Cloning of the complete gene for pig PIT-1 and analysis of PIT-1 protein function

T.-P. Yu, graduate student, H. S. Sun, postdoctoral research associate, M. F. Rothschild, professor, and C. K. Tuggle, associate professor Department of Animal Science Iowa State University

ASL-R1492

Summary and Implications

We have cloned and sequenced the complete proteincoding region of the pig PIT-1 gene. The pig PIT-1 gene is highly similar to the PIT-1 gene in other species (human, rodent, cattle). We also found some alternative forms of the pig PIT-1 gene. We have analyzed the protein function of the pig PIT-1 genes and one of its alternative forms; Δ 3PIT-1. The functional studies showed that the pig PIT-1 protein can function normally at growth hormone (GH) and prolactin (PRL), whereas the pig Δ 3PIT-1 protein cannot. These results imply that the pig PIT-1 gene is important in pig growth through regulation of GH and PRL gene expression, whereas its alternative forms might play different roles on PIT-1 target genes.

Introduction

PIT-1 is a regulatory gene of several important hormone (GH, PRL and thyrotropin- β) genes (1). Dwarf mice and humans have been found that lack PIT-1 gene activity. We have reported that the PIT-1 gene is associated with birth weight and backfat in the pig (2). To understand the biological function of the pig PIT-1 gene and its possible application in swine genetics, we completed cloning the PIT-1 gene in these studies. Several PIT-1 alternative forms also were identified in the pig while we attempted to clone the complete gene of PIT-1. They are the \triangle 3PIT-1 and the \triangle 4PIT-1 that are missing different parts of the PIT-1 gene, and PIT-1\beta that has additional amino acids relative to the PIT-1 gene. The Δ 4PIT-1 and PIT-1 β have functional differences and have previously been found in other species. Therefore, we investigated the function of the Δ 3PIT-1 and the normal pig PIT-1 protein.

Materials and Methods

The cloning of the pig PIT-1 gene and its alternative forms was done by using PCR (polymerase chain reaction) techniques to amplify specific PIT-1 gene sequences from pig pituitary mRNA. Several positive clones for each form of the PIT-1 gene were compared to known genes by using the BLAST molecular biology software. Plasmids containing these genes were engineered to produce recombinant pig PIT-1 protein and Δ 3PIT-1 protein in bacteria. These proteins were isolated and used in a DNA-protein gel electrophoresis binding assay to see if the protein could recognize and bind to the regulatory region near the rat GH or PIT-1 genes. (See T.-P. Yu's ISU Ph.D. dissertation for experimental detail.)

Results and Discussion

The complete pig PIT-1 gene (Genbank accession No. AF016251) shows high similarity to the PIT-1 gene of cattle, humans, and rodents (Table 1). Several alternative forms of the pig PIT-1 gene also were found: Δ 3PIT-1 (Genbank: AF016382), PIT-1 β (Genbank: AF010475), and Δ 4PIT-1 (Genbank: AF016348). PIT-1 β and Δ 4PIT-1, which were previously identified in rodents, have showed different regulatory functions on rodent PIT-1 target genes. The pig PIT-1 β and Δ 4PIT-1 are highly similar to the rodent PIT-1 β and Δ 4PIT-1. The Δ 3PIT-1 has only been found in pig.

Target gene recognition of pig PIT-1 and Δ 3PIT-1 proteins were examined. The coding sequences of each PIT-1 gene form were cloned into plasmids and engineered to express the pig protein in bacteria. Partial purification of the pig PIT-1 and Δ 3PIT-1 were used in a DNA-protein binding assay with two targets of the PIT-1 protein identified in rodents. The results showed that pig PIT-1 can recognize GH and PRL regulatory regions, whereas Δ 3PIT-1 cannot.

The high similarity in the PIT-1 genes between the pig and other mammals (bovine, human and rat), and the recognition of pig PIT-1 to rGH and rPRL regulatory regions reveal the functional conservation of PIT-1 across species. Therefore, the pig PIT-1 gene should play an essential role in the pig's growth. Our earlier work showed that the pig PIT-1 gene was significantly associated with birth weight and backfat in the ISU Chinese x US pig population (2). Also a region of chromosome 13 associated with the early growth was shown to be very close to PIT-1 (3). More work is required to determine if the PIT-1 or another gene near PIT-1 plays a regulatory role in pig growth and carcass differences between pig breeds, and to understand the possible pig breeding applications of PIT-1.

The PIT-1 alternative form that showed functional differences from normal PIT-1 also could be important in PIT-1 function and potentially have a pig breeding application. However, additional work will be required to demonstrate the level of expression of this alternate PIT-1 form.

Acknowledgments

This study was supported in part by the National Pork Producers Council, the USDA, and the Iowa Agric. and Home Econ. Exp. Station. The rGH and rPRL regulatory region were kindly provided by Dr. K. Kozak (Dept. of Molecular Biology, Mass. General Hospital, Boston, MA).

References

1) Tuggle, C.K. and A. Trenkle. 1996. INVITED REVIEW: Control of Growth Hormone Synthesis and release. Domestic Animal Endocrinology 13:1-34.

2) Yu, T.-P., C. K. Tuggle, C. B. Schmitz, and M. F. Rothschild. 1995. PIT-1 genotypes are associated with quantitative growth and carcass traits in swine. J. Anim. Sci. 73:1282-1288.

3) Andersson, L., C.S. Haley, H. Ellegren, et al. 1994. Genetic Mapping of Quantitative Trait Loci for Growth and Fatness in Pigs. Science 263:1771-1774.

Table 1. The percentage of identity of functional region (exons) between the swine PIT-1 gene and the bovine, human, and rat PIT-1 genes, respectively.asl-14

	exon 1	<u>exon 2</u>	<u>exon 3</u>	<u>exon 4</u>	<u>exon 5</u>	exon 6
bovine	92	94	94	96	95	90
human	90	94	91	94	90	91
rat	86	92	86	88	87	85