QUALITY PORK GENES: THE APPLICATION OF TRANSCRIPTOME AND PROTEOME ANALYSIS FOR THE DISCOVERY OF CANDIDATE GENES FOR PORK QUALITY AND PIG WELFARE - AN EU-FUNDED PROJECT

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### Background

Associations have been identified between DNA markers (polymorphisms) and economic traits in the pig including specific defects (porcine stress syndrome), litter size, meat quality, appetite and specific disease resistance. The pork industry has already made substantial use of genetic markers for meat quality with the "Halothane" and "RN" genes. These genes are associated with Pale, Soft, and Exudative meat and "cooking loss" respectively.

Muscle colour and pH (especially 24 hours post mortem) are the most common measures used to assess meat quality as they are correlated with drip loss and tenderness as well as to each other. A higher pH is associated with a higher water holding capacity, translating into lower drip or purge losses during storage, and a higher yield when processing (Eikelenboom et al., 1995).

More recently, several groups have reported Quantitave Trait Loci for meat quality traits and in two cases candidate genes have been identified, which effect pH and colour, on SSC15 and tenderness on SSC2 (Ciobanu et al., 2001, Ciobanu et al. 2002). Table 1 shows the possibilities of one of these markers for ultimate pH and colour.

Table 1: Association results between the genotypes at the I199V substitution site of the PRKAG3 gene and meat quality traits across five commercial pig lines

TRAITS	Least square means of 1199V genotypes*		
	II	IV	VV
Ham pH	5.81 (.01) e	5.74 (.01) <sup>f</sup> ,e	5.71 (.01) <sup>f</sup>
Loin pH	5.78 (.01) <sup>e</sup>	5.74 (.01) f,e	5.71 (.01) f
Ham Minolta L	44.9 (.37) <sup>e</sup>	46.5 (.27) <sup>f</sup>	46.9 (.26) <sup>f</sup>
Loin Minolta L	44.2 (.26) <sup>e</sup>	44.7 (.18) a	45.2 (.18) <sup>f,b</sup>
Ham Minolta b	3.63 (.14) <sup>e</sup>	4.30 (.10) f ,e	4.71 (.10) f
Loin Minolta b	3.15 (.08) e	3.31 (.06) <sup>c</sup>	3.49 (.06) f,d

Significant differences between least squares mean estimates (within a trait and genotype) are indicated with 2-letter superscripts: a-b p<.05, c-d p<.005. e-f p<.0005. An estimate with superscript "a" is significantly different at p <.05 from estimate(s) with superscript "b", same for c-d and e-f at their respective significance levels. Standard errors of the estimates are given in parenthesis.

DNA tests give the ability to produce pigs with more precisely defined characteristics, and give producers and processors greater control over their preferred results. Their use can result in increased rates of annual genetic improvement as well as ensuring that the progeny of selected breeding stock actually have specific desired genes. The outcomes of this EU project will allow a greater control over the genotype and a faster genetic improvement, which will bring higher profitability to the pork chain and better pork to consumers.

## Objectives

This project aims to use new functional genomics and proteomics approaches to identify candidate genes for meat quality and welfare in the pig.

## Methods

Phenotypic data will be collected on a total of 500 animals representing the most commonly used genotypes in Europe e.g. Large White Landrace and Duroc. Many different traits will be measured including growth and measures of stress levels, as well as carcass characteristics measures of quality such as pH, colour and drip loss, muscle biochemical characteristics, lipid classes and fatty acids composition. Samples will be collected from at least two muscles per animal immediately after slaughter in order to allow preparation of RNA and the proteomecDNA libraries will be constructed for the preparation of micro arrays in order to analyse gene expression in muscle at the time of slaughter. Arrays will contain both control and "candidate" genes. Data on the transcriptome and proteome will be analysed in order to identify genes associated with variation in meat quality traits.

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Preliminary characterizations of 8 pig genotypes are presented in Figure 1. Lines A-E will be included in the project.

Figure 1. Characterization of meat quality for 8 different pig lines after applying a Principal Component Analysis



## Project deliverables

This 3-year project began at the end of 2001 and will generate the following deliverables:

• Establishment of a unique project database on 500 pigs

- Potential of 1000 samples for RNA analysis
- New SSH libraries
- Normalised muscle cDNA library
- Porcine micro arrays for transcriptome analysis
- · 2D fingerprints of muscle proteome
- Association analysis of transcriptome and proteome with quality characteristics
- · Identification of candidate genes

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The ultimate aim is to identify new genetic markers that will provide new tools for the improvement of pork quality. More information about this brain the provide new tools for the improvement of pork quality. this EU project can be found on www.qualityporkgenes.com.

# Pertinent literature

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