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Genome wide association test with scrotal hernias in pigs

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Hernia is an abnormal protrusion of an organ or tissue through a defect or natural opening in the covering skin or muscle. In the swine industry, it is considered the most common congenital defect involved with high morbidity and mortality in the herds. The scrotal hernias are found in high frequencies ranging from 1.7 to 6.7%, and they have been linked to several boar lines and breeds, with moderated to high heritability (0.2- 0.86). However, even avoiding the use of those boar lines, hernias have not being completely eliminated from herds. Therefore, new approaches are needed to elucidate the genetic mechanisms involved with this condition to better select animals. Therefore, the objective of this study was to conduct a genome-wide association test (GWAS) in a cross-bred swine population (Landrace, Large-White and Pietrain) for the identification of genetic markers associated with the appearance of scrotal hernias. Animals were all from the same commercial swine herd located in the Northwest region of the RS. Piglets had similar age and were kept with the sow until 28 days of age and then weaned; castration was conducted during the first week of age. After weaning, piglets were moved to a group-housing with 100 piglets per pen with mixed sex. The phenotype classification was based on visual appearance of scrotal hernias. Each affected pig was matched to a healthy control from the same pen. In the total, 68 animals were genotyped using the Porcine SNP60 Beadchip, out of those, 41 animals had the presence of hernias and 27 were healthy animals. Markers and animals were submitted to a quality control process to remove individuals with difference in their genetic background and SNPs with a Minor Allele Frequency< 1% or if they failed in more than 10% of the samples. After after quality control, 50,797 SNPs from 18 healthy animals and 35 piglets with scrotal hernia were tested using an allelic X^2 test. From this test, we have identified two markers (MARC0114274, $P = 1.6 \times 10^{-7}$ and CASI0004285, $P = 1.6 \times 10^{-5}$) located on SSCX at 50,001,848 bp and 55,903,957 bp, respectively, and one with unknown location (MARC0063079, $P < 1.6 \times 10^{-5}$) associated with appearance of scrotal hernias in this population. In this study, we were able to refine the region linked with the appearance of hernias previously identified by Grindflek, E., BMC Genet. V. 7, P.1-12, 2006. We have identified that the segregation of these predisposing alleles for hernias in this population is via maternal inheritance. Therefore new approaches will be needed to eliminate those predisposing alleles to hernias out of this population, by removing the carriers females and replacing the boars being used.

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