

CHAPTER I

INTRODUCTION

Genetic improvement in the quality and production efficiency of pork are needed to maximize success of animal production. The amount of lean becomes the basis for the price paid for the carcasses. Loin-eye area is the one for the estimation of carcass muscle and it is one of the factors that can predict percent of muscle in USDA Grade. However, most traits of agricultural importance such as growth rate, fat levels, meat quality, disease resistance and reproductive performance are quantitative traits. In the past few years the researchers found progress in detecting genomic regions containing quantitative trait loci (QTL) and candidate genes of the traits. The first QTL in pigs detected by this approach was reported by Andersson *et al.* (1994). A QTL accounting for 10% of phenotypic variation for average backfat and abdominal fat on chromosome 4 was detected. There are genes that are candidate genes for growth traits due to the physiologic function of their products in the organisms. The analysis of such genes may provide useful markers for economically important traits or may even lead to the identification of polymorphism that cause phenotypic variation.

Another approach to detect candidate genes is based on the analyses of differences of the expression profile in a particular subsets of cells and/or individuals with certain phenotypes. These genes are functional candidate genes because of their temporo-spatial distribution of expression or their expression in certain phenotypes.

The functional candidate approach benefits from the fact, that it only deals with cDNA, devoid of intronic and intergenic sequences, which represent only a few percent of the total genome (about 3% in mammals). Differential expression screening approaches are therefore more closely associated to gene function. Since it is logistically near impossible to sequence the 100,000 different genes in a pig, the next best approach is to sequence only parts of the genes called ESTs. By the use of the differential display technique Ponsuksili *et al.* (1999, 2000b,c) were able to identify ESTs that represent genes that are functional candidate genes for the trait eye muscle area. One of these genes is the vinculin gene. Knowledge of the function of vinculin indicates that it is likely to be involved in growth and muscle phenotype. Therefore, this study focused on the polymorphism in porcine vinculin gene.