

## CHAPTER 1

### INTRODUCTION

Advances in swine genetics have accelerated rapidly over time. Several genes that cause considerable phenotypic differences in pigs have been identified (halothane, rendement napole, and estrogen sulfate receptor genes). Genetic disorders are conditions caused by mutations in a gene or a set of genes. Gene mutations can result from a complex interplay of multiple genetic changes and environmental influences. Because of this complexity, it is unlikely that an individual health prospect can ever be predicted in a deterministic fashion from a term of genetic tests. Diseases existed at time of birth, before birth, or develop during the first months of life, an regardlessly of causation called congenital disease. Most congenital disorders have a genetic component in their etiology. This may take the form of a single gene or monogenic defect, a mitochondrial disorder, a chromosomal imbalance or a multi-factorial condition, which is partly genetic and partly environmental. Many different abnormalities occur in pig can have a negative effect on production. Congenital defects are common in pigs and the most important ones are cryptorchism, atresia ani and hernias (umbilical and scrotal). The situation of scrotal hernia in Thailand shows that the frequencies of herniated animals range from 1% (industrial pig farms) to 5% (small-size farms). The economic loss is about 300 baht per herniated pig (discount individual price for slaughter), alternatively the costs for castration is 150 baht per head. Selection against this disease is preferable for pig breeders.

To date no primary gene or any clear pattern of inheritance has been identified so far. In humans, a high segregation ratio suggests an autosomal dominant inheritance with incomplete penetrance. Also, sex influence was reported and proposed a possible role of genomic imprinting in the etiology of hernia. Anatomical factors such as an abnormal wide inguinal canal or a not obliterated processus vaginalis are regarded as predisposing for inguinal and scrotal hernia (Beck *et al.*, 2006). Persistence of the smooth muscle of the processus vaginalis or gubernaculum

has been proposed to result from a failure in apoptosis. Thus, *TAC1* and *BAX* genes involved in an expansion of the apoptosis cascade were chosen as putative function candidate genes. The objectives of this study were to localize the porcine preprotachykinin A (*TAC1*) and BCL2-associated x protein (*BAX*) genes on the porcine map and to characterize the structure of the porcine genes including detection of single nucleotide polymorphisms (SNPs).



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