

CHAPTER 1

INTRODUCTION

During the last few decades, pig breeding programs have been based on genetic improvement to achieve profitability. Selections with pressures on economically important traits are considered to improve efficiency of production. The main areas of emphasis in genetic selection are lean yield, growth rate and reproductive performance. However, large improvement in these traits may have undesired impacts on other traits. Hence, some previous reports have revealed a genetic correlation between rapid growth and prevalence of leg weakness. Continued selection for high meat quantity and growth rate are found to exacerbate leg weakness problems (Kadarmideen *et al.*, 2004; Kadarmideen, 2008). That might be beneficial and interesting if genetic marker for leg weakness or its related traits could be identified and are included in the selection program. Osteochondrosis (OC) is one of the major reasons for leg weakness in growing and mature pig as well as in sow. OC lesion is responsible for economic losses and continues to be one of the causes of reduced reproductive performance and increased culling rate in breeding stock with an incidence of 10 to 20% (Jorgensen, 2000). The prevalence of OC is correlated with specific sire lines whose progeny are more susceptible (Frantz, 2006). Failure of chondrocyte differentiation, subchondral bone necrosis, and failure of blood supply to the growth cartilage have been proposed as the initial step in the pathogenesis (Ytrehus *et al.*, 2007). This means that OC lesion involved the disturbance of the endochondral ossification in the articular cartilage. These lesions are thought to form at an early age in the underlying bone and can be aggravated by stress or trauma to tissue. Hereditary dispositions and genetic influence play an important role in aetiology of the OC. Estimated heritability for OC ranging from 0.1 to 0.5 (Lundeheim, 1987; Stern *et al.*, 1995; Serenius *et al.*, 2004) supported that these traits are highly affected by genetic.

The genetic background of OC, which resembles alteration in the tissues degeneration has been examined and identified. A number of investigations in both human and animals have focused on the progression of OC to osteoarthritis (OA), the chronic stages of the disease. To yield information and understanding of the pathogenesis, factors involved in the respective theories have been investigated intensively in many species. However, up to date, the primary cause of OC is still debated. Moreover, genes which link or chromosome location susceptibility to OC in pig are less reported and need to be investigated. Genes previously linked to OA in human could be also considered as molecular markers for OCD in pig. Therefore, the present study was conducted in order to achieve the following aims-

(1) to characterize porcine matrix gla protein (*MGP*) gene (2) to find genetic variants of selected candidate genes. The polymorphism changes in *MGP*, transforming growth factor- β 1 (*TGF β 1*), matrix metalloproteinase-3 (*MMP3*), collagens type II (*COL2A1*) and collagen type X (*COL10A1*) genes were screened by comparative sequencing (3) for genotyping a large scale genotyping, multiplex SNP base extension method were developed and (4) to evaluate the association of identified polymorphisms within *MGP*, *TGF β 1*, *MMP3*, *COL2A1* and *COL10A1* genes with osteochondrosis traits in pig.