

PRELIMINARY ANALYSIS OF GENETIC DIVERSITY IN IMPROVED VALACHIAN AND TSIGAI BREEDS USING GENEALOGICAL INFORMATION

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Abstract. The objective of this study was to analyse genetic variability of Improved Valachian and Tsigai sheep breeds using pedigree information. The programme ENDOG was used for analyses. The reference populations were considered live animals born during a period of four consecutive years from 2007 to 2010 and consisted of 14,652 (Improved Valachian) and 10,601 animals (Tsigai). The pedigree populations were considered all animals with genetic ties to the reference populations and consisted of 45,135 (Improved Valachian) and 28,292 animals (Tsigai). The mean values of inbreeding were 0.22% (Improved Valachian) and 0.49% (Tsigai). The mean values of average relatedness were 0.19% (Improved Valachian) and 0.49% (Tsigai). The mean values of individual increase in inbreeding were 0.06% (Improved Valachian) and 0.12% (Tsigai). The realized population size - computed taking into account individual increase in inbreeding was 893 (Improved Valachian) and 403 animals (Tsigai). The equivalent number of founders was 7,143 (Improved Valachian) and 4,187 animals (Tsigai). The effective number of founders was 1,232 (Improved Valachian) and 434 animals (Tsigai). The effective number of ancestors was 608 (Improved Valachian) and 264 (Tsigai). The number of ancestors explaining 50% of genetic variability was 246 (Improved Valachian) and 107 (Tsigai).

Keywords: sheep, pedigree, identity by descent, gene origin.