

Genetics and genomics of pig meat quality – progress and prospects

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With the genetic improvement in the lean content of pork over recent decades, attention has increasingly focussed on the quality of that lean. Different interest groups attach importance to particular aspects of quality. The consumer is primarily interested in the pleasurable aspects of eating meat, its flavour and particularly its tenderness or lack of toughness (Warkup (1993). Dieticians are concerned with the nutritional value of meat, its fat, protein and moisture content and food retailers look to its appearance, particularly colour and texture, when displayed on meat counters or in supermarket packs.

There are two complementary models for the genetic control of complex traits such as meat quality. The infinitesimal model, that has provided the underpinning quantitative genetics theory for success in animal breeding over the past 50+ years, assumes that complex traits are controlled by large numbers of unlinked genes of which each only has an infinitesimal effect on the trait. In contrast, the major gene model assumes that a small number of (major) genes contribute a substantial proportion of the genetic variation in the trait of interest. The results from quantitative trait locus (QTL) mapping experiments in farm animals indicate that both models are incomplete. Modest numbers of QTL can explain some, but not all of the genetic variation in complex traits.

Major genes associated with significant reductions in quality have been identified. For example, the halothane sensitivity allele that leads to a high risk of porcine stress syndrome (PSS) as well as pale, soft, exudative (PSE) meat was the first allele to be identified and then selected in breeding programmes using molecular genetic tools (Fujii *et al.*, 1991). More recently, the *RN* allele, which reduces yields of cured ham, has been identified and molecular tests developed for animals carrying the undesirable alleles (Milan *et al.*, 2000). A number of genes with potentially desirable effects on traits of importance to the meat industry have now been fully characterised and the underlying molecular basis for the effects determined. A single base pair change in the regulatory sequence controlling the post-natal expression of insulin-like growth factor 2 (*IGF2*) in pigs has been shown to cause a significant increase in lean muscle content (van Laere *et al.*, 2003). With the exceptions noted above meat and product quality traits appear to be under the control of several genes. For example, Bidanel and Rothschild (2002) reviewed the large number of different alleles associated with meat quality traits that had been mapped in pigs. The current release of the pig QTL database (PigQTLdb, <http://www.animalgenome.org/QTLdb/pig.html>) contains information on 1,831 QTL from 113 publications. Of these QTL, the PigQTLdb curators classify 1,425 as Meat Quality QTL.

Our own results are drawn from a genome scan of the F₂ generation of a Large White (LW) x Meishan (MS) cross comprising 308 animals slaughtered at a mean live weight of 87 kg (Lee *et al.*, unpublished). The Meishan and Large White breeds are known to differ significantly for a wide range of traits, including growth rate, fatness, and reproductive performance (Haley and Archibald, 1992) and aspects of meat quality (Serra *et al.*, 1992). We have reported details of the population and QTL influencing boar taint earlier (Lee *et al.*, 2004). Quantitative trait locus (QTL) mapping analyses were performed for laboratory predictors and sensory panel assessments of meat quality. Muscle samples were recorded for pH, moisture, fat and protein percentages, shear force, myofibrillar fragmentation index (MFI) and 5 colour parameters. Fat and lean samples from cooked meat were scored by a trained sensory panel for juiciness, tenderness, flavour and overall acceptability. The F₂ individuals together with their F₁ parents and grand-parents were genotyped for 131 markers spanning the whole genome. Three QTL were detected at the genome wide significance level, these being colour lightness, L*, on chromosome 1, pH 24 hrs on chromosome 12 and juiciness score on chromosome 16. Twenty eight QTL were found at the 5% chromosomal threshold (approximately equivalent to the genome-wide suggestive significance level). One region of chromosome 2 contained putative QTL for yield force and sensory panel scores for tenderness and overall acceptability, with the MS allele favouring all three traits. Three QTL for MFI were found in regions where there were no other tenderness QTL and MFI was generally poorly correlated with other traits. QTL for colour dilution traits were found on chromosome 1, in the same interval as the L* QTL, with the MS allele associated with paler meat, and on chromosomes 2, 12 and 14, with variable allelic effects. QTL for colour saturation were found on chromosomes 1, and 9. The LW allele increased saturation on chromosome 1, but reduced it on chromosome 9. Four independently acting QTL for %protein were observed on separate chromosomes 1, 9, 13 and 16, each with additive and dominance effects, expressed in the female in favour of the MS allele. Of

the observed effects, it was suggested that the locus on chromosome 2 influencing tenderness traits in particular would be worthy of further investigation. In addition to the QTL effects, the results revealed highly significant positive correlations between subcutaneous fat depth and sensory panel scores for tenderness, flavour and acceptability.

Previous QTL studies of meat quality traits include, for example by de Koning *et al.* (2001) in Meishan x Large White and Landrace lines, Malek *et al.* (2001) in a Yorkshire x Berkshire population and Ovilo *et al.* (2002) in an Iberian x Landrace population. Perhaps the most important QTL finding in the current results, given that the factor most highly correlated with the sensory panel's overall acceptability score was tenderness, were the QTL for yield force and sensory panel tenderness score near the adjacent markers SW1879 and S0378 on SSC2, together with a QTL for overall acceptability near marker S0226, 20 cM away. In all three cases, the MS allele was associated with meat that was more tender and thus more acceptable. The combination of the three results gives a strong indication of the presence of a QTL for meat tenderness in this region of chromosome 2. This is further supported by the QTL for tenderness and chewiness scores reported by Malek *et al.* (2001) near the end of chromosome 2. The QTL for MFI on SSC2 was a long distance away and only showed dominance effects. Rohrer *et al.* (2005) have also reported shear force QTL on pig chromosome 2 from a Duroc – Landrace cross.

The calpastatin gene which maps to pig chromosome 2 is a strong positional and physiological candidate for the yield force QTL. Following leads from a genome scan of Berkshire x Yorkshire cross Ciobanu *et al.*, (2004) identified calpastatin haplotypes associated with yield force and juiciness. Meyers *et al.* (2007) also report evidence for a meat quality QTL close to the calpastatin locus as well as meat quality QTL at additional locations on chromosome 2. We have recently genotyped the Roslin population for several additional markers around the calpastatin locus on chromosome 2 in order to compare our findings with those of Meyers *et al.* (2007).

To conclude, the main QTL regions this study has revealed are for tenderness traits, both laboratory and by the sensory panel on SSC2 and for meat colour on SSC 1. Apart from the QTL detection, an interesting relationship between subcutaneous fat depth and muscle tenderness and flavour has been suggested. This putative relationship could be of interest to those promoting early maturing breeds such as the Middle White and Berkshire. Although such breeds have lost commercial popularity, because of their excess fatness, the above correlations suggest that this may be associated with superior quality lean, but further studies would be needed within the breeds to confirm this. Finally, although we and others have mapped QTL, identified genes and in a few cases the molecular variants influencing meat quality, the genetic factors presumed to control the claimed superior meat quality of Durocs, Berkshire and other traditional breeds arguably remain to be discovered.

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