INBREEDING ESTIMATES USING THREE DIFFERENT APPROACHES IN A SWINE BREEDING POPULATION

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Inbreeding, the mating of closely related individuals, is an important parameter in population genetics; it leads to an increased frequency of homozygosity, which often increases the risk of recessive deleterious alleles to be co-expressed and reduces genetic diversity. The standard approach to estimate inbreeding coefficient (*Fx*) in an animal population is based on the classical pedigree-based analysis. However, the availability of high density arrays has allowed more precise calculation of *Fx* using genomic markers. Thus, the aim of this study was to estimate and compare inbreeding coefficients based on pedigree (F_{PED}) and genomic information calculated using Runs of Homozigosity (F_{ROH}) and SNP by SNP inbreeding (F_{SNP}), in a Landrace population. Tissue samples from 300 females and 25 males representative of a company breeding herd were collected. DNA was extracted, and samples were genotyped using the Illumina Porcine60K SNP chip. SNPs and samples quality control was conducted using PLINK. SNPs were removed if they failed in more than 10% of the samples, had unknown positions and were located in sexual chromosomes. Animals were removed if the genotype call rate was <90%. The Pedigree package from the R program was used to estimate the F_{PED} using a 3 generation pedigree. PLINK was used to estimate the genomic inbreeding. ROH were detected with the following criteria: sliding window of 50 SNPs, minimum ROH of 50 SNPs with minimum length of 1000(kb), 1 heterozygous SNP and 1 missing SNP were allowed within the sliding window. The identified ROH were then used to calculate F_{ROH} from the formula: $F_{ROH} = \sum k_{lengh}(ROH_k)/L$; where K is the number of ROH identified for each individual in kb and L is total length of the genome (2,808,525 kb). F_{SNP} were obtained based on the excess of SNP homozygosity for the individual. The animal *Fx* was computed as $F_{SNP(i)} = [(OHi - EH)^2/(EH)]$. After filtering, one of 325 genotyped individuals and 9,384 of 61,565 SNPs were removed to estimate the genomic inbreeding. The average *Fx* calculated from F_{PED}, F_{SNP} and F_{ROH} were 0.00034, 0.037 and 0.119, respectively. With the breeding strategies applied to this Landrace line, the expected level of homozygosity should be higher than the one obtained based on pedigree. The sub estimation of *Fx* based on pedigree suggests possible problems in the animal pedigree in this population, which was confirmed with genomic data analysis. Furthermore, low correlation between *Fx* estimates based on pedigree and genomic data (F_{PED}-F_{ROH}: r^2 <0.04; F_{PED}-F_{SNP}: r^2 <0.08) were observed, while high r^2 between genomic methods (r^2>0.84) was found. These results show the effectiveness of using genome-wide SNP information for quantifying inbreeding when the pedigree was incomplete or incorrect. In addition, ROH length can be used to extract information on the population demographic history and genetic relationships.

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