CHAPTER 5

CONCLUSION

In this study, genomic sequences of porcine MGP genes were characterized and identified for polymorphisms. Therefore, the full length porcine MGP sequence was sequenced and analyzed. Furthermore, three SNPs were detected within this gene, the association between MGP markers and association analysis with osteochondrosis traits and DXA traits were performed. Two SNPs were found in intron1 (MGPC1124A and MGPC1185T) and one SNP was found in exon 3 (MGPC3817T). Four additional candidate genes were selected (TGF\$\beta\$1, MMP3, COL2A1 and COL10A1). Altogether, 10 polymorphisms were identified. For genotyped, a high throughput platform for fast genotype and efficient analysis could be established. This method was able to call the correct genotypes with high degree of accuracy approximately 96%. SNPs in genes MGP, MMP3, TGFβ1, and COL2A1 were found to be significantly associated with BMD, BMC and OC lesions. Of particular note are MGP, MMP3 and COL2A1 genes. Only one SNP of COL10A1 gene was not significantly associated with studied traits. In addition, haplotypes associations of these genes were analyzed. MGP haplotypes (TAA and TAG) were found to be significantly associated with BMD, BMC and OC lesions. COL2A1 haplotype (CA) was found significantly with OC lesion on the knee joint. The results showed that genetic factors play a role in osteogenesis and chondrogenesis which exhibits mild osteochondrosis; abnormal development of the growth plates and degenerative changes in joints. The phenotypes of pig with genes defects show remarkable similarities with human diseases. The polymorphisms of these candidate genes, the human OA had already been characterized in detail of pathogenesis and etiogenesis. These findings provide new information on the association of susceptibility genes for OC in pig. The result could be useful for the development of molecular genetic marker for osteochondrosis in pig. However, future association analysis using commercial breed line will confirm of this result.