

# Estimation of genomic inbreeding ( $F_{ROH}$ ) in Croatian Holstein cattle population

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## Summary

More precise estimates of inbreeding coefficients in a population can be obtained using genotypic data involving long stretches of homozygous genotypes known as runs of homozygosity (ROH). Knowledge of ROH length also provides the possibility to distinguish between distant inbreeding (short segments) and recent inbreeding (long segments). The objective of the study was to estimate inbreeding using ROH ( $F_{ROH}$ ) in the Croatian Holstein cattle population. The study was conducted on 90 genotyped cows (Bovine 50K SNP BeadChip), but after quality control of genomic data (call rate per SNP 0.95 and animal 0.90) using the PLINK software (v1.09), 85 animals and 45,661 SNPs were retained in the inferential statistical analysis. PLINK toolset was also used for estimation of lengths of the ROH segments of different size. The estimation of genomic  $F_{ROH}$  () was conducted in R programme based on the following criteria: the minimal number of SNPs in ROH was calculated by the L-parameter, the maximal gap between SNPs was set to 1 Mb, the minimum SNP density was set to 1 SNP every 150 kb, no heterozygotes allowed, and the minimum length that constituted the ROH was set to 1 Mb. A total of 3,116 autosomal ROHs ranging from 1.0 to 59.5 Mb were detected. On average, there were ~37 ROHs per animal with an average length of ~6.94 Mb. Individual  $F_{ROH>1\text{ Mb}}$  ranged from 4.33% to 19.74% with an average of 10.25%. The frequencies of  $ROH_{1-2\text{ Mb}}$ ,  $ROH_{2-4\text{ Mb}}$ ,  $ROH_{4-8\text{ Mb}}$ ,  $ROH_{8-16\text{ Mb}}$ ,  $ROH_{>16\text{ Mb}}$  were 2.7%, 33.9%, 37.0%, 19.3%, and 7.1%, respectively. The estimated  $F_{ROH1-2\text{ Mb}}$ ,  $F_{ROH2-4\text{ Mb}}$ ,  $F_{ROH4-8\text{ Mb}}$ ,  $F_{ROH8-16\text{ Mb}}$ ,  $F_{ROH>16\text{ Mb}}$  were 0.07%, 1.50%, 3.06%, 3.15%, and 2.47%, respectively. These results suggest that majority of the inbreeding events occurred within 20 generations ago.

**Keywords:** Holstein, SNP data, inbreeding coefficient, matting