71st ICoMST
GIRONA - CATALONIA - SPAIN
3rd-8th August - 2025

COMPARISON OF FATTY ACID PROFILES AND METABOLOMIC SIGNATURES IN THE EARLY-STAGE OF HANWOO STEERS WITH DIFFERENT GENETIC POTENTIALS

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I. INTRODUCTION

Genetic sequencing of Hanwoo steers provides valuable information for selecting individuals with superior potential for high-quality beef production. This study aimed to investigate whether genetic selection for enhanced growth performance and meat quality influences the fatty acid composition and metabolomic profiles of Hanwoo steers during the late growth stage. To the best of our knowledge, this is the first study to assess muscle composition in live Hanwoo steers using surgical biopsy techniques.

II. MATERIALS AND METHODS

Forty-eight Hanwoo steers were categorized by age, 10 months (10M) and 13 months (13M), and further classified based on genetic potential into two groups: growth potential (G) and meat quality potential (Q). Genetic classification was conducted using tail hair samples analyzed by the Animal Gene Testing Center (NongHyup Economic Holdings, Hanwoo Breeding Business Office, Seosan-si, South Korea). All steers were maintained on a standardized diet until the time of sampling. Muscle samples were surgically obtained from the semitendinosus muscle of live animals and analyzed for fatty acid composition using gas chromatography and for metabolite profiles using nuclear magnetic resonance (NMR) spectroscopy. Data were statistically analyzed using Minitab version 19. One-way ANOVA followed by Tukey's post hoc test and independent t-tests were used to determine significant differences at a 95% confidence level ($p<0.05$). Multivariate analyses, including Partial Least Squares Discriminant Analysis (PLS-DA) and Variable Importance in Projection (VIP) scoring, were conducted using MetaboAnalyst 6.0 (https://www.metaboanalyst.ca/).

III. RESULTS AND DISCUSSION

Fourteen major fatty acids were identified, and the statistically significant items are listed in Table 1. Significant differences ($p<0.05$) were observed between age groups for elaidic acid, linolenic acid, and gondoic acid. However, no significant differences were found between genetic groups within the same age. Across age groups, the growth genotype exhibited higher concentrations of linoleic acid, dihomo-γ-linolenic acid, and eicosapentaenoic acid, while the quality genotype showed elevated oleic acid levels. These findings are consistent with previous research indicating that dietary factors and age have a greater influence on fatty acid composition than genetic background during early growth (De Smet et al., 2004). This may be the reason why only four fatty acids show significant differences between the genotype groups and no significant differences between growth and quality potential groups within the same age.

Fatty Acid		Age × Genetic potential					Genetic potential regardless of age		
		10G	10Q	13G	13Q	*P*-Value	G	Q	*P*-Value
Elaidic	18.1T	0.34^{a}	0.29^{ab}	0.22^{bc}	0.19^{c}	0.000	0.28	0.24	0.252
Linoleic	18.2	11.92	9.09	10.33	8.87	0.100	11.13^{d}	8.98^{e}	0.027
Linolenic	18.3	0.36^{b}	0.45^{ab}	0.48^{a}	0.48^{a}	0.014	0.42	0.47	0.179
Godonic	20:1	0.06^{bc}	0.02^{c}	0.22^{ab}	0.27^{a}	0.001	0.14	0.15	0.932
Dihomo-γ-Linolenic	20:3	1.53	1.07	1.37	1.17	0.111	1.46^{d}	1.12^{e}	0.023
Eicosapentaenoic	20:5	1.10	0.81	0.94	0.79	0.143	1.02^{d}	0.80^{e}	0.037

Table 1. Comparison of fatty acids composition of young Hanwoo steers with different genetic potential.

[a-c] Different letters within the same row differ significantly ($p < 0.05$).

[d-e] Different letters within the same row differ significantly ($p < 0.05$).

10G,10 months old group having growth related genetic potential; 10Q, 10 months old group having quality related genetic potential; 13G, 13 months old group having growth related genetic potential; 13Q, 13 months old group having quality related genetic potential; G, potential for growth regardless of age; Q, potential for quality regardless of age.

Analysis of metabolite data revealed significantly higher ($p<0.05$) concentrations of alanine, glutamate, isoleucine, leucine, phenylalanine, valine, N,N-dimethylglycine, and carnitine in the 10-month-old group. Simultaneously, all explored free amino acids except betaine, glycine, methionine, and tyrosine have been shown to have higher levels in the 10M group ($p<0.05$). Free amino acids are crucial for protein synthesis and broader metabolic functions (Chandel et al., 2021), possibly explaining their higher levels in younger steers. Genetic groupings showed no significant differences in metabolite concentrations. The score plot visually represents how well the PLS-DA model distinguishes between the four groups (Figure 1a). The 10 and 13-month Hanwoo steers are distinctly separated along Component 1, which explains 54.5% of the variation. The VIP (Variable Importance in Projection) score plot identifies the most important metabolites for distinguishing between the two age groups based on their VIP scores (Figure 1b). Betaine, carnosine, creatine, isoleucine, anserine, inosine, and IMP have the highest VIP scores, indicating they are the most significant in differentiating between 10 and 13-month Hanwoo steers.

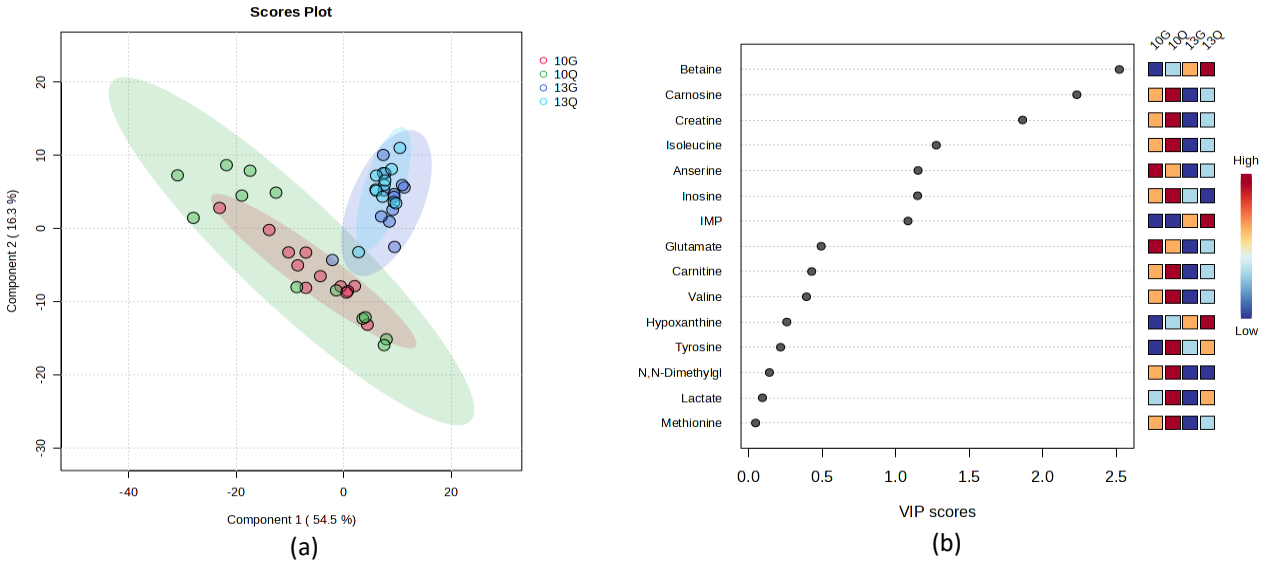


Figure 1. Results of (a) PLS-DA and (b) VIP score of metabolite compounds between 10 and 13 months of Hanwoo steers

IV. CONCLUSION

This study indicates that age, rather than genetic selection for growth or meat quality, has a more pronounced effect on the fatty acid composition and metabolomic profile of Hanwoo steers in the late growth phase. Both fatty acid and metabolite data collected during this study showed that the free amino acids related to protein synthesis and compounds related to energy metabolism were observed in higher concentrations in the 10-month-old group. However, a significantly clear demarcation was not observed between the genetic traits of each age group. These findings suggest that physiological maturity has a stronger influence on metabolic composition than genetic potential at this stage of development.

ACKNOWLEDGEMENT

This research was funded by Korea Institute of Planning and Evaluation for Technology in Food, Agriculture, and Forestry (IPET), through the Smart Farm Innovation and Technology in Food, Agriculture, and Forestry (IPET), through the Smart Farm Innovation and Technology Development Program funded by the Ministry of Agriculture, Food, and Rural Affairs (MAFRA) (421022-04).

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