Mapping and Investigation of Two Novel Candidate Genes for Growth and Meat Quality traits in the Pig

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ASL-R 663

Summary and Implications

Two new candidate genes for growth and meat quality traits were studied. The porcine beta-tropomyosin (*TPM2*) and the agouti-related protein (*AGRP*) genes were chosen based on their presumed role in growth and meat quality traits. These genes were genetically mapped and were linked to several markers on porcine chromosomes (SSC) 1 and 6, respectively. Both genes also were physically mapped using a pig/rodent somatic cell hybrid panel. The physical locations of the genes are consistent with linkage results and previous chromosome painting results indicating conserved (similar) regions between human and pig chromosomes. Association studies of the *AGRP* and *TPM2* polymorphisms with growth and meat quality traits in commercial pig populations provided preliminary evidence that an *AGRP* polymorphism may be associated with variation in several traits of interest for pig breeding.

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 (3). In this study, our objective was to determine the linkage and physical locations of the porcine agouti-related protein (AGRP) and the beta-tropomyosin (TPM2) genes to improve the comparative the pig gene map and to evaluate the genotypic effects of *AGRP* and *TPM2* on several growth and meat quality traits.

Materials and Methods

Physical gene mapping was carried out using typical molecular biology methods and a pig-rodent somatic cell hybrid panel (4). Linkage mapping was initiated after identifying polymorphisms (different gene forms) using DNA sequencing. The PiGMaP reference families (1) were used for two and multipoint linkage analyses using standard statistical approaches (2). The polymorphisms also were genotyped in animals from PIC USA to investigate the association of these genes with the phenotypic traits.

Results and Discussion

The *TPM2* gene was assigned to chromosome 1 (probability =1.00) and the q23-q27 region (probability = 0.86) and showed significant linkage to several markers on porcine chromosome 1. Most significant linkages between *TPM2* and PiGMaP gene markers were obtained from microsatellite S0155 (recombination fraction = 0.02 and LOD = 24.48) and S0311 (recombination fraction = 0.04 and LOD = 22.58). We investigated the association between the polymorphism of *TPM2* and economic traits in several commercial lines of pigs. The overall analysis of the phenotypic data from the commercial lines of pigs revealed that there was no significant relationship between the phenotypic data and the polymorphism found in *TPM2*. However, the *TPM2* gene was found to be moderately associated with a difference in a pork color measurement in two of the three commercial populations in which the polymorphism exists. In one of the populations, heterozygous animals demonstrated a slightly lower Japanese color score value (3.25) than the animals homozygous for allele 2 (3.42). The other population also exhibited a similar tendency (the heterozygous animals had a lower Japanese color score (2.33) than allele 2 homozygous animals (2.51). These results indicate that although there was little overall phenotypic association with the *TPM2* gene, it may still have economic value in some populations.

The porcine *AGRP* gene was assigned to chromosome 6 (probability = 1.00) and the (1/2)p12-(1/2)p14 region (probability = 0.81) and showed significant linkage to several markers on the porcine chromosome 6. Most significant linkages between *AGRP* and PiGMaP markers were obtained from microsatellite S0087 (recombination fraction = 0.00 and LOD = 3.01) and S0297 (recombination fraction = 0.00 and LOD = 3.31) on porcine chromosome 6. No overall significant associations between *AGRP* genotypes and phenotypic trait data were found, but some of the individual results suggested that the rare allele 2 is preferred for better growth and overall meat quality traits. In the Landrace based population, the heterozygous animals (since only a few animals were allele 2 homozygotes) tended to exhibit lower ham minolta score (46.64) and drip loss (2.27%), higher ham pH (5.71) and loin depth (62.03 mm) than the allele 1 homozygous animals (47.7, 2.65%, 5.68 and 59.34 mm, respectively). These heterozygous animals also showed higher daily gain (917 g/day) than allele 1 homozygous animals (897 g/day). In the Large White based population (allele 2 homozygous animals were not present in the sample), the allele 1 homozygous animals showed better Japanese loin color score (3.74) than the heterozygous animals (3.32), but the presence of allele 2 showed better growth as in the Landrace based population. These results indicated that this *AGRP* gene could be associated with several traits in these commercial pig populations based on linkage disequilibrium with QTLs responsible for the phenotypic variation of these traits.

Conclusions

The localization of these genes is reasonably consistent with previous chromosome painting results indicating conserved regions between human and pig chromosomes. Furthermore, 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. Current data from *TPM2* shows very little association between the genotypic and phenotypic data analyzed, but further study is under way to search for other links between *TPM2* and meat quality traits. The *AGRP* gene locus on SSC6 is a possible marker for identification of quantitative trait loci associated with growth and meat quality traits and further investigation of this region will be useful for the marker-assisted selection for efficient and superior pork production.

Acknowledgments

We are grateful to Jeannine Helm for technical assistance, Regina Holzbauer (PIC USA) for the association analyses and Massoud Malek for the help with the linkage analysis. The sharing of the PiGMaP family DNA and database information (Alan Archibald and PiGMaP collaborators) and the SCH panel (Martini Yerle) are appreciated. Financial support provided by PIC and the Iowa Agriculture and Home Economics Experimental Station are also appreciated.

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Table 1. Effect of *AGRP* genotype on growth and meat quality traits in pigs from the Landrace based commercial population.

AGRP Genotypes	N	Days[a]	ADG[b]	BF[c]	Loin D[d]	Loin JCS[e]	Ham Min L[f]	Ham pH	Drip%[g]
11	382	163.33	896.65	12.39	59.34	3.39	47.71	5.68	2.65
12	81	162.53	917.45	11.92	62.03	3.43	46.64	5.71	2.27
22	7	158.62	917.50	12.19	62.25	3.46	44.52	5.76	3.93
P<0.32	P<0.13	P<0.55	P<0.03	P<0.89	P<0.11	P<0.22	P<0.06		

[a] Days to 110 kg.
[b] Daily gain (gm/day).
[c] Tenth rib backfat (mm).
[d] Loin depth (mm)-higher value better.
[e] Japanese Color Score - higher value better.
[f] Ham Minolta Score - lower value better.
[g] Drip Loss (%) - lower value better.

Table 2. Effect of *AGRP* genotype on growth and meat quality traits in pigs from the Large White based commercial population.

AGRP Genotypes[a]	N	Days	ADG	BF	Loin D	Loin JCS	Ham Min L	Ham pH	Drip%
11	75	169.12	846.40	13.61	57.52	3.74	45.56	5.65	2.22
12	18	165.14	889.64	13.00	58.85	3.32	44.98	5.73	2.50
P<0.12		P<0.03	P<0.46	P<0.52	P<0.07	P<0.79	P<0.28	P<0.72	

[a] Allele 2 homozygous animals were not present in the population.