IOWA STATE UNIVERSITY
Department of Animal Science

2023 DataFEWSion Symposium
January 10, 2023

Utilizing Proteomic and Metabolomic Data to Predict Fresh Pork Loin Quality

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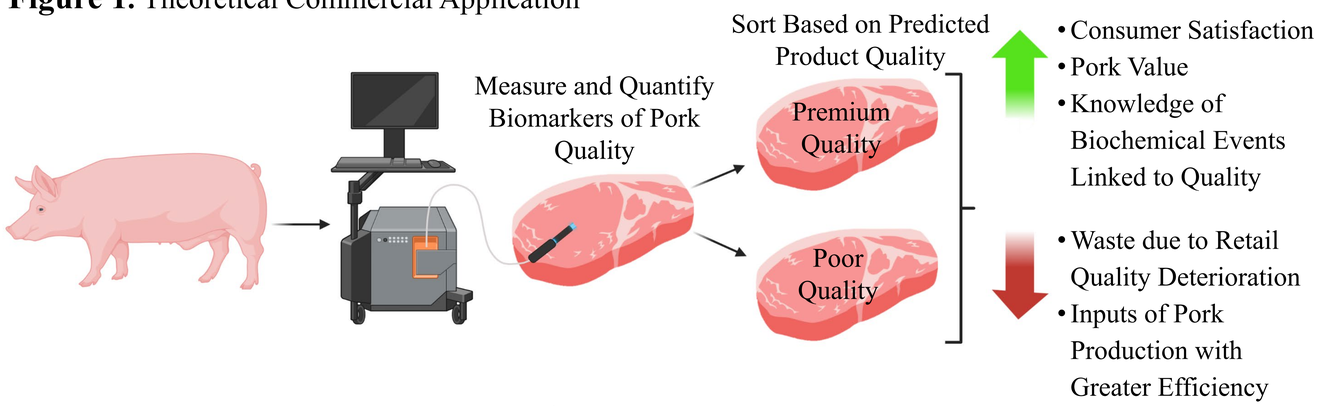
Introduction

- Iowa is the leading producer of pork in the United States, producing one-third or approximately 9 billion pounds of pork annually for domestic and export markets.
- There is no current applied industry standard for sorting pork based on product quality. Predicting the ultimate quality of fresh pork is challenging as numerous factors influence pork quality, including genetics, nutrition, postmortem handling, and other undefined variation.
- If pork producers and processors had a means of predicting the quality of fresh pork products, they could sort and merchandize products for different markets, increase pork value, and improve consumers' satisfaction when purchasing and consuming pork products.
- Previous research has determined certain proteins and metabolites are associated with pork quality measurements, including tenderness, color, and water-holding capacity.

Objective: To evaluate the proteome and metabolome of aged pork loins to understand better the association with measures of pork quality, including tenderness, color, and water-holding capacity.

Figure 1. Theoretical Commercial Application



Materials and Methods

- Fresh pork loins (N = 100) were collected from a commercial pork harvest facility. Loins were aged for 12 to 14 d postmortem, and pork chops (2.54 cm) were fabricated and evaluated for chop purge, cook loss, moisture content, ultimate pH, color, star probe, and sensory traits.
- Pork chops were uniformly powdered in liquid nitrogen. Proteins were extracted in a low-ionic strength buffer, and metabolites were extracted using 80% methanol.
- Proteins were reduced, alkylated, and digested with trypsin. Tandem mass tags were used to label individual samples to allow for quantification. Peptides were evaluated using liquid chromatography-mass spectrometry. Metabolomic analysis was conducted using gas chromatography-mass spectrometry.

Figure 2. Overview of the Current Research Workflow

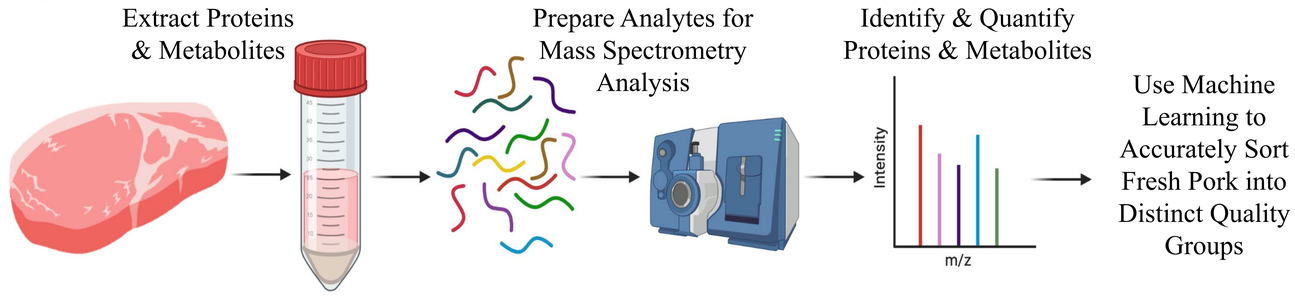


Table 1. Summary of quality, proteome, and metabolome differences based on sub-setting the initial (N = 100) pork loins by different measures of pork quality

Pork Quality Classification	Premium Quality	Poor Quality	Number of Different Proteins	Number of Different Metabolites
Tenderness/ Star Probe (SP)	n = 25; SP ≤ 4.5 kg	n = 25; SP ≥ 5.7 kg	84	22
Instrumental Color	n = 29; L^* ≤ 47	n = 28; L^* ≥ 49.7	43	22
Water-Holding Capacity	n = 27; Purge Loss ≤ 0.45%	n = 27; Purge Loss ≥ 0.95%	40	25

Results & Discussion

- Pork chops that are more tender, darker in color, and have lower purge loss could be considered more premium in quality. The proteomic and metabolomic analysis showed that pork chops of different quality groups have different proteomic and metabolomic phenotypes.
- A greater abundance of sugars was observed in pork chops of poorer quality groups. Premium pork chops had greater proteolytic degradation of key myofibrillar and structural proteins, such as desmin. These data support previous studies while extending the knowledge of new associations between pork quality and proteomic and metabolomic phenotypes.

Implications & Future Work

- These data distinctly show that the proteome and metabolome of pork loins vary greatly and are associated with distinct pork quality attributes. Continued work to validate and use these data to predict ultimate pork quality will be crucial in efforts to sort and merchandise fresh pork.
- Improving pork quality will improve pork value. Higher quality pork will maintain color in retail settings for longer, reducing retail waste and the need for greater food, energy, and water inputs in producing pork products.

Acknowledgements: Partial funding was provided from the Iowa Agricultural and Home Economics Experiment Station project no. IOW04121 and the Iowa Pork Producers Association.