

# The Challenge: Molecular Mapping of Meat Protein Modification through Processing

Jolon M Dyer<sup>1-4\*</sup>, Tzer-Yang Yu<sup>1</sup>, Anita J Grosvenor<sup>1</sup>, Santanu Deb-Choudhury<sup>1</sup>, Stephen Haines<sup>1</sup>, Duane Harland<sup>1</sup>, James Morton<sup>2,4</sup>, Stefan Clerens<sup>1,2</sup>

<sup>1</sup>Food & Bio-based Products, AgResearch Lincoln Research Centre, Private Bag 4749, Christchurch, New Zealand

<sup>2</sup>Biomolecular Interaction Centre, University of Canterbury, Christchurch, New Zealand

<sup>3</sup>Riddet Institute, based at Massey University, Palmerston North, New Zealand

<sup>4</sup>Centre of Food Science & Innovation, Lincoln University, Canterbury, New Zealand

\*Corresponding author (Jolon.Dyer@agresearch.co.nz)

**Abstract-** Protein modification occurring during production, environment, processing, transport, storage and food preparation can affect all key quality attributes of meat-derived products. This includes effects on texture, mouthfeel, solubility, taste, color, nutrition and health. We here summarize developing proteomics-based approaches to characterizing and understanding these modifications, and tracking modification through meat processing.

**Key words: Meat, Proteins, Modification, Processing, Oxidation**

## I. INTRODUCTION

Post-production modification of muscle components at the molecular level, particularly proteins and lipids, affects all key quality attributes of meat-based ingredients and foods, including nutritional value and eating quality. This modification is induced through both natural degradative processes and also through common food handling and processing steps. Development and utilization of highly sensitive analytical techniques to characterize and track modification at the molecular level is therefore increasingly of interest to the food industry, as a means to facilitate control of product quality, functional attributes and consistency. The emerging discipline of redox proteomics provides new tools and approaches to achieving these goals. We here briefly summarize the underpinning concepts which provide a basis to map and track a wide array of protein primary structural level modifications through meat processing.

## II. DISCUSSION

Traditionally, the food industry has used relatively empirical, one-dimensional approaches to measuring food modification. For example, overall levels of oxidation are typically assessed via reaction with dinitrophenylhydrazine and subsequent colorimetric assay. However, these types of evaluation cannot assess specifically what modification types are occurring, where these are located in the protein primary structure and how the relative abundance of these change through processing. To fully understand and ultimately control modification of meat proteins and subsequent product quality, more advanced tools are required.

### *The Challenges*

Modification of food proteins when considered at the molecular level is highly complex. Oxidation is an example of a key modification process associated with changes in meat quality. Protein oxidation is not underpinned by any one type of modification at the molecular level, but is in fact a complex cascade of oxidative products. Initially formed primary oxidation products, such as tryptophan oxidation to hydroxytryptophan, are progressively further modified to secondary products, such as dihydroxytryptophan, and so on. For any given amino acid residue within any given protein, the relative abundance of the native unmodified residue to its modified products will be progressively changed over time, in response to oxidative and other insult. Although any specific modification may be present in low overall relative abundance, the accumulation and interaction of the wide array of modifications within the meat proteins directly impact all product quality attributes.

### *Redox Proteomics*

Redox proteomics is a sub-discipline derived from classical proteomics but focused explicitly on the characterization of oxidative and reductive (redox) changes in proteins [1]. The key underpinning step is initial characterization of the modifications. Oxidative insult of food proteins results in differing types of protein

modification, including amino acid residue side-chain modification, Maillard modification, side-chain scission, terminal modification, protein backbone cleavage, and protein-protein crosslinking. Summarized, many of these modifications can be mapped via initial separation to enrich specific protein fractions, typically based on liquid chromatography, and followed by mass spectrometric evaluation. Recent advances have incorporated a redox scoring system into the evaluation [2]. This type of scoring system ranks observed molecular products according to their degree of modification from the native unmodified amino acid residue. So, using the example cited earlier, each observed hydroxytryptophan would be assigned a score of 1, while each observed dihydroxytryptophan is assigned a score of 2, and so forth. This scoring allows a good overview of the modifications occurring, and can be broken down to summarize specific categories of modification. To account for variation in extraction and observation of meat proteins between samples, a weighting factor can be applied that allows highly robust comparison between differing samples [3]. Utilizing this approach, samples can in principle be taken throughout production and processing, to track the formation of specific products. For a more detailed example of the application of redox proteomics to mapping meat protein modification during thermal processing/cooking, please refer to these references [4-6].

### III. FUTURE DIRECTIONS

Redox proteomics tools offer significant advantages over empirical assays. However, limitations still remain to be overcome. Mapping all forms of potential protein modification simultaneously, including crosslinked modifications, will ultimately provide the full understanding required to correlate molecular level modifications robustly to higher order structural changes and holistic meat product properties. In tandem, advances in techniques that provide absolute quantitation of each and every modification type are required for proteomic approaches to achieve their full potential.

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