IOCAN 2026 Conference
The 4th International Online Conference on Animals
17–19 March 2026 | Online
MDPI

Effects of Steam-Flaked Corn on Rumen Microbial Composition and Metabolism in Yaks

Zhengge Zhao, Shuli Yang, Jianmin Chai (jchai@uark.edu)

Guangdong Provincial Key Laboratory of Animal Molecular Design and Precise Breeding, School of Animal Science and Technology, Foshan University, Foshan, China

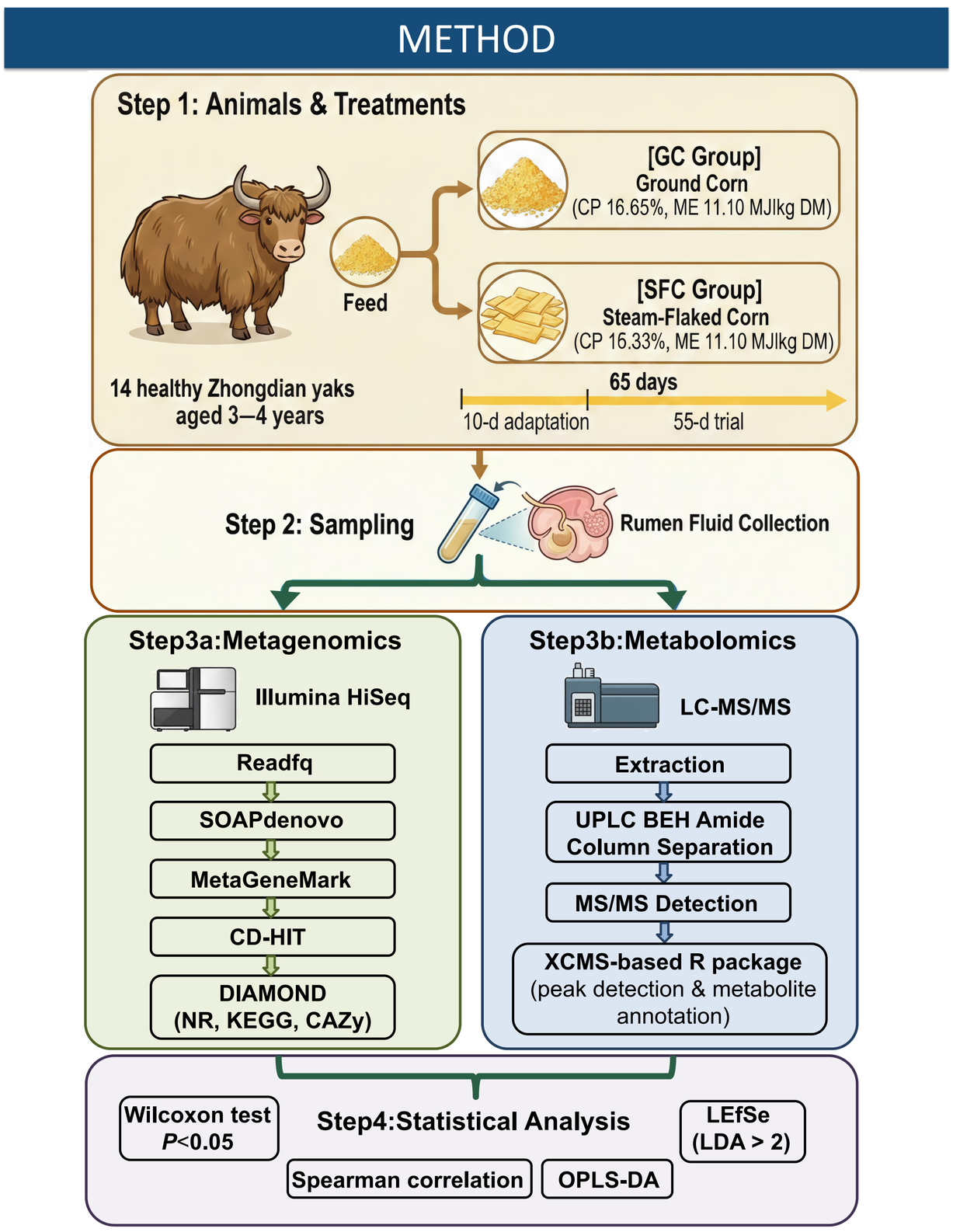
INTRODUCTION & AIM

Yak, a unique domestic animal from the Qinghai-Tibet Plateau, is China's third-most populous cattle breed. Living in high-altitude, low-oxygen, cold environments, they face year-round grazing and nutritional shortages. During winter and spring, house feeding with enhanced nutrition is key to boosting their performance and reducing grazing pressure.

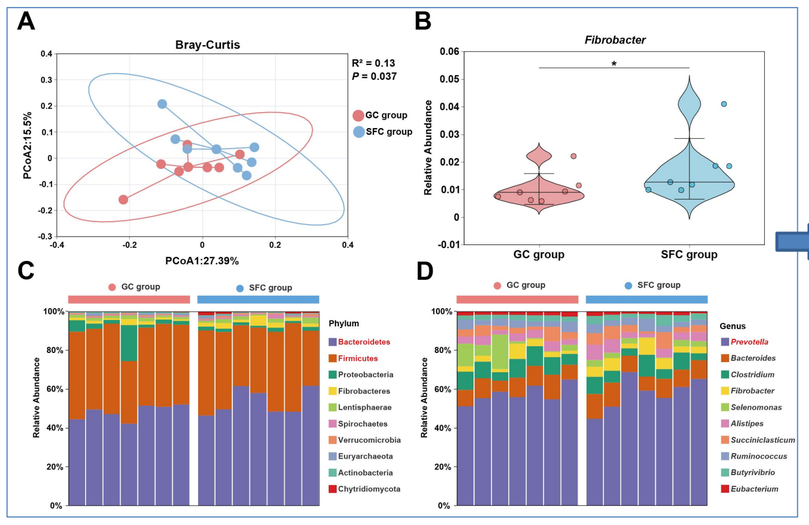
Corn is the primary energy feed for housed livestock, and its digestibility directly determines animal production performance. Appropriate processing can disrupt the structure of corn starch, enhancing its availability in the body. Steam flaking alters the endosperm structure of corn, increasing particle size and the surface area for microbial attachment, thereby improving starch gelatinization, digestibility, and the utilization of energy and nitrogen.

Therefore, this study aims to investigate the effects of steam-flaked corn on rumen fermentation parameters, microbial community composition, species function, and metabolism in yaks using metagenomics and metabolomics technologies, with ground corn as the control. This approach aligns with the demand for "precision feeding" in animal husbandry.

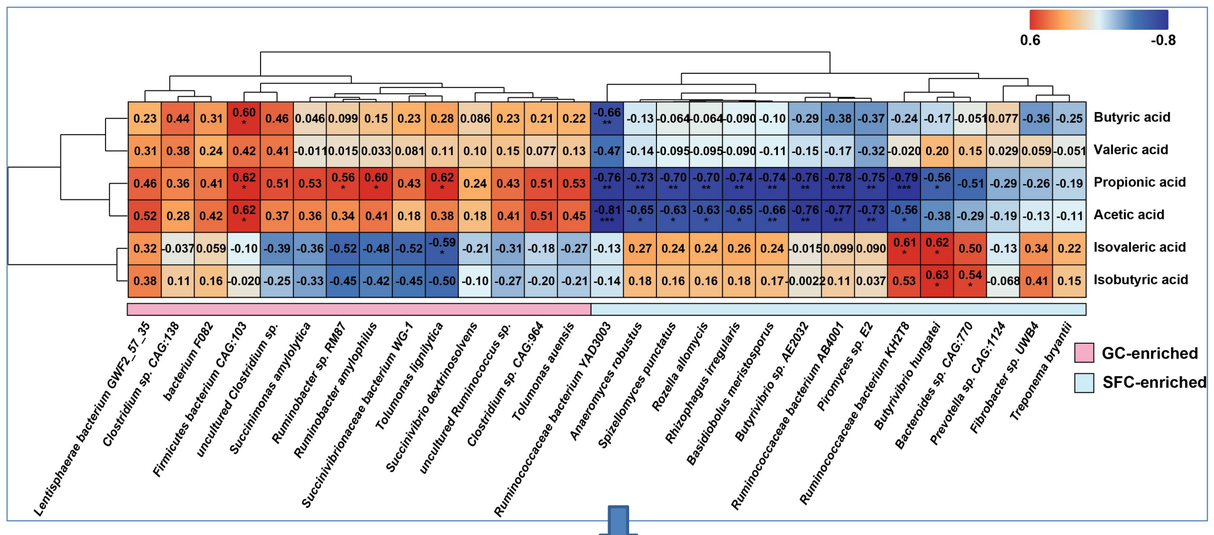
METHOD



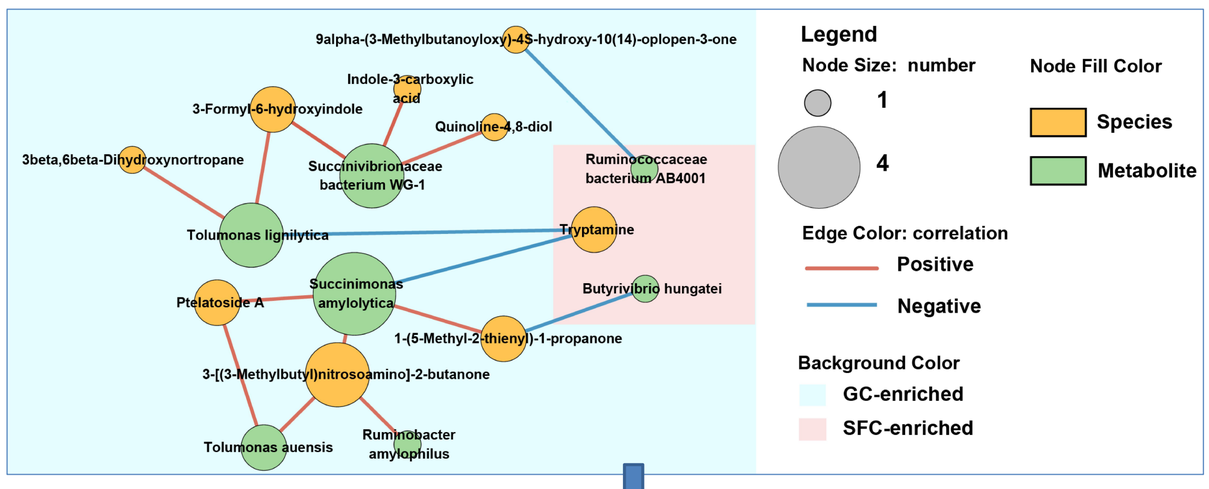
RESULTS & DISCUSSION



Steam-flaked corn (SFC) significantly altered the rumen microbial community in yaks: *Fibrobacter* was enriched, while Bacteroidetes and *Prevotella* remained the dominant taxa.



Correlation analysis between differential microbes and short-chain fatty acids (SCFAs)



Correlation analysis between differential microbes and differential metabolites.

CONCLUSION

This study found that steam-flaking treatment promoted the proliferation of carbohydrate-degrading microorganisms (e.g., *Fibrobacter*) by altering feed structure, enhanced carbohydrate digestion and utilization, and subsequently improved nutrient absorption and metabolism in yaks.

FUTURE WORK / REFERENCES

Our laboratory employs multidisciplinary approaches, including multi-omics (such as metagenomics, metatranscriptomics, metabolomics, and culturomics), bioinformatics, statistics, and machine learning, to understand the role of the animal and human microbiome in nutritional metabolism, health, and various diseases.