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 [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.

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 *HMGI* genes to improve the comparative the pig gene map and to eventually evaluate the genotypic effects of *HMGI* genes on several growth and composition traits in pigs. Recent studies indicate that the HMG-I 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 a 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 *HMGI(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 *HMGI(Y)* gene with 92 and 86.2% identities at the amino acid and nucleotide levels, respectively, to the corresponding human *HMGI(Y)* sequence. One polymorphism was identified and used for linkage analysis in the Berkshire-Yorkshire cross family. *HMGI(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 *HMGI(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. The discrepancy could simply suggest the presence of a pseudogene. However, the discrepancy might be evidence of the possible chromosomal rearrangement (or break) within the pig *HMGIC* gene because *HMGI* 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 *HMGI(Y)* gene in the pig chromosome 7 agrees with other comparative mapping studies. The positioning of *HMGI(Y)* under a fat QTL suggests that the HMGI(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

1. Anand A, Chada K (2000) In vivo modulation of Hmgic reduces obesity. Nature Genetics 24, 377–380.
2. Goureau A., M. Yerle, A. Schmitz, J. Riquet, D. Milan, P. Pinton, G. Frelat and J. Gellin. 1996. Human and porcine correspondence of chromosome segments using bidirectional chromosome painting. Genomics 36: 252–262.
3. Malek, M., J. C. M. Dekkers, H. K. Lee, T. J. Baas, and M. F. Rothschild. 2001. A molecular genome scan analysis to identify chromosomal regions influencing economic traits in the pig. I. Growth and body composition. Mammalian Genome 12. 630–636.
4. Melillo RM, Pierantoni GM, Scala S, Battista S, Fedele M, et al. (2001) Critical role of the HMGI(Y) proteins in adipocytic cell growth and differentiation. Molecular and Cellular Biology 21, 2485–2495.
5. Rothschild, M. F., Soller, M. (1997). Candidate gene analysis to detect trait of economic importance in domestic livestock. Probe 8:13–20.
6. Yerle, M., Echard, G., Robic, A., Mairal, A., Dubut-Fontana, C., Riquet, J., Pinton, P., Milan, D., Lahbib-Mansais, Y., Gellin, J. (1996). A somatic cell hybrid panel for pig regional gene mapping characterized by molecular cytogenetics. Cytogenet. Cell Genet.73:194–202