

# DISTINCTION OF BEEF WITH DIFFERENT STORAGE PERIODS BY ARTIFICIAL INTELLIGENCE-BASED TECHNOLOGY

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## I. INTRODUCTION

Aging is a method that enhances the tenderness and flavor of meat by decomposing meat proteins into various substances, such as peptides and amino acids, by endogenous proteolytic enzymes [1,2]. Changes in proteome or peptide distribution characteristics due to proteolysis are crucial indicators of the aging period [2]. Although HPLC and mass spectrometry can perform precise and accurate quantitative and qualitative analyses of proteomes and peptides, identifying significant markers in the vast amount of data, ranging from dozens to tens of thousands, remains challenging. Recently, artificial intelligence-based technology has made it possible to quickly and accurately analyse big data, which is useful in both research and industry [3]. In this study, we applied artificial intelligence-based technologies to discriminate aged meat from fresh meat using vast amounts of peptide data obtained from beef.

## II. MATERIALS AND METHODS

Strip loins (*M. longissimus lumborum*) were obtained from 10 Hanwoo (Korean native cattle) steers (30 months of age, 453±12 kg of carcass weight) at a commercial slaughterhouse at 48 h postmortem. Six chops were prepared per strip loin by cutting approximately 3 cm and vacuum-packing. The chops were randomly divided into two groups: Day-1, stored at 1°C for 1 d; and Day-14, stored at 1°C for 14 d. Peptide extraction, LC-MS/MS analysis, identification, and quantification were performed as described by Kim *et al.* [2]. The MS spectra identified as unique peptides were transformed into spectrograms based on their m/z values and relative intensities. The spectrograms were used as input data for transfer learning (a modified learning model of the existing deep learning model) using AlexNet [4] and MATLAB (R2023a, MathWorks, Inc., MA, USA). The initial learning rate was set at 0.0001, and the iteration size and the number of epochs were 16 and 100, respectively.

## III. RESULTS AND DISCUSSION

A total of 7411 peptides derived from 212 proteins were identified in fresh and aged beef samples (Fig. 1A). Among these peptides, 110 showed significantly different intensities between the two groups ( $p < 0.05$ ); however, trends in the change of intensity were different (increased or decreased by 14 days of storage) between these peptides. In addition, the regression equations with the relative intensity and m/z values did not clearly distinguish between the two groups (Day-1 vs. Day-14) (Fig. 1B). Transfer learning modified by the deep learning model (AlexNet) allowed us to distinguish between the two beef groups with high accuracy (100%), as shown in Fig. 1C. As previously reported [4], this approach also allowed for time savings and reduced analytical procedures despite the preprocessing of MS spectra to obtain a spectrogram. These results indicate that all peptide fragments (MS spectra),

regardless of the significance of the change in relative intensity, can be used to discriminate beef with different storage periods, and that deep learning can maximize the accuracy of discrimination.

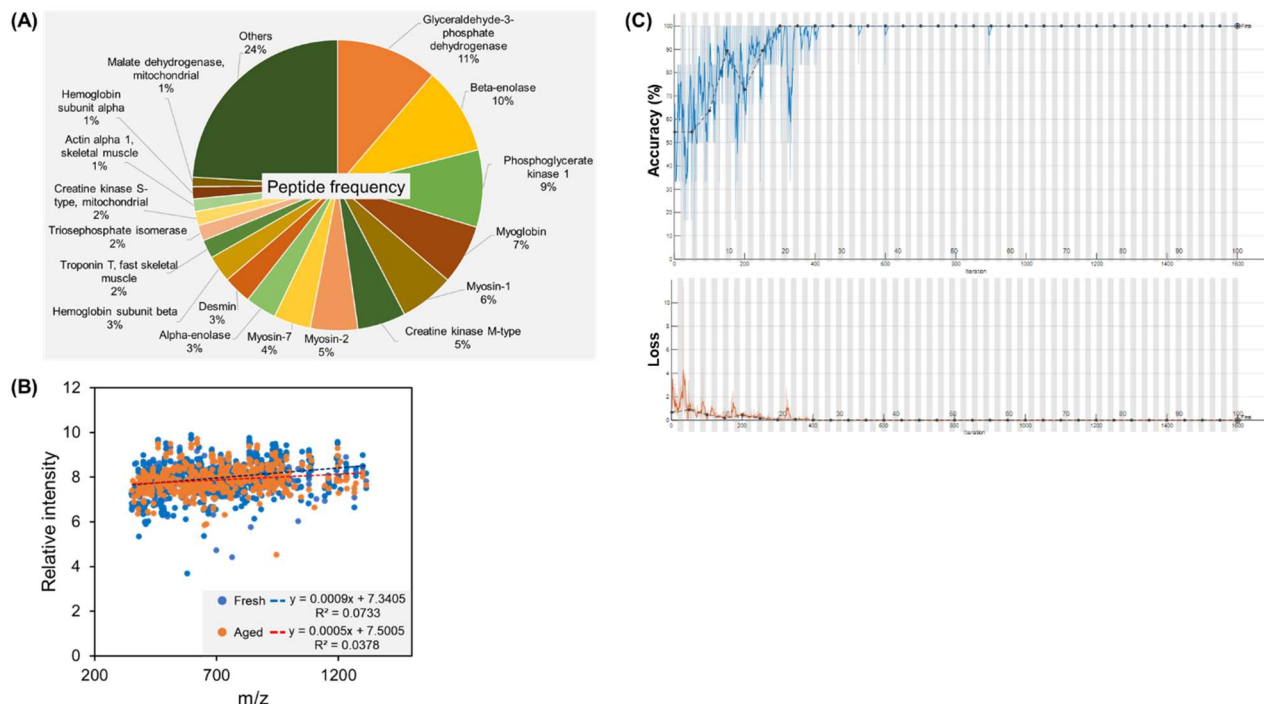


Fig. 1. Frequency (A) and linear regressions (B) of mass spectra and relative intensity of peptides derived from beef with different storage periods, and the result of transfer learning for distinction of beef with different storage periods (C).

#### IV. CONCLUSION

Artificial intelligence-based technologies, such as deep learning, can be applied to distinguish beef with different storage periods using vast MS spectra (peptide data). This technology will be useful for discrimination, classification, and prediction in the field of food, including meat and meat products.

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