ASSESSING GENETIC VARIABILITY IN A FLOCK OF AFSHARI SHEEP BY GENEALOGICAL DATA

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ABSTRACT

The aim of this study was to investigate genetic diversity in a nucleus flock of Afshari sheep using measures based on the probability of identity-by-descend of genes (coancestry, $f$, inbreeding, $F$, average relatedness, $AR$, and effective population size, $N_e$), as well as measures based on probabilities of gene origin (effective number of founders, $f_e$, effective number of ancestors, $f_a$, effective number of founder genomes, $f_g$, and effective number of non-founder genomes, $f_n$). The average coancestry ($f$), inbreeding ($F$), and relatedness ($AR$) in the whole population were 1%, 0.5%, and 2%, respectively. The estimated value of the effective population size ($\bar{N}_e$) was 58. Effective number of founders was estimated to be 62 which was one fourth of the total number of founders, indicating the loss of diversity due to the unequal contribution of founders in such a way that only 62 founders covered 75% of the total genetic diversity. The effective number of ancestors ($f_a$) was 49. Only 18 ancestors were needed to explain 50% of the genetic diversity in the population. The marginal contribution of the most influential ancestor was 6.5%. This was 5.8% and 4.8% for the 2nd and 3rd most influential ancestors. Effective number of founder genomes which covered all of the losses in genetic diversity during segregation was computed to be 41 and the effective number of non-founder genomes was 125. While the level of inbreeding was low, it was concluded that the rate of inbreeding needs to be controlled in the future to avoid further decline in genetic diversity.

Key words: Genetic diversity, Inbreeding, Pedigree, Sheep.

INTRODUCTION

The genetic change of the population mean of a quantitative trait is the outcome of the action of two antagonistic forces: selection and genetic drift. The latter may generate inbreeding depression and erosion of the genetic variance, both for production and fitness traits (Falconer and MacKay, 1996). The harmful effects of inbreeding on production and reproduction performance of farm animals have been well documented (Mandal et al., 2002; Brah et al., 2012). Owing to the undesirable effects of low heterozygosity, preserving genetic diversity is, therefore, one of the goals in livestock management and knowledge of this diversity is the basis for effective selection and conservation programs.

In general, two groups of criteria are used for monitoring genetic diversity. They are obtained either based on probability of identity-by-descend (IBD) of genes or based on probabilities of gene origin. Effective population size ($N_e$) (Wright, 1931) is the most famous IBD criteria used for describing genetic diversity in animal populations. Upto late 1980s, it was the only parameter used for monitoring genetic diversity. Lacy (1989) introduced the concepts of effective number of founders ($f_e$) and effective number of founder genomes ($f_g$), two members of the second group, to evaluate genetic diversity. The former only accounts for the unequal contribution of founders, but the later accounts for the unequal contributions of founders, bottlenecks, and random loss of alleles due to genetic drift. Boichard et al., (1997) were among the first researchers who used the criteria proposed by Lacy (1989) to analyse genetic diversity in livestock populations. Besides discussing the value of these new criteria to study genetic diversity, Boichard et al.

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(1997) developed the concept of effective number of ancestors ($f_a$) to supplement the effective number of founders. The number obtained from the calculation of $f_a$ are essentially the same as $f_e$, but takes into account the decrease in genetic variation in populations that have passed through a bottleneck. Caballero and Toro (2000) introduced the effective number of non-founder genomes ($f_n$) to assess the loss of genetic diversity via random genetic drift accumulated in non-founder generations.

The aim of the present study was to evaluate genetic diversity in a nucleus flock of Afshari sheep using different measures of genetic variability (Wright, 1931; Lacy, 1989; Boichard et al., 1997; Caballero and Toro, 2000). The results will give breeders a viewpoint concerning the genetic size of the population and provide them an opportunity to plan more efficient mating programs aimed at minimizing the future loss of genetic diversity.

**MATERIALS AND METHODS**

**Data:** Pedigree information (Table 1) used in this study was from a nucleus flock of Afshari sheep maintained at the department of Animal Science at the Zanjan University, Zanjan, located in Iran, 1663 m above mean sea level and 35°35´S, and 47°15´E. The location of the experimental flock and husbandry practices were described comprehensively by Eskandarinasab et al., (2010). Briefly, the flock was closed in 1998 with 11 fertile rams and 110 breeding ewes. The aim of the project was to set up a nucleus resource of Afshari sheep to improve other flocks in the region. Natural service was applied once a year between September and October and lasted for three oestrus cycles (51 days). One breeding ram was allowed to mate with 15 ewes. The corresponding lambing season took place in February and continued to May. At birth each lamb was identified and date of birth, sex, type of birth and weight were recorded. Lambs were weaned at an average age of 120 days. Animals were maintained on natural pasture during spring, summer and autumn and kept indoors during winter months and manually fed according to NRC (1985).

**Genetic variability parameters**

Coancestry, $f$: Coancestry (kinship, Malécot, 1948) is defined as the probability that any two alleles, sampled at random (one from each individual), are identical copies of an ancestral allele.

Individual inbreeding coefficient, $F$: It describes the probability that two alleles at any locus are identical by descent (Wright, 1931). Coefficients of $F$ were computed for each individual following Meuwissen and Luo (1992).

Individual average relatedness, $AR$: The $AR$ coefficient for each individual in the pedigree is computed as the average of the coefficients in the row correspondent to the individual in the numerator relationship matrix, $A$ (Gutiérrez and Goyache, 2005).

The effective number of population size, $N_e$: This parameter was obtained following Gutiérrez et al., (2009) based on individual increase in inbreeding ($\Delta F$). The $\Delta F_i$ coefficients are computed as $\Delta F_i = 1 - \frac{1}{\sqrt{1 - F_i}}$, where $F_i$ is the individual coefficient of inbreeding and $t$ is the equivalent complete generations. This estimate of effective population size ($N_e$) can be computed from, that can be computed by averaging the $\Delta F_i$ of the $n$ individuals included in a given reference subpopulation, as $N_e = 1/2 \Delta F$.

The effective number of founders, $f_e$: Lacy (1989) estimated the effective number of founders as $f_e = 1/\Sigma_{k=1}^{m} q^2 k$, where $q_k$ is the expected proportional genetic contribution of founder $k$, calculated by the average relationship of the founder to each animal in the current population, and $m$ is the total number of founders.

The effective number of ancestors, $f_a$: This parameter complements the information offered by the effective number of founders accounting for the losses of genetic variability produced for the unbalanced use of reproductive individuals producing bottlenecks and computed as $f_a = 1/\Sigma_{k=1}^{n} P^2 k$, where $P$ is the marginal contribution of each ancestor, i.e., the contribution made by an ancestor which is not already explained by a previously chosen ancestor. The sum of marginal contributions of all ancestors is one.

The effective number of founder genomes, $f_g$: Following Caballero and Toro (2000), parameter $f_g$ was obtained by the inverse of twice the average coancestry of the individuals included in a predefined reference population. Since $f_g$ accounts for
all causes of gene loss during segregations, \( f_g \) always is a smaller number than both \( f_a \) and \( f_e \).

The effective number of non-founder genomes, \( f_{ne} \): The 5th type of effective number of animals, the effective number of non-founder genomes, accounts only for the effect of genetic drift in non-founder generations. This effective number is obtained as \( f_{ne}^{-1} = f_{g}^{-1} - f_{e}^{-1} \) (Caballero and Toro, 2000).

Genealogical analyses on pedigree information were carried out using the program ENDOG, version 4.6 (Gutiérrez and Goyache, 2005).

**RESULTS AND DISCUSSION**

The results of the pedigree analysis are presented in Table 2. The mean coancestry (\( f \)) in the whole population is 1.00%. It means that 1% of the loci carry the same ancestral alleles. Coancestry highlights the degree of genetic similarity of individuals in a breeding population. High coancestry means low diversity which decreases the ability of selecting better animals, as the difference between individuals is narrower. From a conservation genetics perspective, coancestry is the most important criteria of genetic variability because it determines the future rate of inbreeding. The mean inbreeding (\( F \)) in the whole pedigree was 0.5%. However, this was almost 9% in the inbred animal population. The average relatedness (\( AR \)) in the whole population was 2%, higher than both \( f \) and \( F \). \( f \) and \( AR \) are of value in planning conservation programs. Using these parameters, it becomes possible to decrease the rate of inbreeding through controlling the contribution of each parent to the next generation.

The effective population size \( N_e \) was 58. The current estimate is intermediate among other estimates, smaller than of the literature values summarized by Pirchner (1983) for breeds of domestic animals (\( N_e \approx 100 \)) and of estimated value reported by Ghafoori-Kesbi (2010) for a close population of Zandi sheep as 71, but is higher than that reported by Oravcová and Krupa (2011) for Valachian sheep as 21 (a population consisted of 137 individuals). According to Bijma (2000) for an effective selection an effective population size between 50 to 100 is necessary. Although, current estimate of \( N_e \) falls between this range, this figure can be decreased following an increase in the inbreeding level of the population. For this reason, the inbreeding level of the population should be controlled.

235 founders contributed in the population, however as shown in Figure1, their contributions is unbalanced. As shown, 62 founders cover 75% of the total genetic diversity. It means that the rest 173 founders only cover 25% of the total genetic diversity. The estimated value of the effective number of founders (\( f_f \)) was 62 which is lower than that reported by Goyache et al., (2003) as 80 for Spanish Xalda sheep and that estimated by Ghafoori-Kesbi (2010) as 70 for a close population of Zandi sheep, but is higher than that reported by Oravcová and Krupa (2011) for Valachian sheep as 21 (a population consisted of 62 founders). The ratio of effective number of founders to the actual number of founders is almost 0.25. A large difference between the number of founders and the effective number of founders is a direct consequence of the excessive use of some founders as parents which resulted in a high disequilibrium between founder contributions (Ghafoori-Kesbi, 2010).

The effective size of ancestors (\( f_a \)) was 49. The calculation of effective number of ancestors (\( f_a \))

<table>
<thead>
<tr>
<th>TABLE 1: Description of the pedigree information.</th>
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<tbody>
<tr>
<td>Item</td>
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<tr>
<td>No. of animals</td>
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<tr>
<td>No. of sires-grandsires</td>
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<tr>
<td>No. of dams-granddams</td>
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<td>No. of animals with progeny</td>
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<td>No. of animals without progeny</td>
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<tr>
<td>No. of animals with unknown sire</td>
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<td>No. of animals with unknown dam</td>
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<th>TABLE 2: Results of the pedigree analysis.</th>
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<tr>
<td>Item</td>
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<tr>
<td>Average coancestry (%)</td>
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<tr>
<td>Mean inbreeding (%)</td>
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<tr>
<td>Mean inbreeding in inbred animals (%)</td>
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<tr>
<td>Average relatedness (%)</td>
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<tr>
<td>Effective no. of population (( N_e ))</td>
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<tr>
<td>No. of founders</td>
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<tr>
<td>Effective no. of founders (( f_f ))</td>
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<tr>
<td>No. of ancestors</td>
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<tr>
<td>Effective no. of ancestors (( f_a ))</td>
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<tr>
<td>No. of ancestors explaining 50%</td>
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<tr>
<td>Effective no. of founder genomes (( f_g ))</td>
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<tr>
<td>Effective no. of non-founder genomes (( f_{ne} ))</td>
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involves the looking for marginal contributions of each ancestor. The most influential ancestor, who was also a founder, contributed almost 6.5% to the gene pool of the population. This was 5.8% and 4.8% for the 2nd and 3rd most influential ancestors, respectively. \( f_a \) is more informative than \( f_e \) because besides considering the unequal contribution of ancestors, it considers bottleneck effects. Moreover, estimation of \( f_e \) is influenced by several factors which make \( f_e \) estimates to be unreliable (Sørensen et al., 2005).

The most informative effective number, effective size of founder genomes (\( f_g \)) was estimated to be 41 which is lower than both \( f_a \) and \( f_e \) for the reason that \( f_g \) accounts for all causes of gene loss during segregations. Ghafouri-Kesbi (2010) estimated \( f_g \) for a population of Zandi sheep as 42 which is close to current estimate. Besides dealing with the total loss in diversity, \( f_g \) is directly related to genetic diversity itself. Lacy (1995) showed that the relationship between the current population’s mean coancestry and \( f_g \) is \( f_g = (1/2c) \). According to the formula, as the population becomes more related, as would happen with any closed population, \( f_g \) decreases.

Effective number of non-founder genomes (\( f_{ne} \)) was 125. This parameter describes the relation between effective number of founders and effective number of founder genomes and shows that with respect to loss in genetic diversity which one is more important, random genetic drift accumulated in non-founder generations or unequal contribution of the founders. When \( f_{ne} \) is larger than \( f_e \), as observed here, it means that for the reduction of genetic diversity, unequal contribution of founders is more serious than the random genetic drift.

**CONCLUSIONS**

Deviation of the effective size of the founders and the effective size of ancestors from the actual number of founders and ancestors indicates that the population has lost part of its genetic diversity since its foundation mainly because of the unequal contribution of founder animals. However, the level of inbreeding shows that genetic variability reduction is low. In spite of this, breeders should be concerned about the future rate of inbreeding because as time passes, the pedigree becomes more complicated with a higher percentage of relative animals.

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REFERENCES


