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Genetic diversity of a nucleus flock of Malpura sheep through pedigree analyses

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ABSTRACT

Malpura sheep is one of the heaviest sheep breed of India, known for its adaptability to harsh environment and potential for high meat production. It is distributed in the semi-arid region of Rajasthan, India. The pedigree information estimated by the number of equivalent generation traced was good (7.21). For reference cohort, effective number of founders (f_e) was 58, representing 29.15% of the potential number of founders. The effective number of ancestors (f_a) was 36 and the genetic contribution of the 13 most influent ancestors explained 50% of the genetic variability in reference cohort. The realised effective population size of the flock was 91.74 ± 2.02. The ratio f_e/f_a which expresses the effect of population bottlenecks was 1.61. The average inbreeding coefficient for reference population was 3.32%. The average relatedness coefficient between individuals of the reference population was 5.10%. The generation interval was lowest for ram daughter pathway (2.72 years) and highest for ewe to son (4.13 years). Study revealed non-significant effect of individual inbreeding or change in inbreeding on the lamb live weights. Introduction of new sires with the lowest possible average relatedness coefficient and the use of appropriate mating strategies are recommended to keep inbreeding at acceptable levels and increase the genetic variability.

1. Introduction

India is endowed with rich genetic diversity of livestock and ranks second in the sheep population with 73.99 million heads (FAOSTAT, 2010). Many reviews described 40 breeds (Acharya, 1982; DAHD, 1996; Arora and Garg, 1998; Singh et al., 2007), but details of 42 distinguished sheep breeds of India are available in the literature (Naqvi and Gowane, 2013). However, there is still a vast diversity of sheep genetic resources in India that remains undocumented. These sheep breeds are well adapted to specific environment in specific agro-climatic regions of the country. Malpura sheep is one amongst the heaviest sheep breed of India, widely distributed in the semi-arid region of Rajasthan, mostly Tonk, Jaipur and Sawai Madhopur districts. As per the 17th livestock census, Government of India, the total population of Malpura sheep is 375,336. Malpura sheep are reared by small and marginal land holders who graze them on fallow land, crop residue and also take them on migration during period of scarcity of feed. They are mainly reared for mutton purpose, as the earnings from their coarse wool are of little market value. The Central Sheep & Wool Research Institute (CSWRI) Avikanagar is involved in genetic improvement and conservation of Malpura sheep since many years.

A complete pedigree is essential for evaluating inbreeding, effective population size, generation interval, genetic diversity, and several other important population parameters (Martínez et al., 2008). Scientific management of sheep flock that takes into consideration the genetics of sheep breeding should aim at controlling the level of inbreeding in future generations in order to prevent a fall in the

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Table 1
Average meteorological parameters for last three years during breeding season at the farm.

Parameter		Minor breeding season (March–April)	Major breeding season (August–September)
Humidity (%)	7.30 AM	55.74	88.34
	2.30 PM	31.96	76.21
Rainfall (mm)		2.27	247.97
Temperature (°C)	Min	18.45	23.77
	Max	36.20	31.70
Photoperiod (h)		8.11	5.20

performance or a threat to the sustainability of selection programmes. A number of concepts and methods have been proposed to monitor the amount of genetic diversity in a population (Lacy, 1989; Alderson, 1991; Boichard et al., 1997).

The major objective of the present study was to evaluate the diversity of a nucleus flock of Malpura sheep through pedigree analyses, status of inbreeding in the reference population along with assessing the impact of inbreeding on the lamb live weights.

2. Materials and methods

2.1. Data and management of sheep

Data on 5872 animals spread over 38 years (1975–2012) were collected for the pedigree analysis from the breeding flock of Malpura sheep. Reference population (1039) was a subset of the main population, considered as the cohort born from 2009 to 2012 for which different population demographic parameters were estimated (Table 2). The sheep flock was maintained at Central Sheep & Wool Research Institute (CSWRI), Avikanagar, located in the semi-arid region of Rajasthan, India at 75°28′ E Longitude and 26°17′ N Latitude at an altitude of 320 m above mean sea level. The meteorological parameters for the breeding seasons of Malpura sheep at the research station are tabulated in Table 1. A flock of Malpura sheep was maintained under a semi-intensive management system, which was similar to the management of flocks by farmers. In this flock, all the animal practices along the period of study were in agreement to international guidelines. The flock was closed where nearly 300 breeding females were maintained during each year. Nearly 15–20 sires were used for breeding every year. Males were selected for breeding on the basis of an index involving six month live weight and greasy fleece weight at six month of age. The intensity of selection for males was nearly 10%. A sire was typically used for 2 years. The improved rams from this flock of research station are supplied to the farmers for improving their sheep on fixed value (book value basis). Ewes were unselected. Ewes usually remained in the flock for 7 years and culling was done only on the basis of health and low production. Lambing was restricted in two seasons, first (January–March) and second (August–September). For nutritional management, concentrate mixture was offered ad libitum to suckling lambs from 20 days age until weaning (90 days). From three weeks of age until weaning, lambs were grazed separately from their dams for 2 h each morning and evening. In addition to 8–10 h grazing and dry fodder supplementation, 300 g of concentrate mixture was provided during the post weaning period. The grazing area consisted of forestland with natural fodder trees like Khejri (*Prosopis cineraria*), Ardu (*Ailanthus* spp.), and Neem (*Azadiracta indica*). Bushes and surface vegetation, including the improved pastures of *Cenchrus ciliaris* were also available. Due to scarce grazing resources from March to June, the sheep were supplemented with hay of Cenchrus, Cowpea and Dolichos. Additionally pala leaves (Zizyphus) and fodder tree lopping was provided.

2.2. Statistical analysis

Pedigree information was obtained for the whole pedigree of the research station Malpura sheep flock. Pedigree analysis and parameter estimates based on gene origin probabilities were performed on reference population cohort (animals born from 2009 to 2012) using the ENDOG (version 4.8) programme (Gutiérrez and Goyache, 2005). The completeness of pedigree was assessed by computing the equivalent number of generations and it was studied by analysing the account of the completeness of each ancestor in the pedigree several generations back. The average relatedness (AR) coefficient of each individual was computed. It is defined as the probability that an allele randomly chosen from the whole population in the pedigree belongs to a given animal (Gutiérrez and Goyache, 2005). The AR coefficient can thus be interpreted as a representation of the animal in the whole pedigree regardless of the knowledge of its pedigree.

Genetic history was assessed by calculating the effective number of founders (f_e) and the effective number of ancestors (f_a) for reference population. The effective number of founders is defined as the number of equally contributing founders that would be expected to produce the same genetic diversity as in the population under study (Lacy, 1989). This is computed as:

$$f_e = \frac{1}{\sum_{k=1}^{f} q_k^2}$$

where q_k is the probability of gene origin for ancestor k.

Boichard et al. (1997) proposed the effective number of ancestors (f_a) that represents the minimum number of animals (founders or non-founders) which are necessary to explain the complete genetic diversity of the study population and as a metric to assess bottlenecks in the population a major cause of gene loss in captive and domestic populations. This parameter complements the information offered by the effective number of founders by accounting for the losses of genetic variability produced by the unbalanced use of reproductive individuals producing bottlenecks. It is calculated as:

$$f_a = \frac{1}{\sum_{j=1}^{a} q_j^2}$$

where q_j is the marginal contribution of ancestor j, which represents the genetic contribution made by an ancestor that is not explained by another ancestor chosen previously. The effective number of ancestors is expected to be smaller than the effective number of founders due to bottlenecks that decrease genetic variation.

The inbreeding coefficient (F) is computed following Meuwissen and Luo (1992). The change in inbreeding (ΔF) is calculated for each generation using the standard formula as introduced by González-Recio et al. (2007) and modified by Gutierrez et al. (2009):

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

where F_i is the individual inbreeding coefficient and t is the equivalent complete generations for this individual.

The estimate of effective population size ($\bar{N}_e$) (Gutiérrez et al., 2008), called realised effective size by Cervantes et al. (2008), was computed from $\bar{\Delta F}$ by averaging ΔF_i of the n individuals included in a given reference subpopulation, as $\bar{N}_e = 1/2\bar{\Delta F}$. The standard error was approximated as:

$$\sigma\bar{N}_e = \frac{2}{\sqrt{n}} \bar{N}_e^2 \sigma\Delta F_i$$

With n being the reference population size and $\sigma_{\Delta F_i}$ the standard deviation of ΔF_i.

The following parameters were calculated for each individual: (1) the number of fully traced generations, defined as the number of generations separating the offspring of the furthest generation where the second generation ancestors of the individual are known. Ancestors with no known