Mapping of Two High Mobility Group Protein Genes for Growth and Composition traits in Pig

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Abstract
Using information from the human genome two new candidate genes for growth and composition traits were studied. The porcine high mobility group isoforms protein [HMGI(Y) and HMGIC] genes were chosen based on their presumed role in fat cell growth and differentiation. The HMGI(Y) gene was assigned to pig chromosome 7 by both linkage and physical mapping methods. This assignment agrees with other comparative mapping studies as the human HMGI(Y) gene maps to human chromosome 6p21, which is known to share a homology with pig chromosome 7. Interestingly, the pig HMGIC gene was assigned to the pig chromosome 1 by both methods. The localization of these candidate genes in the pig genome could improve the power of analyses for quantitative traits associated with growth and meat quality traits.

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Mapping of Two High Mobility Group Protein Genes for Growth and Composition traits in Pig

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Summary and Implications
Using information from the human genome two new candidate genes for growth and composition traits were studied. The porcine high mobility group isoforms protein [HMG1(Y) and HMGIC] genes were chosen based on their presumed role in fat cell growth and differentiation. The HMG1(Y) gene was assigned to pig chromosome 7 by both linkage and physical mapping methods. This assignment agrees with other comparative mapping studies as the human HMG1(Y) gene maps to human chromosome 6p21, which is known to share a homology with pig chromosome 7. Interestingly, the pig HMGIC gene was assigned to the pig chromosome 1 by both methods. The localization of these candidate genes in the pig genome could improve the power of analyses for quantitative traits associated with growth and meat quality traits.

Introduction
Identifying major genes or quantitative trait loci (QTL) related to economically important traits and selecting animals based on genotype is an efficient tool to improve livestock production and product quality. Two primary methods, the candidate gene approach or QTL linkage mapping, have been used for gene identification. Some candidate gene studies have shown that this approach can be useful in generating tools for marker-assisted selection in livestock as well as serving as genes for the comparative gene map between species (5). In this study, our objective was to determine the linkage and physical gene map locations of the porcine HMG1 genes to improve the comparative pig gene map and to eventually evaluate the genotypic effects of HMG1 genes on several growth and composition traits in pigs. Recent studies indicate that the HMG1 gene products may be involved in fat cell proliferation and differentiation (1,4).

Materials and Methods
Physical gene mapping was carried out using typical molecular biology methods and pig-rodent somatic cell hybrid panel (6). Linkage mapping was initiated after identifying polymorphisms (different gene forms) by using DNA sequencing. The Berkshire and Yorkshire crossed ISU reference families were used for two and multipoint linkage analyses by using standard statistical approaches (3).

Results and Discussion
Approximately 700 bp products of the porcine HMG1(Y) gene spanning exons 6 and 7 were amplified by the combination primers. The sequence of the polymerase chain reaction (PCR) product confirmed that the PCR product is the HMG1(Y) gene with 92 and 86.2% identities at the amino acid and nucleotide levels, respectively, to the corresponding human HMG1(Y) sequence. One polymorphism was identified and used for linkage analysis in the Berkshire-Yorkshire cross family. HMG1(Y) was significantly linked to several markers on the published porcine chromosome 7. By analyzing the pattern of clones amplified on the somatic cell hybrid panel, the HMG1(Y) was physically mapped to SSC7q12-q23 as would be expected from survey of the chromosome painting available.

The porcine HMGIC gene fragments amplified from polymerase chain reaction were sequenced and analyzed. The sequence of the porcine HMGIC gene fragment, spanning exon 5 and the 3' UTR showed approximately 79% identity at the DNA level to the corresponding human sequence. We identified several polymorphisms in the porcine HMGIC gene. DNA samples from animals of three generation of the Berkshire x Yorkshire family were used to map the gene. The HMGIC gene was significantly linked to several markers on the published porcine chromosome 1 and the HMGIC also was physically mapped to the same chromosome.

This result is striking because human HMGIC maps to human chromosome 12q15, so the pig HMGIC was expected to map on pig chromosome 5, a region corresponding to that chromosome. However, the discrepancy might be evidence of the possible chromosomal rearrangement (or break) within the pig HMGIC gene because HMG1 genes have been evolved through gene duplication and exon shuffling events and the human HMGIC gene is known to contain chromosomal breakpoints associated with many cancers.

Conclusions
The localization of the HMG1(Y) gene in the pig chromosome 7 agrees with other comparative mapping studies. The positioning of HMG1(Y) under a fat QTL suggests that the HMG1(Y) is a possible candidate gene for the phenotypic variation of interest. Interestingly, the pig HMGIC was mapped to pig chromosome 1 by both methods.

Both genes were located, according to the linkage analyses, near chromosome regions that may be associated with several fatness traits. Additional analysis is underway to see if these genes are associated with some
the variation in fat related traits.

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**References**