

Genetic Structure Analysis through Pedigree Information in a Closed Herd of the New Zealand White Rabbits

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Abstract : The New Zealand White breed of rabbit is one of the most commonly used, well adapted exotic breeds in India. Earlier studies were limited only to analyze the environmental factors affecting the growth and reproductive performance. In the present study, the population of the New Zealand White rabbits in a closed herd was evaluated for its genetic structure. Data on pedigree information (n=2508) for 18 years (1995-2012) were utilized for the study. Pedigree analysis and the estimates of population genetic parameters based on gene origin probabilities were performed using the software program ENDOG (version 4.8). The analysis revealed that the mean values of generation interval, coefficients of inbreeding and equivalent inbreeding were 1.489 years, 13.233 percent and 17.585 percent, respectively. The proportion of population inbred was 100 percent. The estimated mean values of average relatedness and the individual increase in inbreeding were 22.727 and 3.004 percent, respectively. The percent increase in inbreeding over generations was 1.94, 3.06 and 3.98 estimated through maximum generations, equivalent generations, and complete generations, respectively. The number of ancestors contributing the most of 50% genes (f_{a50}) to the gene pool of reference population was 4 which might have led to the reduction in genetic variability and increased amount of inbreeding. The extent of genetic bottleneck assessed by calculating the effective number of founders (f_e) and the effective number of ancestors (f_a), as expressed by the f_e/f_a ratio was 1.1 which is indicative of the absence of stringent bottlenecks. Up to 5th generation, 71.29 percent pedigree was complete reflecting the well-maintained pedigree records. The maximum known generations were 15 with an average of 7.9 and the average equivalent generations traced were 5.6 indicating of a fairly good depth in pedigree. The realized effective population size was 14.93 which is very critical, and with the increasing trend of inbreeding, the situation has been assessed to be worse in future. The proportion of animals with the genetic conservation index (GCI) greater than 9 was 39.10 percent which can be used as a scale to use such animals with higher GCI to maintain balanced contribution from the founders. From the study, it was evident that the herd was completely inbred with very high inbreeding coefficient and the effective population size was critical. Recommendations were made to reduce the probability of deleterious effects of inbreeding and to improve the genetic variability in the herd. The present study can help in carrying out similar studies to meet the demand for animal protein in developing countries.

Keywords : effective population size, genetic structure, pedigree analysis, rabbit genetics

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