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Identification of Porcine *Hernia inguinalis/scrotalis* Using Single Nucleotide Polymorphism in INSL3 and Bax Genes

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Abstract

Scrotal hernia is a congenital defect of great concern to pig producers that leads to economic loss and poor animal welfare. Several candidate genes have been proposed to be causative for the disorder. This study focused on the analysis of single nucleotide polymorphisms in the genes encoding the Leydig insulin-like hormone (INSL3) and the BCL2-associated X protein (BAX). INSL3 has recently been mapped to SSC2q12-q13 and BAX to SSC6q21. In total, 250 bp in INSL3 (promotor region) and 416 bp in BAX (Intron1) were comparatively sequenced using affected and un-affected commercial pigs as well as autochthonous Thai pigs. PCR-RFLP was used to screen SNPG-224A (INSL3) and C119T (BAX). A total of 212 commercial pigs (179 unaffected (u) and 33 herniated (h) pigs) were used for INSL3 genotyping. Allele frequency estimations revealed no significant differences between the two phenotypes at this loci ($G_u = 0.97$; $A_u = 0.03$; $G_h = 0.91$; $A_h = 0.09$) indicating that this mutation cannot be used to identify the disease. Interestingly, the allele frequency for G in Thai native pigs ($n=7$) was 0.07. It appears that the breed differences exist in the INSL3 gene. Screening of BAX was done in 151 commercial pigs (125 unaffected and 26 herniated pigs) showing significant differences in allele frequencies between unaffected and herniated pigs (C:T = 0.62:0.38 and 0.83:0.17) ($p < 0.01$). Allele C in Thai native pigs ($n=7$) was 1.00. Currently, further mutations in the regulatory and coding regions of BAX are identified to assess their possible role in this congenital disorder.

Keywords: BAX, INSL3, porcine *Hernia inguinalis*