *Anim. Genet. Resources.* 57: 51-56.
- Portolano, B., R. Finocchiaro, M. Todaro, J.T. van Kaam and P. Giaccone (2004). Demographic characterization and genetic variability of the Girgentana goat breed by the analysis of genealogical data. *Ital. J. Anim. Sci.* 3(1): 41-45.
- Rashidi, A., M.S. Mokhtari and J.P. Gutiérrez (2015). Pedigree analysis and inbreeding effects on early growth traits and greasy fleece weight in Markhoz goat. *Small Rum. Res.* 124: 1-8.
- Sargolzaei, M., H. Iwaisaki and J.J. Colleau (2006). CFC: A tool for monitoring genetic diversity. *Proc 8th World Congr. Genet. Appl. Livest. Prod. CD-ROM Communication*, (27-28): 13-18.
- Scherf, B.D. (2000). *World watch list for domestic animal diversity*. 3th ed. Food Agric. Org. United Nations, Rome, Italy.
- Sölkner, J., L. Filipic and N. Hampshire (1998). Genetic variability of populations and similarity of subpopulations in Austrian cattle breeds determined by analysis of pedigrees. *Anim. Sci.* 67(2): 249-256.
- Szabó, P., I. Komlósi and J. Posta (2015). Pedigree analysis of Mangalica pig breeds. *Annals Anim. Sci.* DOI: 10.1515/aoas-2015-0075.
- Tahmoorespur, M., and M. Sheikhlou (2011). Pedigree analysis of the closed nucleus of Iranian Baluchi sheep. *Small Rum. Res.* 99: 1-6.
- Veroneze, R., P.S. Lopes, S.E.F. Guimarães, J.D. Guimarães, E.V. Costa, V.R. Faria and K.A. Costa (2014). Using pedigree analysis to monitor the local Piau pig breed conservation program. *Archivos de Zootecnia.* 63: 45-54.
- Vozzi, P.A., C.R. Marcondes, C.D.U. Magnabosco, L.A.F. Bezerra and R.B. Lôbo (2006). Structure and genetic variability in Nellore (*Bos indicus*) cattle by pedigree analysis. *Genet. Mol. Biol.* 29: 482-485.
- Vozzi, P.A., C.R. Marcondes, L.A. Bezerra and R.B. Lôbo (2007). Pedigree analyses in the Breeding Program for Nellore Cattle. *Genet. Mol. Res.* 6(4): 1044-1050.
- Yazdanshenas, M. S., R. VaezTorshizi, N. Emam Jome Kashan and M. Aminafshar (2013). Estimation of genetic parameters for direct and maternal effects of growth traits in Iranian Adani goats. *Annals Biol. Res.* 4(7): 20-26.