Title: Inbreeding and pedigree analysis of the Elsenburg Merino flock

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The Elsenburg Merino resource flock has been divergently selected for 25 years and a retrospective pedigree analysis could provide useful information to conserve these lines in the future. The study of inbreeding and pedigree analysis is pertinent to modern livestock improvement programmes; which use intense selection of a small number of individuals or families to greatly improve genetic gains but results in a corresponding increase in rates of inbreeding (Weigel 2001). The objectives of this study were to describe the population dynamics, analyse the pedigree and calculate inbreeding parameters for the two lines of the divergently selected Elsenburg Merino flock. The pedigree was analysed and inbreeding trends computed for the Elsenburg Merino flock using ENDOG v4.8 and POPREP web analysis software. The complete pedigree data used in this study comprised of 7446 records of the Elsenburg Merino flock collected from 1979 to 2011. The average inbreeding coefficients (F) were 1.47% and 0.73% for the divergently selected High (H) and Low (L) lines. Mean average relatedness is higher in the H line than in the L line, 4.17% compared to 2.48%, respectively. The generation intervals for males and females were similar in both lines, amounting to 2.3 and 4.4 in the H line and 2.4 and 4.2 in the L line. The rate of inbreeding (ΔF) per generation was 0.5% for the H line and 0.6% in the L line. The effective number of founders (fe) and effective number of ancestors (fa) were 48 and 322 in the H line and 90 and 227 for the L line. The overall rate of inbreeding per generation in the H and L lines are within acceptable levels. However, the low effective population size, high proportion of inbred animals and increase in ΔF in the most recent breeding year is of concern in the L line if this population is to be conserved.

Keywords: Inbreeding, H and L lines, pedigree analysis inbreeding coefficients, effective population size, rate of inbreeding