ABSTRACT

Pedigree data of 18315 animals born from 1961 to 2008 from the National Sahiwal Stud, Kenya was used to assess and predict genetic diversity for the Kenyan Sahiwal population. Current (Ne_c) and predicted effective population sizes (Ne_f) were calculated from rates of inbreeding (ΔF) and coancestry (Δf) per generation, respectively. Population structure was inferred by computing Nei's minimum distance and Wright's F statistics. Genetic conservation index (GCI) was computed from the genetic contributions of all identified founders. In the most recent population group, the rate of inbreeding per generation was 0.79% with a rate of coancestry per generation of 0.85%. Predicted rate of inbreeding per generation for individuals with at least 3 and 6 complete generations were 0.82 and 1.19% and Ne of 54 and 35, respectively. The respective coancestries were 0.89 and 1.36%. Values of predicted rate of inbreeding for individuals with more complete pedigrees were >1%, implying that the population is losing genetic diversity and may not be viable in the longterm. GCI for the whole population was 5.93% whereas individuals with at least three complete generations and the reference population had values of 7.87% and 9.87%, respectively. Parameters of genetic differentiation for the whole population under study (1961-2008) were F_{IS}=- 0.0071, F_{ST}= 0.0036 and F_{IT} =- 0.0034. Loss in genetic diversity for the whole population was -0.023, an indication of random genetic drift and unequal contribution of founders. Improved pedigree completeness led to higher estimates of parameters describing the structure of the population (GCI, Ne_c, Ne_f,, ΔF and Δf). Mating should be carried out between mates with low coancestries and also by allowing more animals that are not related into breeding herd. Pedigree recording should be improved for accurate estimation of parameters.

Key words: breeding structure, coancestry, conservation index, genetic differentiation