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National Food Centre

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GENOMICS AND MEAT QUALITY

Ashtown Food Research Centre,
(formerly National Food Centre),
TEAGASC, Dublin, Ireland.
Mission Statement

To further our understanding of meat quality traits through the analysis of molecular components of muscle, and their interaction with environmental factors, with a view to predicting, enhancing and controlling meat quality.
Objectives

Application of tools of molecular biology to investigate the relationship of the following with meat quality:

1. Gene expression & environmental factors
2. Protein expression & environmental factors
3. DNA markers

The frequency at which genotypes of interest occur in the Irish herd will also be determined.
Functional Genomics
Functional genomics to date

- RNA stability studies
- Gene expression
  - SSH libraries tenderness/IMF/WHC
  - real time PCR
  - arrays

Functional genomics short to medium term

- Interaction of diet, breed and gene expression – relationship with quality
- Postmortem carcass intervention
- PACCP based management system

Partners – Michigan State University; University College Dublin/Conway Institute; NDC-Galway; Australia,
Proteomics
Proteomics to date

- Detection of novel quality indicators
- Focused on muscle and exudate extracts (1D & 2D)
- Protein expression
  - 1D - 5 new potential markers identified
  - 2D - 21 differentially expressed
- Muscle model for molecular studies (tough/tender)
- Development and factory testing of immunoassays

Proteomics short to medium term

- Interaction of pre/post slaughter events with protein signatures – relationship with quality

Partners - Michigan State University; INRA
DNA markers
## Tenderness

### Association analysis between genotypes and Warner Bratzler shear force

<table>
<thead>
<tr>
<th>Gene</th>
<th>Genotype</th>
<th>Warner-Bratzler Shear Force (N) (mean±stdev)</th>
<th>n</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Calpain I, exon 9</td>
<td>GG</td>
<td>49.42 ± 23.61</td>
<td>208</td>
<td>0.0033</td>
</tr>
<tr>
<td></td>
<td>GA</td>
<td>39.05 ± 11.50</td>
<td>63</td>
<td></td>
</tr>
<tr>
<td></td>
<td>AA</td>
<td>34.15</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>Calpain I, exon 14</td>
<td>VV</td>
<td>46.20 ± 19.3</td>
<td>177</td>
<td>NS</td>
</tr>
<tr>
<td></td>
<td>VI</td>
<td>51.82 ± 30.58</td>
<td>57</td>
<td></td>
</tr>
<tr>
<td>Calpain II</td>
<td>AA</td>
<td>46.02 ± 16.36</td>
<td>41</td>
<td>NS</td>
</tr>
<tr>
<td></td>
<td>AB</td>
<td>43.80 ± 16.63</td>
<td>143</td>
<td></td>
</tr>
<tr>
<td></td>
<td>BB</td>
<td>49.06 ± 27.58</td>
<td>86</td>
<td></td>
</tr>
<tr>
<td>Growth Hormone</td>
<td>DD</td>
<td>33.53 ± 11.44</td>
<td>5</td>
<td>NS</td>
</tr>
<tr>
<td></td>
<td>CD</td>
<td>46.61 ± 27.12</td>
<td>43</td>
<td></td>
</tr>
<tr>
<td></td>
<td>CC</td>
<td>47.59 ± 20.89</td>
<td>220</td>
<td></td>
</tr>
</tbody>
</table>

NS = non significant; N = newtons
Others markers currently being assessed

- Leptin,
- Thyroglobulin
- DGAT
- ...
- Associations with quality traits
- Frequency in Irish herd
- Breeding, production groups
- Partners University College Dublin/Conway Institute, Michigan State University
Applications

- Marker assisted selection breeding programmes.
- Diagnostic test for quality.
- Integrate into a PACCP based management system. Interaction between genotype and pre/post slaughter management system.
- Integrate into a similar system for healthier meat.
- Cost benefit analysis.
Acknowledgements

- Research team – Dr Patricia Stapleton, Dr Elaine O’Doherty, Dr Deirdre Corocoran, Dr Annamaria White, Dr Karen O’Reilly, Dr Aidan Moloney, Veronica Sanchez, Shane Costello, Liselotte Pannier, Paul Sullivan.

- Funding sources – Teagasc Biotechnology Initiative, Enterprise Ireland, Department of Agriculture and Food, EU – Marie Curie.
Design of Meat Products with Proteomics (Meatomics)
Projects in MeatOmics at KVL

- Specific activity markers for post mortem proteolysis
- Protein modifications related to meat quality
- Fungal stress in relation to preservation of meat products
- Regulation of calpain
- Effect of mechanical stimulation on muscle cells
- Genetic variation in chicken
- Effect of compensatory growth in pigs
Dr Eva Veiseth
Agricultural University of Norway
Norway
Proteomics at Ås Campus Norway

Eva Veiseth

Dept. Mathematical Sciences and Technology, Norwegian University of Life Sciences & MATFORSK, Norwegian Food Research Institute
Salmon aquaculture in Norway

  - 44% of world total production

- Accounts for more than twice the sum of all other farmed meat products in Norway

- Salmon meat quality affected by:
  - Genetics
  - Production and slaughter conditions
  - Postmortem treatments
Stress and salmon quality

HANDLING
CROWDING
TEMPERATURE
TRANSPORTATION

MUSCLE pH
RIGOR MORTIS
GAPING
TEXTURE
COLOUR
WHC
Research goals

• Better understanding of:
  • mechanisms that regulate fish meat quality
  • stress response in salmon
  • connection between stress and meat quality

• Find biomarkers
  • Stress (process control)
  • Meat quality traits (sorting)
Myosin regulatory light chain 2
Fast myotomal muscle tropomyosin
Fast myotomal muscle actin
Myosin heavy chain
Glycogen phosphorylase fragment
Myosin heavy chain
Myosin regulatory light chain 2
TES-soluble muscle proteins

Blood plasma
Proteome activities at MATFORSK, Norwegian Food Research Institute
Research areas

- Proteome changes during tenderisation
  - Identify protein changes that are related to tenderisation
  - Biomarkers for tenderness?

- Heritability (Genetics)
  - Identify heritable protein changes related to tenderisation
• Protein degradation in dry-cured hams
  • Biomarkers for good quality?
• Changes in metabolic proteins

• Early postmortem period (Poster # Th56, Jia et al.)

• Electrical stimulation
INRA: Institut National de la Recherche Agronomique

Proteomics all of INRA: groups working on trout, pig, cattle, chicken, sheep
Our research center: Clermont-Ferrand
Our research unit: Food Product Quality
QuaPA meat proteomics

Proteomic approach to characterize pale and dark turkey breast meat sorted by image video Santé-Lhoutellier V, Le Pottier G, Sayd T & Monin G ICoMST 2004

*Image analysis of 2DGE shows 18 to 26 spots change between the groups*

Proteomic characterization of normal and pasty Spanish dry-cured hams. Maria H, Sante-Lhoutellier V, Jacinto A & Monin G. ICoMST 2004

*Image analysis of 2DGE shows 10 spots characterize this problem*

Proteome analysis of the sarcoplasmic fraction of pig semimembranosus muscle: correlation with meat $L^*$ value. Morzel, M., Sayd, T., Chambon, C., Franck, M., Larzul, C., Le Roy, P., Monin, G., Chérel, P. and Laville, E. 2005. 51st ICoMST, Baltimore, USA 7th-12th August 2005. *This paper is preliminary: proteins of glycolytic and oxidative metabolisms, but also chaperone proteins are associated preferable with light or dark samples.*


*Preliminary results show that glycogen myophosphorylase fragments and GST-pi are associated with muscle hypertrophy.*
QuaPA meat & stress


Pub Med: « proteome & muscle & stress » = 14, 2 = skeletal muscle
ibid replace stress with calpain = 0

- Age = oxidative stress, chronic inflammation
- 2DGE “fiber type = enolase, TP isomerase, CK etc”, apobec2 and galectin
- Ab chip (700 Ab) markers = telethonin, C9, lamin, cathepsin, NFkB


- Surgery = trauma as systemic stress; muscle markers = enolase and actinin only
How to use this type of information

- **Meat mechanisms**: calpain degradation of cytoskeleton

- **Strategy for biomarkers**:
  - PNAS, 2005, 102 (21) 7677-7682
  - Serum protein markers for early detection of ovarian cancer
  - Gil Mor, Irene Visintin, Yinglei Lai, Hongyu Zhao, Peter Schwartz, Thomas Rutherford, Luo Yue, Patricia Bray-Ward, and David C. Ward
  - No single protein could completely distinguish the cancer group from the healthy controls. However, the combination of the four analytes exhibited the following: sensitivity 95%, positive predictive value (PPV) 95%, specificity 95%, and negative predictive value (NPV) 94%, a considerable improvement on current methodology. (IGF-1, leptin, prolactin)
Keynote review: Recent advances in biomarkers for cancer diagnosis and treatment
Upender Manne, Rashmi-Gopal Srivastava, and Sudhir Srivastava

During the past two decades, fewer than 12 biomarkers have been approved by the US Food and Drug Administration (FDA) for monitoring response, surveillance or recurrence of cancer [1]. This is surprising because hundreds of thousands of biomarkers have been discovered or declared to be potential biomarkers for cancer diagnosis and detection. However to date none have proven to be effective.