

Comparison of genetic diversity between Holstein and Simmental breeds reared in Croatia

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Summary

Conventional dairy cattle breeding programs usually lead to substantial genetic progress, but also to depletion of genetic pool in selected populations. The objective of the study was to compare some pedigree based estimates of genetic diversity between Holstein (HOL) and Simmental (SIM) breeds in Croatia. The pedigrees with 307486 (HOL) and 330556 (SIM) animals were prepared by tracing back all known ancestors for the 200760 (HOL) and 231329 (SIM) routinely phenotyped cows. The SIM breed had more informative pedigree. The number of full generation, number of equivalent complete generations (*equiGen*), and index of pedigree completeness (*PCI*) for SIM were 1.47, 3.35, and 0.58, and for HOL 1.22, 2.99, and 0.51, respectively. SIM had longer generation interval than HOL (6.2 vs 5.7 years). The coefficient of inbreeding (*F*) and effective population size (*N_e*) were obtained for animals with *equiGen*>3 which were born in the last six years which corresponds to the size of the estimated generation interval ($N_{ref}(SIM) = 45807$, $N_{ref}(HOL) = 54540$). The average $F_{ref}(SIM)$ and $F_{ref}(HOL)$ were 0.0097 and 0.0163, respectively. Cows ($F_{ref}(SIM) = 0.0097$, $F_{ref}(HOL) = 0.0163$) were more inbred than bulls in both breeds ($F_{ref}(SIM) = 0.0071$, $F_{ref}(HOL) = 0.0118$). The estimated $N_{ref}(SIM)$ and $N_{ref}(HOL)$ were 227 and 140, respectively. The obtained results suggest greater genetic variability of SIM breed which is in accordance with the expectations based on the known history of intensive selection work in HOL.

Key words: genetic diversity, pedigree, completeness, inbreeding, effective population size