

**Estimation of inbreeding and effective population size in Simmental cattle using genomic information***N. Karapandža<sup>1</sup>, I. Curik<sup>2</sup>, M. Špehar<sup>1</sup> and M. Ferenčaković<sup>2</sup>**<sup>1</sup>Croatian Agricultural Agency, Ilica 101, 10000 Zagreb, Croatia, <sup>2</sup>Faculty of Agriculture, Department of Livestock Sciences, Svetosimunska 25, 10000 Zagreb, Croatia; nkarapandza@hpa.hr*

Precise estimates of effective population size and a degree of inbreeding are of great importance for population and conservation genetics. Experience has shown that estimates based on pedigree data are often unreliable and imprecise. High resolute genomic information, as one of the most polymorphic types of information, was highlighted as much more precise for this kind of calculations. In this research, we used genotypes of 107 Simmental young animals. Dual purpose Simmental breed represents dominant part of Croatian cattle population (62.8%) under selection scheme. Effective population size ( $N_e$ ) was estimated based on a functional relationship of  $N_e$  and correlation  $r^2$  and recombination rate ( $c$ ). To estimate  $N_e$  through generations we used a multithreaded tool SNeP. Regression analysis was used to estimate current effective population size, and a value of  $N_e=110$  (95%CI: 101.98-118.02) was obtained. Historical estimates of the  $N_e$  during the last 100 generations showed linear decrease of 29.24 per generation. We also estimated inbreeding levels based on runs of homozygosity (ROH) for every animal. Averaged values were as follows: FROH1=0.026 (0.015-0.045), FROH2=0.01 (0.004-0.019), FROH4=0.002 (0-0.006) while we did not detect any inbreeding originating from up to 6.25 generations ago. ROH and LD calculations were done by PLINK while data manipulation, regression analysis and visualizations were done using SAS 9.4. For comparison, we calculated  $N_e$  based on pedigree information using ENDOG software, which computes  $N_e$  via individual increase in inbreeding. For a population of 107 genotyped animals we obtained a value of 229.18, and for the population of 682 bulls that are of great importance for artificial insemination value of 264.92. Mean inbreeding was 0.42 and 0.27%. We can conclude that genomic information will be very useful to understand genetic diversity of the Simmental population with respect to genetic selection. In addition, it will help to identify genomic regions which have been preferentially selected.