

**Inbreeding estimates using two different approaches in Gyr cattle.**

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The development of high-density SNP arrays led to an increasing interest in calculating the inbreeding coefficients using molecular information, instead of from pedigree data ( $F_{PED}$ ). The aim of this study was to estimate and compare inbreeding coefficients from  $F_{PED}$  and from runs of homozygosity (ROH) genomic data ( $F_{ROH}$ ). A total of 585 sires comprising the progeny test program from the National Program for Improvement of Dairy Gyr were genotyped with the BovineHD BeadChip (Illumina Inc.). Eight sires were removed due to low call rate (0.1); 7,411 markers were excluded based on HWE test ( $p \leq 0.00000001$ ); 14,351 SNPs failed on missing genotype rate; and 286,289 SNPs failed on MAF test ( $MAF < 0.05$ ). The ROH were identified using PLINK v1.07. Regions of homozygosity were extracted just in autosomes. The parameters set to perform ROH analyses were: homozyg-window-snp 50, homozyg-window-het 0, homozyg-window-missing 5, homozyg-snp 100, homozyg-gap 500, homozyg-kb 1000, homozyg-density 50. The ROH segments were classified into five length categories ( $L_{ROHj}$ ): 1 to 2; 2 to 4; 4 to 8; 8 to 16 and more than 16 Mb. The  $F_{ROH}$  were estimated for each animal dividing each  $L_{ROHj}$  by the autosome length covered by markers. The  $F_{PED}$  was calculated using INBUPGF90 software. The pedigree dataset contained 92,807 animals, in which 5,449 were sires and 38,704 dams, distributed into 7.7 generations. The  $F_{PED}$  ranged from  $7,62e^{-006}$  to 0.41, and  $F_{ROH}$  ranged from 0.001 ( $F_{ROH4,8}$ ) to 0.10 ( $F_{ROH8,16}$ ). Pearson's correlations were low to moderate:  $F_{PED:F_{ROH1,2}}$  (0.10);  $F_{PED:F_{ROH2,4}}$  (0.24);  $F_{PED:F_{ROH4,8}}$  (0.31);  $F_{PED:F_{ROH8,16}}$  (0.37), and  $F_{PED:F_{ROH>16}}$  (0.34). These results might be explained by the fact that the pedigree is not deep enough, poorly correlating with short segments arising from ancient inbreeding (up to 20 generations) and correlating moderately with long segments arising from recent inbreeding (0-5 generations).

**Key words:** autozygosity, *Bos Taurus Indicus*

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