COMPARISON OF CHEMICAL COMPOSITION AND LIPID METABOLISM-RELATED GENES EXPRESSION BETWEEN KOREAN HANWOO AND BRINDLE CHIKSO CATTLE

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I. INTRODUCTION

In many countries, intramuscular fat (IMF) is considered as the most important determinant of purchasing decision by consumers for beef [1]. Because the IMF content positively affects the eating quality of beef [2]. Additionally, fatty acid composition of beef has received a considerable interest due to their effects on human health and organoleptic characteristics of the beef [3]. It is known that adipogenesis and de novo fatty acids synthesis are the major pathways of fat deposition [2], which are tightly regulated by adipogenic transcription factors such as; peroxisome proliferator activated receptor gamma (PPAR), fatty acid binding protein 4 (FABP4), stearoyl-CoA desaturase 1 (SCD1), and Acetyl-CoA carboxylase (ACACA) etc. [4]. Hanwoo, as the major beef cattle in Korea, is known worldwide because of high IMF level and unique palatability of its meat [1]. Beside the Hanwoo, another cattle breed named Chikso, has recently been used for beef production in Korea [5]. Since beef breeds may have different capabilities for adipose tissues accumulation. However, it still remains known whether there is a difference in molecular factors underlying the lipid metabolism, IMF content and fatty acid profiles in beef between the Hanwoo and Chikso. The aim of this study was to elucidate the effect of cattle breed on the lipid metabolism-related genes, IMF and fatty acid profiles in beef.

II. MATERIALS AND METHODS

A total of 12 same-age cattle (n=6 per breed, 30 months old) reared in commercial cattle farms (Korea) under identical condition was used. Immediately after slaughter, approximately 20 g of muscle tissues from *longissimus lumborum* (LL) at 1st lumbar vertebrae were taken for mRNA analysis. After 24 h chilling at 4 °C, the carcasses were evaluated for marbling score (1: devoid; 9: abundant), and all the LL muscles were collected from the left side of carcasses and used for the IMF and fatty acids analysis. Total RNA in muscle tissue was extracted using TRIzol reagent (Sigma-Aldrich, CA, USA) according to manufacturer's instruction. Thereafter, 1 µg of total RNA from each the sample was reversely transcribed into cDNA using iScript[™] cDNA Synthesis Kit (Bio-Rad, Seoul, Korea). Real-time polymerase chain reaction (RT-PCR) was carried using SSoAdvanced Universal SYBR Green Supermix (Bio-Rad, Seoul, Korea), a cDNA equivalent of 10 ng of total RNA from each sample, and primers as shown in our previous study [6]. The thermal conditions for amplification of genes and calculation of genes expression were same as those described by Hoa et al. [6]. The IMF content in meat was determined using a Food Scan™ Lab 78810 (Foss Tecator Co., Ltd, Denmark). The lipid content in the meat samples was extracted using the protocol as described by Hoa et al. [6]. Individual fatty acids were expressed as relative percent (%) of total fatty acids. Each sample was analysed in duplicate. Data was analysed with a SAS Enterprise software (version 7.1; SAS Inst. Inc., Cary, NY), using the General Linear Model procedure where the cattle breed was considered as a fixed effect, and the IMF, fatty acids and mRNA expressions were considered as dependent variables.

III. RESULTS AND DISCUSSION

Our results (Fig 1) showed that the Hanwoo exhibited a higher expression of lipoprotein lipase (LPL), peroxisome proliferator activated receptor gamma (PPARG) and fatty acid binding protein 4 (FABP4) compared with the Chikso (P<0.05). While, Chikso had an upregulated expression of Stearoyl CoA desaturase 1 (SCD1) compared with the Hanwoo (P<0.05).

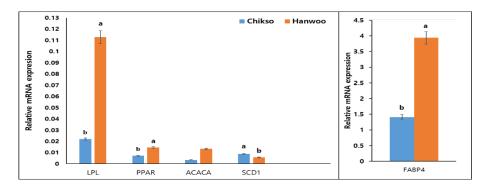


Figure 1. The effect of cattle breed on the expression of lipid metabolisms-related genes: Lipoprotein lipase (LPL), Peroxisome proliferator activated receptor gamma (PPARG), Acetyl-CoA-carboxylase alpha (ACACA), Stearoyl CoA desaturase 1 (SCD1), Fatty acid binding protein 4 (FABP4) in the LL muscles. The expression levels were calculated using the $2^{-\Delta Ct}$ method and were normalized to the Glyceraldehyde-3-phosphate dehydrogenase (GAPDH). Different letters (a,b) indicate the statistical difference (P<0.05).

As shown in Table 1, the breed also showed a significant effect on the IMF and fatty acids in the LL muscles in which Hanwoo had a higher marbling score and IMF content compared with Chikso (P<0.05).

Items	Chikso (n=6)	Hanwoo (n=6)	SEM	P-value
Marbling score (1: devoid; 9: abundant)	2.83	6.33	1.91	0.02
Intramuscular fat (%)	8.83	23.9	2.02	0.001
Saturated fatty acids (%)	43.1	46.3	0.08	0.03
Monounsaturated fatty acids	56.8	53.6	0.07	0.05
Polyunsaturated fatty acids	2.80	1.52	0.32	0.02

Table 1. Marbling, intramuscular fat and fatty acids of beef LL muscles as affected by breed.

IV. CONCLUSION

The breed affected the expression pattern of lipid metabolism-related genes such as PPAR, LPL and FABP4, which might affect the IMF level and fatty acid profiles in the beef between two cattle breeds. Furthermore, the PPAR, LPL and FABP4 could be considered as the key molecular factors underlying the fat deposition and fatty acids synthesis in beef.

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REFERENCES

- 1. Chung, K. Y., Lee, S. H., Cho, S. H., Kwon, E. G. &Lee, J. H. (2018). Current situation and future prospects for beef production in South Korea A review. Animal Bioscience 31:951-960.
- 2. Schumacher, M., DelCurto-Wyffels, H., Thomson, J.& Boles, J. (2022). Fat deposition and fat effects on meat quality—A Review. Animals12:1550.
- Listrat, A., Gagaoua, M., Andueza, D., Gruffat, D., Normand, J., Mairessec, G., Picard, B. & Hocquettea, J.F. (2020). What are the drivers of beef sensory quality using metadata of intramuscular connective tissue, fatty acids and muscle fiber characteristics? Livestock Science 240:104209.
- Liu, L., Cao, P., Zhang, L., Qi, M., Wang, L., Li, Z., Shao, G., Ding, L., et al. (2021). Comparisons of adipogenesis- and lipid metabolism-related gene expression levels in muscle, adipose tissue and liver from Wagyucross and Holstein steers. *PLoS ONE* 16: e0247559.
- 5. Park, B.; Choi, T.J.; Park, M.N.; Oh, S.H. (2020). Estimation of environmental effects and genetic parameters of carcass traits on Chikso (Korean brindle cattle). Animal Bioscience 33:525-530.
- 6. Hoa, V. B., Song, D. H., Seol K. H., Kang S. M., Kim, H. W., Bae S. B., Cho, S. H. 2023. A comparative study on the carcass and meat chemical composition, and lipid metabolism-related genes expression between Korean Hanwoo and Brindle Chikso Cattle. Current Issues in Molecular Biology 45:3279-3290.