

# Using Pig Genomic Sequence to Determine Underlying Mutations Affecting a Pig SSC17 Meat Quality QTL: New Developments

## A.S. Leaflet R2232

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### Summary and Implications

Improving pork quality is a high priority and a challenging task for the current pig industry. Because of the complicated properties of meat quality, breeding innovations for improved meat quality meat traits requires more knowledge of modern molecular and quantitative genetics than traditional breeding approaches. On the basis of previous quantitative trait loci (QTL) mapping results of our research group, additional SNPs markers were further mined and QTL fine mapping was implemented. We continue to search for additional markers to explain the meat quality effects seen on chromosome 17.

### Introduction

Meat quality is now a more important consideration when consumers decide to purchase pork, and pork with fine color, odor and flavor can be easily sold with an increased price. Therefore, improving meat quality is one of primary breeding goals in pig industry. However, in view of the general genetics, meat quality traits are usually regarded as quantitative traits that are controlled by polygenic genes and easily influenced by environmental factors. It is difficult and less efficient to carry out meat quality breeding schemes with traditional breeding techniques.

In the last decade, efforts have been put into pig QTL mapping and more than 900 QTLs relevant to pork quality have been reported (PigQTLdb). In previous studies by our group (Ramos et al., 2007), several meat quality QTL with significant effects were discovered on SSC17. There still remains an obstacle between discovery of these QTL and making genetic improvement. The biggest problem is that the QTL region spanned an interval of 30cM and contains at least 60 genes. So it is impossible to know which genes are really responsible for the individual traits. Increasing numbers of genetic markers in a QTL region and narrowing intervals between markers were previously undertaken. The objective of this continued study was to carry out QTL fine mapping on SSC17 and identify the possible causative mutations responsible for the observed meat quality QTL.

### Material and Methods

A total of five new genes to study were chosen using new sequence information from the ongoing porcine genome sequencing results from the Sanger Center and distributed by the International Swine Genome Sequencing

### Consortium

[http://vega.sanger.ac.uk/Sus\\_scrofa/index.html](http://vega.sanger.ac.uk/Sus_scrofa/index.html)). Genetic tests to detect mutations (called single nucleotide polymorphisms, SNPs) were then developed for genotyping and those mutations causing large genetic changes were given priority. Genotyping was accomplished in our ISU Berkshire × Yorkshire resource family. All genes were linkage mapped with two and multiple point analysis using standard programs of CRIMAP. Further QTL mapping and association analyses were performed in the BY population using QTL Express (<http://qtl.cap.ed.ac.uk>) and PROC MIXED procedure of SAS, respectively.

### Results and Discussions

More than forty SNPs were detected in the three selected genes and two novel transcripts. PCR-RFLP genotyping of two SNPs of interest were developed for each gene or transcript. The length of the new linkage map of SSC17 has added up to 128.1 cM. The QTL mapping results revealed that there were several significant positions, which confirmed the existence of meat quality QTL previously mapped (Ramos et al., 2007). A new peak was identified at position 128 cM with a light reflectance trait after a new gene was included in this region. The further association analysis indicated that this gene was highly associated with two light reflectance measures ( $P < 0.001$ ) and color score ( $P < 0.01$ ). Another new gene located at 103.5 cM was also associated with color and tenderness score ( $P < 0.05$ ). Three other genes had no significant associations with meat quality traits. Additional genes in this QTL region will soon be analyzed.

This new gene study demonstrated QTL related to meat quality in SSC17 can be further dissected by integrating a variety of approaches from molecular genetics, bioinformatics, and sequence information. It is hoped that these and future results will lead to useful genetic tests for the pig industry.

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