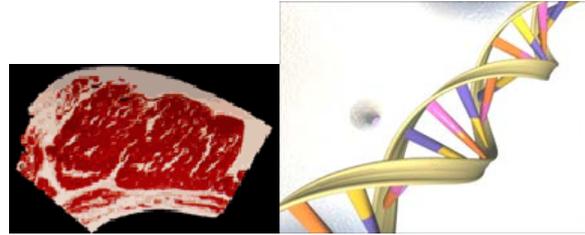


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## Assessment of DNA markers for meat quality traits in Irish beef and pork



### Key external stakeholders:

Breeders, meat processors, diagnostics companies

### Practical implications for stakeholders:

Variability in meat quality presents many problems for the industry and for consumer satisfaction. The underlying causes are multi-factorial in nature and are considered to include difference in the genetic profile (genotype) of the animal. Attributes of relevance to the consumer sensory experience include tenderness, colour, juiciness, flavour, texture, while those directly impacting on industry management systems include water holding capacity and colour. Management systems to predict and optimize these attributes require clear understanding of the factors underpinning variability. Currently eating quality is a major deficiency in breeding programmes and this is reflected along the beef chain from processors to retailers, who have highlighted the necessity for tools to accurately predict quality, in particular tenderness. Water-holding capacity has additional importance due to its ability to influence processed product quality and the financial losses incurred when it is sub-optimal. There is thus a need for tools to discriminate meat on the basis of quality and select sires for improved quality.

- A number of candidate genes have been identified as potentially relevant to beef sensory and technological traits.
- DNA markers have been tested and were shown to be associated with quality parameters.
- These hold potential quality prediction tools for meat management systems and/or to provide a basis for the inclusion of meat quality in selection goals.
- The outcomes highlight the importance of investigating and understanding the molecular basis of quality traits with a view to optimisation of management systems for quality.

### Main results:

- Novel single nucleotide polymorphisms (SNPs) developed which are associated with tenderness (shear force on day 14 and sensory tenderness) and intra-muscular fat (flavour, juiciness) content.
- SNP in CAST, PRKAG3, GHR and SCD genes were associated with muscle colour and PRKAG3 was also shown to be associated with cook loss in beef.
- SNP in CAPN1 and ANK1 were confirmed to be associated with shear force (tenderness).
- A GHR polymorphism was associated with composition of muscle including moisture, intra-muscular fat and protein content in loin and rump muscles.
- Commercially available markers tested (and subset validated) for association with Irish beef quality.

### Opportunity / Benefit:

The present research has validated some of the DNA markers tested in Irish crossbred cattle populations. Novel SNP markers associated with tenderness in Irish crossbred cattle have been identified. This research validates the genomic approach to meat quality and expansion of this research area is recommended. The further development of these and other markers for independent traits to create tools for prediction of quality would have a wide range of potential applications spanning animal production and meat management systems.

### Collaborating Institutions:

UCD

**Teagasc project team:** Dr. Anne Maria Mullen (PI)  
Dr. Ruth Hamill  
Dr. Wesley Reardon  
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**External collaborators:** Prof. Torres Sweeney, UCD

### 1. Project background:

Ireland has a good reputation internationally for producing high quality beef and pork, but variability in quality still remains. Defining the association between the genome and quality attributes is a first step to enable the prediction and management of the ultimate quality of pork and beef using genetic markers. Research has led to the identification of multiple genes and genetic markers that are reported to affect economically important traits in beef and pork. Many DNA single nucleotide polymorphisms (SNPs) have been identified which have shown potential as markers for meat quality traits. This project was established to test known SNPs for association with economically important traits in crossbred cattle and pigs and consequently for their relevance to the meat industry. We also identified and tested novel SNP for association with meat quality. Advances in meat genomics and knowledge gained from these approaches can be beneficial in defining and optimising management systems for quality, providing assurance of meat quality and in tailoring quality to suit market needs.

### 2. Questions addressed by the project:

- Are internationally developed genetic markers for meat quality relevant in Irish cattle and pig populations?
- Is it possible to identify novel genetic markers that are significantly associated with meat quality in Irish animal populations?

### 3. The experimental studies:

- A survey of commercially available markers and candidate gene markers from the literature was performed and communication established with two leading commercial companies, Genetic Solutions/Pfizer and Igenity. A panel of candidate DNA markers was selected to form the basis of the work.
- Selected candidate markers from the literature were studied in Irish crossbred cattle populations. They were tested for their influence on meat quality traits in loin [M. longissimus thoracis et lumborum (LTL)] and rump [M. semimembranosus (SM)] muscles.
- Selected DNA markers were also tested in 113 pork samples for which meat quality traits and sensory analysis were also available.
- Novel candidate genes whose expression levels correlated with beef quality were sequenced and novel DNA markers (SNP) identified and tested for association with beef quality.
- Polymorphisms were genotyped by TaqMan® assays, direct sequence analysis, PCR-RFLP or commercially by Genetic Solutions Australia/ Pfizer.
- Association analysis was carried out using the General Linear Model (GLM) procedure in SAS.

### 4. Main results:

- A detailed literature review resulted in 75 SNP in 42 bovine genes and 41 SNP in 35 porcine genes being identified for consideration.
- For the bovine we, tested published SNPs in candidate genes in bovine DNA samples from the following genes: Calpastatin (CAST), Protein kinase adenosine monophosphate activated gamma3-subunit (PRKAG3), Growth Hormone Receptor (GHR), Stearoyl-coA Desaturase (SCD), Calpain I (CAPN1), Carboxypeptidase E (CPE), Heat Shock Protein 70 (HSP 70), Fatty Acid Binding Protein 4 (FABP4), Diglyceride acyltransferase (DGAT1), Thyroglobulin (TG) and CCAATT/Enhancer Binding Protein Alpha (C/EBP- $\alpha$ ) genes. Many of the markers tested displayed a significant relationship with eating and technological traits of interest to the industry and consumer alike.
- A SNP in CAPN1 was confirmed to be associated with shear force (tenderness) in LTL but other CAPN1 SNP were not associated with shear force. Reported associations of SNP in DGAT1,

FABP4, TG and leptin genes with intra-muscular fat content were not confirmed. A GHR polymorphism was associated with composition of muscle including moisture, intra-muscular fat and protein content in LTL and SM. SNP in CAST, PRKAG3, GHR and SCD genes were associated with muscle colour and PRKAG3 was also shown to be associated with cook loss in beef for the first time.

- Novel SNPs in the bovine Ankyrin 1 gene were identified using RACE-PCR, followed by sequencing of 1.1 kilobases of the gene promoter region. Ten identified novel SNP markers in the Ankyrin 1 gene were tested for association with beef quality. Significant associations with tenderness (shear force on day 14 and sensory tenderness) and intra-muscular fat content were identified. Using the genotypes obtained it was possible to discriminate tender from intermediate to tough beef.
- For commercially available markers, one molecular marker (of 4 tested) showed significant association with beef Warner Bratzler shear force. None of the 4 commercial markers for marbling were found to be associated with intramuscular fat % in the sample set used.
- We also tested published SNPs in candidate genes in porcine DNA samples: Protein kinase adenosine monophosphate activated gamma3-subunit (PRKAG3), Calpastatin (CAST), Agouti signalling protein (ASIP) and Succinate dehydrogenase complex, subunit D (SDHD) genes were genotyped. Association analysis of genotype frequencies with phenotypic traits revealed a number of significant associations between alleles at SDHD SNP with four meat quality traits.
- Associations were also observed between alleles at the ASIP SNP with several meat quality traits. Associations were also observed between alleles at the CAST Arg249Lys SNP and 4 meat quality traits relevant to water-holding capacity.

#### 5. Opportunity/Benefit:

Novel SNP associations have potential utility in breeding programmes or for processors in meat management systems. Because genetic improvement is a permanent and cumulative procedure, investing in selection can be highly profitable for livestock producers. Identified markers hold potential in forming SNP panels for incorporation into management systems for delivery of consistency in quality. At Ashtown, we have tested a palatability-based grading system for Irish beef. A number of inputs along the meat chain are modelled against consumer based palatability evaluation of beef to provide prediction equations for the eating quality of each cut. Information on an individual genotype may augment these equations. Further information on potential exploitation of the project outputs can be provided by contacting the researchers.

#### 6. Dissemination:

Dissemination has taken the form of peer-reviewed publications, technical publications, conference presentations and posters, RELAY workshop presentations, popular publications and industry information days. RELAY workshop presentations may be accessed on the RELAY website <http://www.relayresearch.ie/Public/WorkshopList.aspx>. Popular presentations included an article for FeedInfo.com and presentation of the results during Science Week.

#### Main publications:

Aslan, O., Sweeney, T., Mullen, A.M. and Hamill, R.M. (2010). 'Regulatory polymorphisms in the bovine Ankyrin 1 gene promoter are associated with tenderness and intra-muscular fat content.' *BMC Genetics* 11: 111

Reardon, W., Mullen, A.M., Sweeney, T. and Hamill, R.M. (2010). 'Association of polymorphisms in candidate genes with colour, water-holding capacity, and composition traits in bovine *M. longissimus* and *M. semimembranosus*.' *Meat Science*, 86 (2): 270-275

Pannier, L., Mullen, A.M., Hamill, R.M., Stapleton, P.C. and Sweeney, T. (2010). 'Association analysis of single nucleotide polymorphisms in DGAT1, TG and FABP4 genes and intramuscular fat in crossbred *Bos taurus* cattle.' *Meat Science* 85 (3): 515-518

#### Popular publications:

Hamill, R.M. (2008). 'The genomic component of beef quality.' *The Ashtown Food Innovator*, Spring 2008, Issue 1, p.2.

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Pannier, L. and Wesley Reardon (2008). 'Addressing cook loss and palatability in beef through genomics.' *The Ashtown Food Innovator*, Issue 2, Summer 2008, p. 3.

Mullen, A.M., Corcoran, D., Hughes, L. and Hamill, R.M. (2007) 'Genomic and proteomic approaches to understanding and enhancing meat quality.' *FeedInfo.com*. Available [www.feedinfo.com](http://www.feedinfo.com)

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**7. Compiled by:** Dr. Ruth Hamill, Dr. Anne Maria Mullen

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