

Research

Generation Interval and Inbreeding in a Population of Poll Dorset Sheep

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ABSTRACT

Pedigree records of 342 Poll Dorset sheep maintained at Mountain Research Centre for Sheep and Goat (MRSCG), Shuhama, during 1990 to 2024 were analysed for generation interval and relatedness using ENDOG version 4.8 software package. Lambs born during 2016 and 2024 were considered as reference population. The mean generation interval for the reference population was 5.27 years, with longer Ram-Lamb interval than Ewe-Lamb pathway, indicating prolonged use of breeding rams and slower genetic gain. The average inbreeding coefficients for complete and reference populations were 5.65 and 15.47%, respectively, with average relatedness of 14.26 and 21.24%. The average numbers of maximum, complete and equivalent generation for the entire pedigree were 3.22, 1.92 and 2.45 respectively with corresponding inbreeding rate as 2.68%, 4.88% and 4.22% per generation, respectively. The effective number of founders (f_e) and ancestors (f_a) were 8 and 5, respectively. The Poll Dorset population exhibits critically high generation interval and inbreeding levels with a narrow genetic base where two ancestors contribute 50% of the gene pool. Immediate implementation of optimized rotational mating schemes is recommended to restore genetic variability and ensure sustainable management of this unique genetic resource.

Keywords: Generation interval, Inbreeding, Poll Dorset sheep.

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INTRODUCTION

Poll Dorset sheep is a globally recognized terminal sire, valued for rapid growth, exceptional carcass quality and non-seasonal breeding, making it a cornerstone of intensive meat production systems in Australia and New Zealand. Poll Dorset sheep are medium-sized animals, known for prolificacy, heavy milk production and good meaty conformation. Adult weight in ewes and Rams range from 67 to 91 kg and 102 to 125 kg, respectively (Mir *et al.*, 2024). This flock represents a unique genetic resource, being the only one of its kind in the temperate Himalayan region of Kashmir. While extensive pedigree studies are common for national breeds, analysis of small, closed flocks are equally important for on farm conservation and management. In small, closed populations, loss of genetic diversity is observed due to selection and increased inbreeding (Boon, 2014). Inbreeding leads to genetic drift and poses a risk if it exceeds 1% per generation (FAO, 1998). Preserving genetic diversity is critically important as it reflects physiological, behavioural and morphological variation within populations (Illa *et al.*, 2020). Pedigree analysis has emerged as an essential tool for efficient herd management, enabling the estimation of coefficient of inbreeding, relatedness, and generation interval (Martinez *et al.*, 2008; Ghavi Hosseini-Zadeh, 2016). High quality pedigree information is useful for

maintaining genetic diversity and identifying factors influencing population genetic history (Fernandez *et al.*, 2005; Valera *et al.*, 2005). To date, no published report exists on population structure analysis of Poll Dorset sheep under these specific agro-climatic conditions. Therefore, the aim of this study was to undertake a comprehensive pedigree analysis of the closed nucleus flock at MRSCG, with the goal of providing recommendations for its sustainable management and genetic improvement.

MATERIALS AND METHODS

Data collection

The research was conducted on 342 records spanning from 1990 to 2024 of Poll Dorset sheep maintained at Mountain Sheep and Goat Research Station (MRCS&G), SKUAST-Kashmir, under organized conditions. Lambs born between 2016 to 2024 were utilized as reference population. The total number of animals $N=342$ is characteristic of a nucleus flock with the depth of pedigree records (1990-2024) providing a robust foundation for analyzing trends within this closed system. ENDOG v4.8 program was used for analysis (Gutierrez and Goyache, 2005). The following parameters were estimated: *Generation Interval (GI)*: (Falconer and Mackay, 1996); *Inbreeding coefficient (F)*:

(Meuwissen and Luo, 1992); *Average Relatedness (AR)*: (Dunner *et al.*, 1998);

RESULTS AND DISCUSSION

The pedigree analysis of Poll Dorset sheep revealed that 90.35% of lambs had both parents known, while 9.65% had unknown parentage, indicating a good pedigree depth based on completeness. The highest number of generations recorded for Poll Dorset sheep was nine. The effective population size (N_e) estimated from individual increase in inbreeding was 10.73. The effective population size (N_e) varied across generations due to different rate of inbreeding (ΔF) and relatedness among animals in that generation. The average inbreeding coefficients and relatedness for whole population were estimated as 5.65 and 14.26%, respectively, whereas the reference population had corresponding values of 15.47 and 21.24%. Inbred lambs constituted 42.40% of the total population, with an average inbreeding coefficient of 13.31%. Overall, females showed higher estimates of inbreeding compared to males (6.06 vs 5.23 %, respectively). For the complete population, the proportion of inbred animals increased from 0.02% in 2nd generation to 0.92% in 7th generation. Similarly, the inbreeding coefficient increased from 0.0025% in 2nd generation to 0.29% in 9th generation (Table 1). The inbreeding rate per generation was 2.68%, 4.88% and 4.22% based on maximum generations, complete generations and equivalent generations, respectively (Fig.1). The population showed an upward trend in inbreeding coefficients over the years with a similar trend observed for average relatedness (Fig. 2). These results suggest accumulation of homozygosity through limited breeding Rams and repeated use of related Rams across generations. The average inbreeding obtained were higher than Kermani sheep (0.51%) (Mokhtari *et al.*, 2013); Guilan sheep (0.15%) (Eteqadi *et al.*, 2014); Malpura sheep (3.32%) (Gowane *et al.*, 2014); Segurena sheep (0.60%) (Barros *et al.*, 2017); Dorper sheep (0.32%) (Kiya *et al.*, 2019); Brazilian Somali sheep (8.74%) (Figueredo *et al.*, 2019); Nellore Sheep (1.38%) (Illa *et al.*, 2020); Bharat Merino sheep (2.36%) (Mallick *et al.*, 2020); Shall sheep (1.62%) (Hashemi and Hossein-Zadeh, 2020); Mecheri sheep (0.16%) (Kannan *et al.*, 2022); Intercross sheep (0.49%) (Rahim *et al.*, 2024); Afshari sheep (0.50%) (Eskandarinasab and Ghafouri-Kesbi, 2024); Magra sheep (0.80%) (Kumar *et al.*, 2024). Janbaz *et al.* (2025) reported much higher inbreeding coefficient of 23.19% in Bhakarwal sheep. The findings suggest critical level of inbreeding in the flock possibly due to restricted mating choices and repeated use of certain rams across generations.

Table 1: Estimates of population parameters for complete number of generations in Poll Dorset Sheep.

Generation	N	F (%)	POR (%)	FP (%)	AR (%)	Ne
0	41	0.00			0.02	
1	57	0.00			0.08	
2	50	0.00	0.02	0.13	0.14	200
3	55	0.03	0.40	0.07	0.15	19.20
4	35	0.08	0.94	0.09	0.17	9
5	36	0.12	0.86	0.14	0.21	12.80
6	37	0.13	0.76	0.17	0.20	47.5
7	14	0.14	0.93	0.15	0.21	33.2
8	13	0.21	1.00	0.21	0.24	6.6
9	4	0.29	1.00	0.29	0.24	4.8

N, Number of observations; F, Mean inbreeding coefficient; POR, Proportion of inbred animals; FP, Average inbreeding coefficient for inbred animals; Ne, effective population size and AR, Average relatedness for complete generations

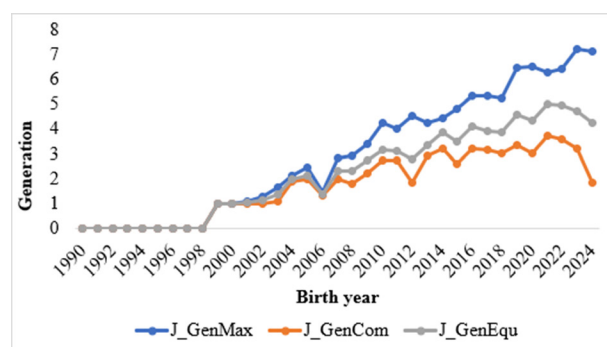


Fig. 1: Annual trends for Maximum (GenMax), Equivalent (GenEqu) and Complete (GenCom) generations traced for the whole pedigree in Poll Dorset sheep.

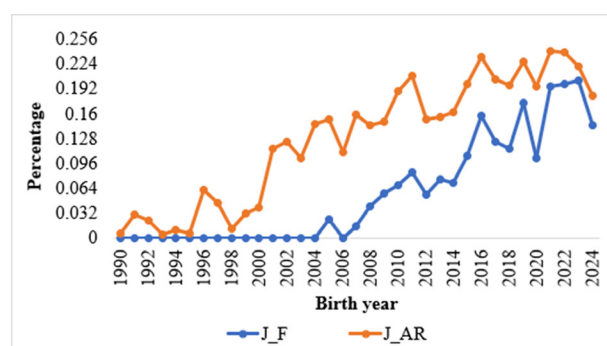


Fig. 2: Trends for Inbreeding coefficient (F) and Average relatedness (AR) of Poll Dorset sheep by year of birth for the whole pedigree.

In the present study, 4 matings (1.17%) were between parent-offspring and 46 (13.45%) between half-sibs. Gowane *et al.* (2014) in Malpura reported 0.44% and 0.12% closely related mating between half sibs and between parent-offspring mating. Similarly, Mokhtari *et al.* (2014) also reported 0.30% between full-sibs, 8.20% between half-sibs and 1.40% between parent and offspring in Iran-Black sheep. Rahim *et al.* (2024)

observed 16 (0.49%) matings between parent-offspring and 10 (0.31%) matings between half-sibs. Janbaz *et al.* (2025) reported 1 (0.46%) and 61 (27.85%) matings between full and half sibs in Bhakarwal sheep. Implementation of rotational mating schemes and optimal contribution selection can help in controlling mating of related animals.

The mean generation interval (GI) was 5.27 ± 0.31 years and mean age of parents at birth of first offspring for the reference population was 5.66 ± 0.16 years. The GI obtained in this study was higher than the optimal GI of ~ 3 years reported by Ghafouri-Kesbi, 2012 and higher than reports of 3.33 years for Iranian Baluchi sheep (Tahmoorespur and Sheikhloo 2011), 3.22 years in Guilan sheep (Eteqadi *et al.*, 2014), 3.37 years for Malpura sheep (Gowane *et al.*, 2014), 3.39 years for

Iran-Black sheep (Mokhtari *et al.*, 2014), 3.38 years for Nellore sheep (Illa *et al.*, 2020) and 3.20 years for intercross sheep by Rahim *et al.* (2024). On the contrary, Morada Nova and Lori-Bakhtiari sheep breeds reported higher GI estimates of 4.98 and 4.95 years, respectively (Rodrigues *et al.*, 2009; Vatankhah *et al.* 2019). Janbaz *et al.* (2025) reported higher estimates of 4.97 years in Bhakarwal sheep. In current study, average generation interval of sire-offspring pathways was longer than dam-offspring pathways (Fig. 3). Comparable results were reported in French and Iranian Baluchi sheep by (Huby *et al.*, 2003 and Tahmoorespur and Sheikhloo, 2011). The overall extended GI, which slows the annual rate of genetic gain, appears to be primarily driven by the long productive lifespan of the sires and the delayed age at which sires produce their first offspring.

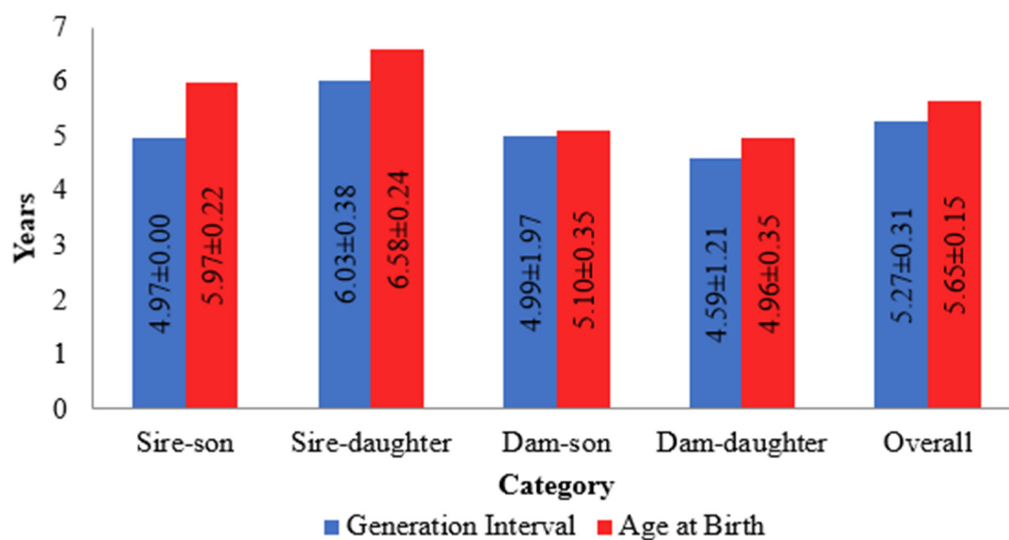


Fig. 3. Generation interval and age at birth of first offspring in Poll Dorset sheep for reference population.

CONCLUSION

The Poll Dorset population exhibited reduced genetic diversity, and a narrow genetic base where just two ancestors contribute 50% of the gene pool. Implementation of pedigree-based mate selection algorithms and replacement of breeding males should be prioritized to restore and maintain genetic variability.

CONFLICT OF INTEREST

The authors declare that there is no conflict of interest regarding this manuscript.

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