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Detecting levels of autozygosity in two pure lines of pigs using genomic and pedigree data

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Introduction

Intense animal selection and breeding strategies have been used to improve several animal traits within the livestock sector. The fewer animals kept for breeding, the greater is the selection intensity; therefore, faster genetic progress can be accomplished (5). One of the concerns involving the massive use of specific sire lines to improve desirable traits is the loss of genetic diversity and the accumulation of high levels of homozygosity among animals, which could be detrimental to reproduction, conformation, and growth traits (2). The objectives of this study were to estimate and to compare levels of homozygosity using both pedigree and genotype data in two female pure lines of pigs, Landrace (LA) and Large White (LW).

Materials and Methods

The animals used in this study were from the BRF/SA private company (BRF-Brazilian Foods). The complete pedigree records for the LA breed contained information on 84,611 animals and for the LW 50,348 animals under selection. They traced back 12 generations, with an average length of 6.41generations for the LA and 5.55 generations for the LW. The pedigree records for the LA and LW were evaluated using the R-statistical environment with the pedigree package. The inbreeding coefficient (F_x) based on the pedigree of the animals was calculated using Wright's Coefficient (3). Animals were genotyped with Illumina 60K SNP Chip. The genomic inbreeding estimated with runs of homozygosity (ROHs) were calculated with PLINK using a sliding window of 50 SNPs, a minimum ROH of 50 SNPs with a minimum length of 1000 kb. One heterozygous SNP and one missing SNP genotype were allowed within the sliding window (4). Identified ROH were then used to estimate individual genomic inbreeding coefficients (FROH):

$$F_{ROH} = \frac{\Sigma_k \text{ Lenght } (ROH_k)}{L}$$

Where "k" was the number of ROH for each individual in Kb and "L" was the total swine genome length (2,808,525Kb, Sscrofa10.2, Aug 2011).

Results

After sample and SNP quality control, 1168 LA (91 M and 1077 F) and 1094 LW (114 M and 980 F) with 58,911 SNPs remained for the analysis. When all the generations were included in the analysis, the Fx calculated based on the pedigree ranged from 0 to 0.139, with an average of 0.014 in the LA, and from 0 to 0.062 for LW, with an average of 0.021. The average inbreeding of the LA animals using the ROH was 0.094 ranging from 0.012 to 0.184 and for LW was 0.106 ranging from 0.008 to 0.181. None of the homozygous regions were shared among all the animals within or across breeds. A region on SSC14 was identified with the highest number of homozygous regions among LA animals. This region harbors two important genes: *CXCL12* and *TFAM*. The *CXCL12* gene was associated with immunological traits in LA piglets, especially with disease resistance, being very important for the survivability of the animals (4). The *TFAM* gene plays an important role in porcine gametogenesis and embryo preimplantation and development, having broad implications for cell physiology and evolutionary biology (1).

Conclusions and Discussion

For diversity studies, the levels of recombination, inbreeding and segregation can be fairly estimated based on pedigree information. However, such parameters can be accurately calculated using high-density genomic data. The use of pedigree information alone to calculate levels of homozygosity and degree of relationship between animals underestimated the levels of inbreeding in both swine breeds analyzed, because of the limited number of generations that are traced back. Implementation of genomic tools to better estimate the correlation coefficient between animals will improve the accuracy of EBVs, consequently the selection efficiency, among other potential advantages. Although no inbreeding differences between breeds were found using FROH, the identification of conserved homozygous regions among individuals might reveal important findings related to the evolutionary standpoint for the pork industry.

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