TRANSCRIPTOME ANALYSIS REVEALS THE NUTRITIONAL METABOLIC MECHANISM OF IMF DEPOSITION IN YAK AT DIFFERENT AGES

Qin Bai[1], Jiuqiang Guan[1], Tianwu An[1], Hongwen Zhao[1], Xiaolin Luo[1,*] and Xiangfei Zhang[1,*]

[1]Institute of Plateau Animals, Sichuan Academy of Grassland Sciences, P. R. China

*Corresponding author email: Luoxl2004@sina.com, zxfsicau@foxmail.com

I. INTRODUCTION

Intramuscular Fat (IMF) is the adipose tissue deposited in endomysium, perimysium and epimysium of muscle. It was reported that IMF was closely related to the shear force, tenderness and sensory scores of meat quality [1]. Transcriptional control of adipogenesis is a highly complex and orchestrated process which is mediated by a cascade of expression events of molecules, including coding and non-coding RNA [2,3]. Therefore, this experiment was conducted to elucidate the metabolic mechanism of IMF deposition in yak muscle by transcriptome analysis.

II. MATERIALS AND METHODS

In the preliminary study, the IMF content in *Longissimus dorsi* of yaks at different ages (0.5, 1.5, 2.5, 3.5, and 4.5 years old, 6 yaks per age group) was detected to explore the depositon pattern of yak meat. The results showed the lowest IMF content at 0.5 years old and highest IMF at 4.5 years old. With the purpose of further investigation on nutritional metabolic mechanism, *Longissimus dorsi* samples of yaks with lowest and highest IMF (0.5 and 4.5 years old, LF and HF) were selected for RNA sequencing (RNA-Seq) analysis. Differentially expressed genes were analysed and identified using DESeq2 software with a cut-off of abs(log2FC)>1 and P_{adj}<0.05.

III. RESULTS AND DISCUSSION

Differentially Expressed Gene Screening

Differential gene screening between the LF and HF groups resulted in the identification of 1527 significantly differentially expressed genes, with 749 genes up-regulated and 778 genes down-regulated in the longissimus dorsal muscle when HF group compared to the LF group.

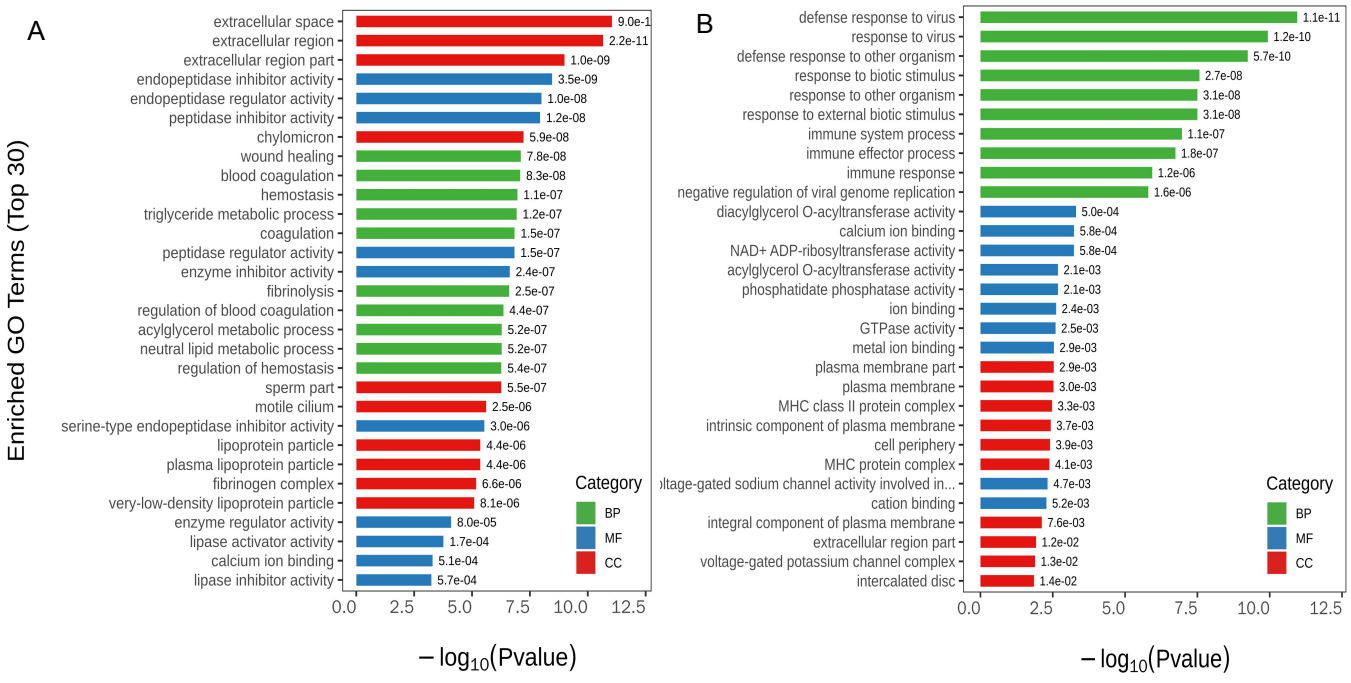

Figure 1. The top 30 significantly enriched GO terms of up-regulation (A) and down-regulation (B)

GO function enrichment analysis

Among the three major GO categories, 708, 137, and 61 significantly different terms were enriched for Biological Process (BP), Molecular Function (MF), and Cellular Component (CC), respectively ($P < 0.05$) . Terms related to lipid metabolism under the MF classification included Acylglycerol metabolic process, Triglyceride metabolic process, Neutral lipid metabolic process, Chylomicron, Lipoprotein particle, Very-Low-Density Lipoprotein particle (VLDL), Lipase activator activity, and lipase inhibitor activity which were significantly upregulated ($P < 0.05$).

KEGG pathway enrichment analysis

The pathways related to lipid metabolism among 54 KEGG significantly enriched pathways are the PPAR signaling pathway, Synthesis and degradation of ketone bodies, Linoleic acid metabolism, Cholesterol metabolism, Glycerolipid metabolism, Fat digestion and absorption. The PPAR signaling pathway is the most significantly enriched of the above six pathways, and has the highest number of DEGs. APOA2, APOC3, APOA5, HMGCS2, and PLPP2 were screened for possible candidate genes associated with IMF.

Table 1 The significantly enriched KEGG pathways related to lipid metabolism

ID	Description	P-value
bom03320	PPAR signaling pathway	<0.001
bom00072	Synthesis and degradation of ketone bodies	0.006
bom00591	Linoleic acid metabolism	0.012
bom04979	Cholesterol metabolism	0.014
bom00561	Glycerolipid metabolism	0.018
bom04975	Fat digestion and absorption	0.037

IV. CONCLUSION

Overall, our results showed several GO terms and signaling pathways involved in IMF deposition of yak by transcriptome analysis, such as the Triglyceride metabolic process, Chylomicron and Lipase activator activity terms, and PPAR signaling pathway, Fat digestion and absorption, and Cholesterol metabolism pathways. These findings suggest that the IMF deposition of yak was accomplished through promoting adipocyte differentiation, enhancing absorption and transport of lipid and lipase regulation.

ACKNOWLEDGEMENTS

The authors gratefully acknowledge the funding support of Basic Scientific Research Project of Academic Institute in Sichuan and CARS-37. The authors have not stated any conflict of interest.

REFERENCES

1. Lambe, N. R., McLean, K. A., Gordon, J., Evans, D., Clelland,N. & Bunger, L. (2017). Prediction of intramuscular fat content using CT scanning of packaged lamb cuts and relationships with meat eating quality. Meat Science 123: 112-119.
2. Lowe, C. E., O'Rahilly, S. & Rochford, J. J. (2011). Adipogenesis at a glance. Journal of Cell Science 124: 2681-2686.
3. De Sá, P. M., Richard, A. J., Hang, H. & Stephens, J. M. (2017). Transcriptional Regulation of Adipogenesis. Comprehensive Physiology 7: 635-674.