

College of Fisheries Henan Normal University



读书报告

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Succession and Fermentation Products of Grass Carp (*Ctenopharyngodon idellus*) Hindgut Microbiota in Response to an Extreme Dietary Shift

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目录
CONTENTS

01 | INTRODUCTION

02 | MATERIALS AND METHODS

03 | RESULT

04 | DISCUSSION

INTRODUCTION



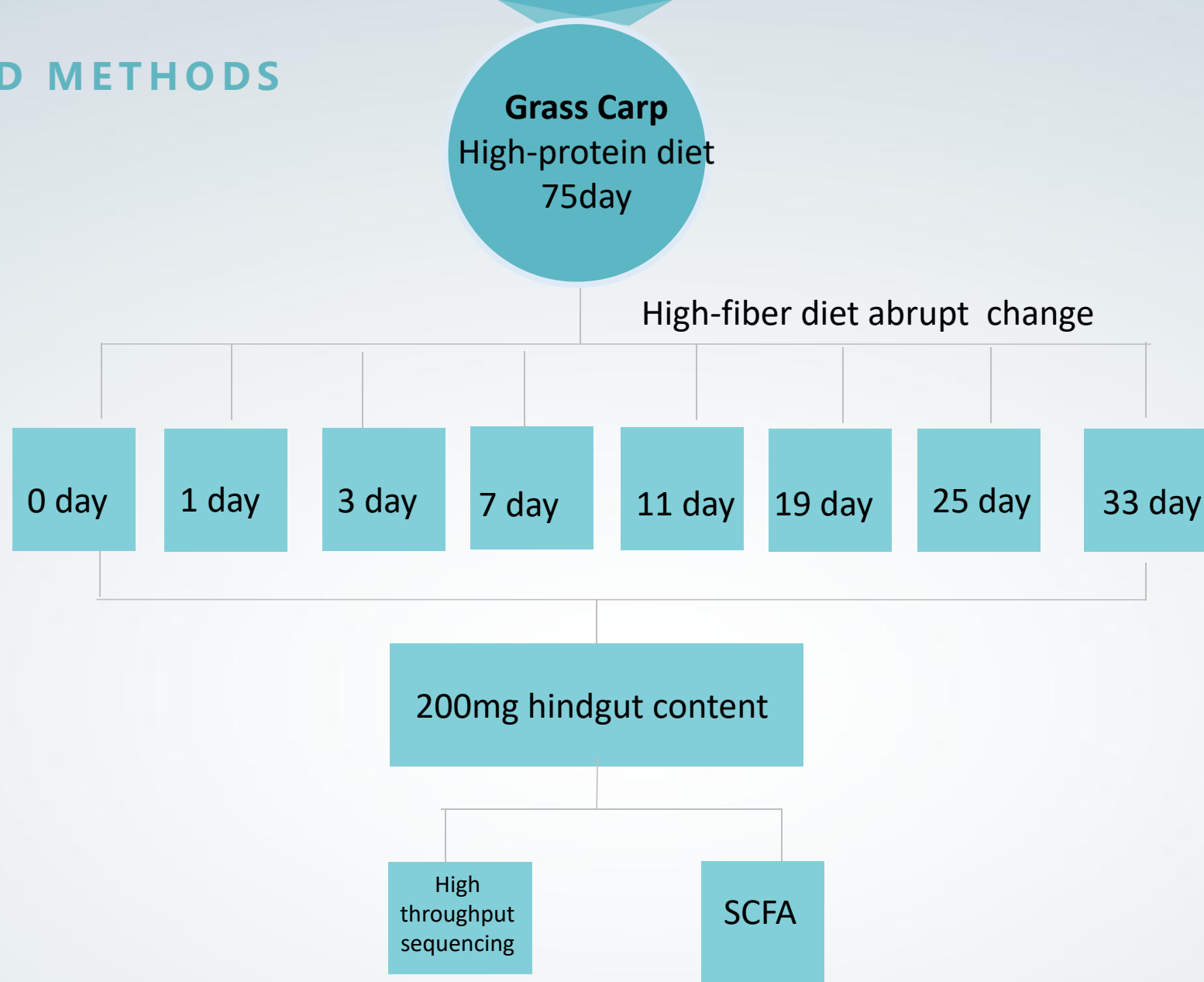
肠道微生物在机体分解和吸收营养物质中起着重要的作用。其结构与功能也受饲料成分的影响。



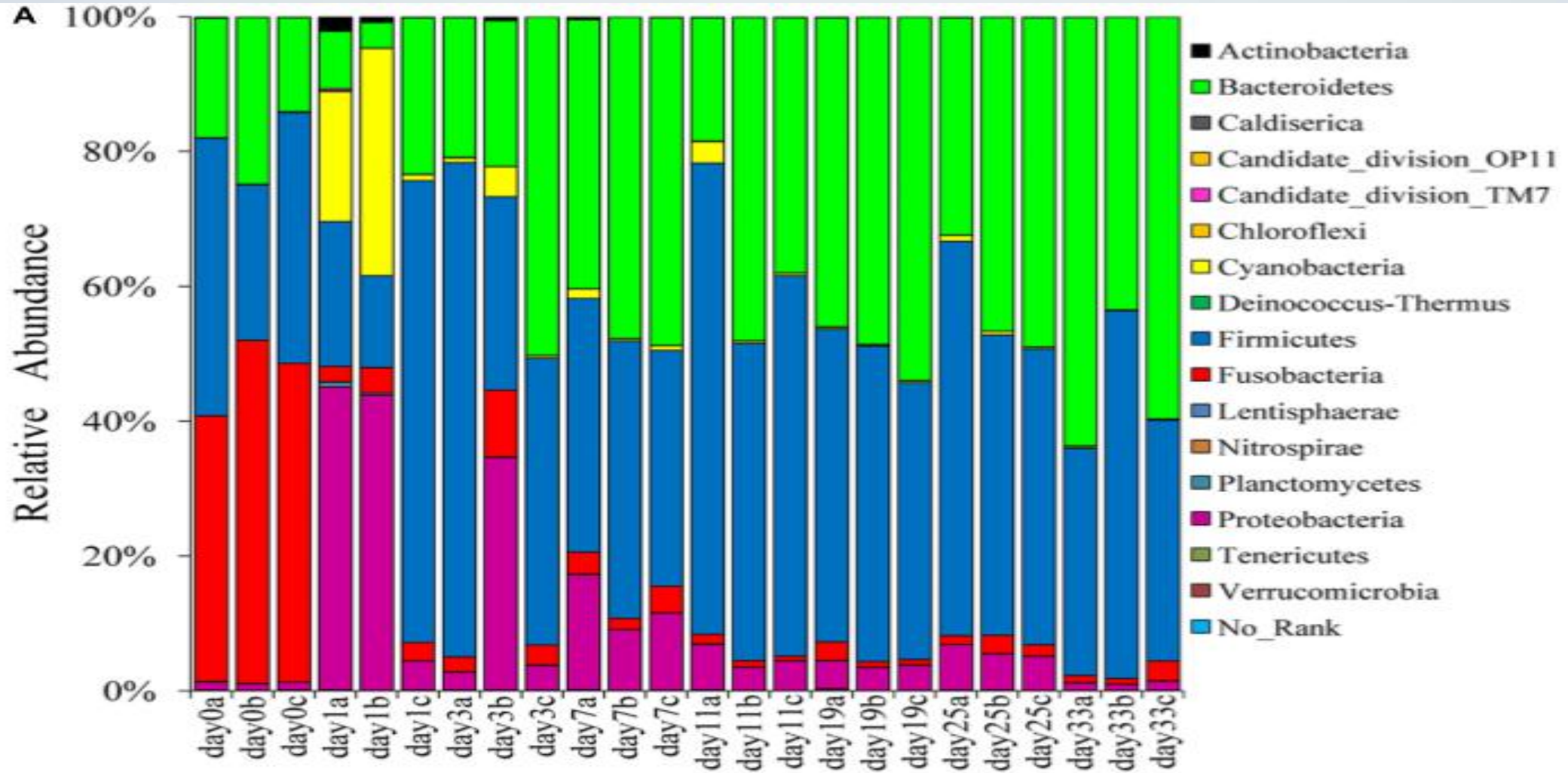
以往的研究大多聚焦于，在特定的饲料喂养下鱼类肠道微生物的结构组成、丰度和多样性的研究。然而在肠道菌群应对营养物质极端改变的条件下，菌群组成及产物变化的研究却鲜有报道。



MATERIALS AND METHODS



RESULT



RESULT

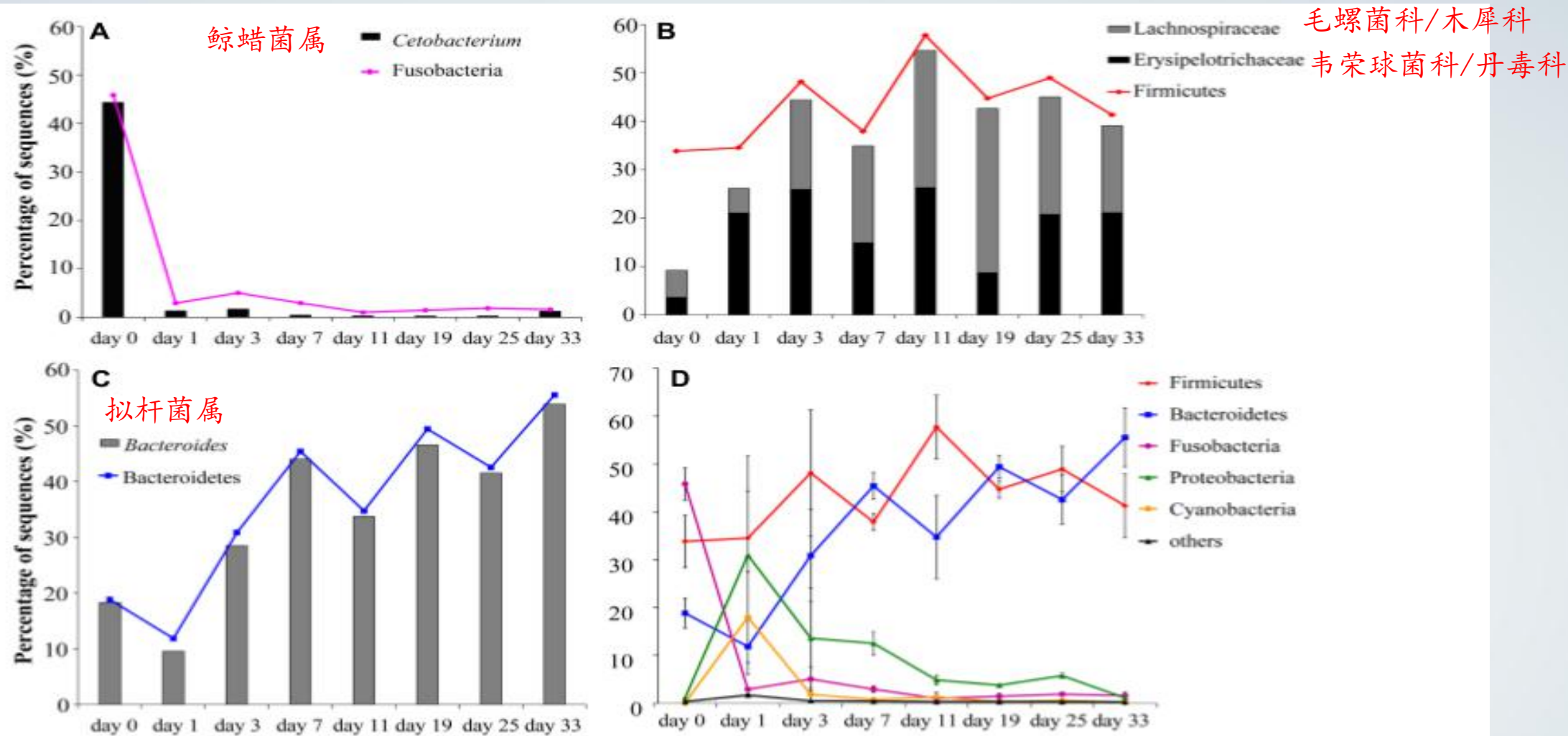


FIGURE 2 | Changes in relative abundances of the main bacterial communities (shown as means of the values of three individual fishes) in the grass carp hindgut after a sudden transition from animal-based diet (fish meal, day 0) to plant-based diet (Sudan grass, day 1–33): **(A)** Fusobacteria and *Cetobacterium*; **(B)** Lachnospiraceae, Erysipelotrichaceae and Firmicutes; **(C)** Bacteroidetes and *Bacteroides*; **(D)** comparison of the changes in the five main phyla, with standard deviation values shown as error bars.

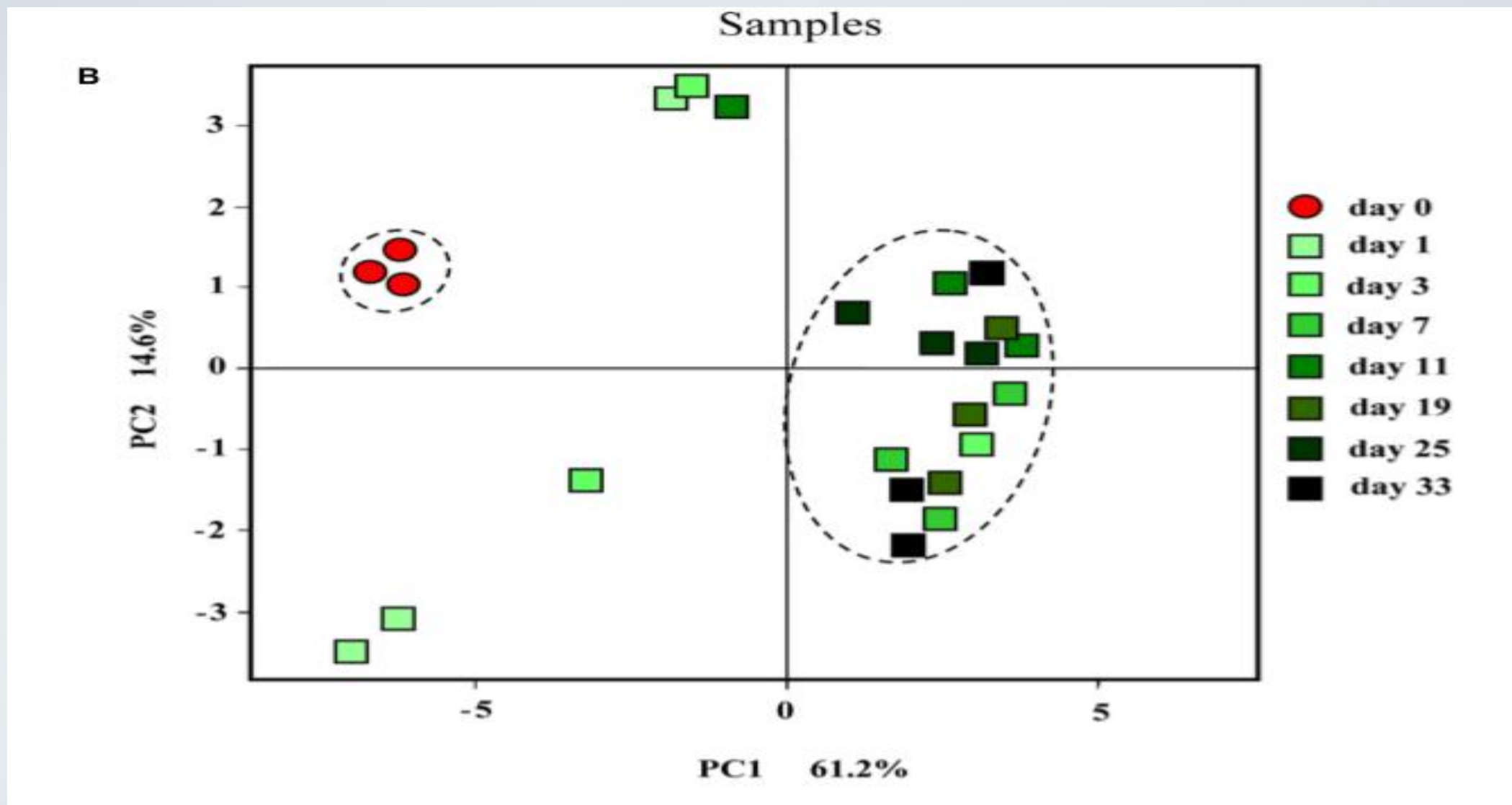
RESULT

TABLE 2 | Summary of diversity indices and coverage estimators of different time-point samples.

Sample ID (n D 3)	Coverage (%)	α -diversity				β -diversity
		Shannon	Simpson	Ace	Chao	UniFrac distance ^r
day 0	97.70 ± 0.06	3.14 ± 0.21	0.16 ± 0.02	1751 ± 226	1277 ± 126	0.09 ± 0.01
day 1	98.25 ± 0.78	3.61 ± 0.60	0.12 ± 0.08	1741 ± 1041	1419 ± 583	0.48 ± 0.01
day 3	97.23 ± 0.77	3.56 ± 0.65	0.13 ± 0.12	2917 ± 752*	2006 ± 370*	0.48 ± 0.02
day 7	97.28 ± 0.20	3.84 ± 0.21*	0.06 ± 0.01*	2546 ± 263*	1877 ± 143*	0.54 ± 0.01
day 11	96.91 ± 0.45	3.47 ± 0.13	0.11 ± 0.03	2833 ± 445*	1990 ± 266*	0.52 ± 0.01
day 19	96.99 ± 0.17	3.33 ± 0.15	0.11 ± 0.02	2810 ± 312*	1876 ± 121*	0.53 ± 0.01
day 25	96.76 ± 0.70	3.42 ± 0.13	0.10 ± 0.01	3077 ± 492*	2060 ± 293*	0.54 ± 0.01
day 33	96.31 ± 0.23	3.35 ± 0.09	0.12 ± 0.00	3509 ± 310*	2292 ± 203*	0.60 ± 0.01

*Significant difference from day 0 samples ($P < 0.05$). ^rUniFrac distance relative to day 0; for day 0, among day 0 samples only.

RESULT



PERMANOVA分析

RESULT

Predicted GH (Glycoside hydrolases) and PL (Polysaccharide Lyases) Families in Host and Intestinal Microbiota

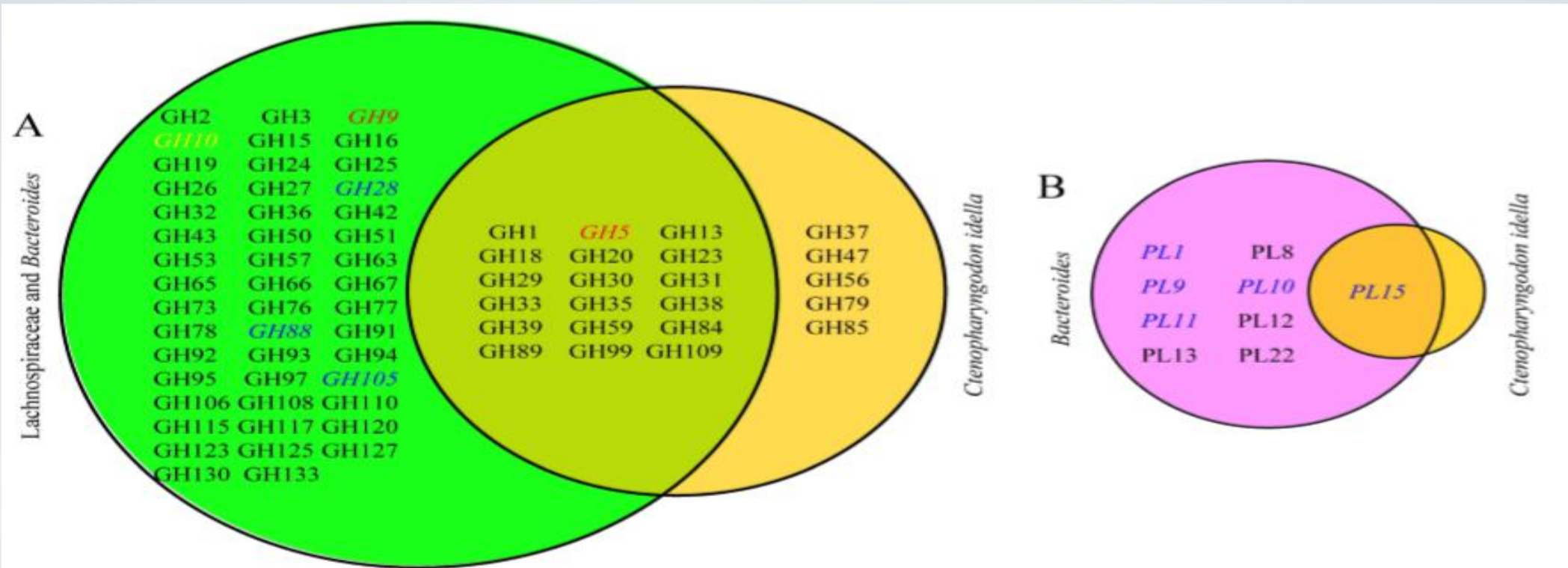


Figure S7: Venn diagrams showing the Carbohydrate-Active enZymes (CAZy) families in grass carp, Bacteroides, and Lachnospiraceae. (A) The comparison of GH families between grass carp and bacterial groups of Bacteroides and Lachnospiraceae. (B) The comparison of PL families between grass carp and Bacteroides. The CAZy families highlighted in red are associated with cellulase-encoding genes, in yellow are associated with xylanase-encoding genes and in blue are associated with pectinase encoding genes. GH5 in bacteria is cellulase, but it is β -glucuronidase in grass carp; PL15 in bacteria is pectinase, but it is dermatan-sulfate epimerase in grass carp.

RESULT

Quantification of the Intestinal Microbiota by qPCR

Major SCFA concentrations in hindgut content samples

TABLE 3 | Major SCFA concentrations in hindgut content samples (mmol/kg wet weight).

Sample ID (n D 3)	Acetic	Propionic	Iso-butyric	Butyric	Total
Day 0	4.50 ± 0.45	1.58 ± 0.51	0.23 ± 0.01	2.07 ± 0.11	7.68 ± 1.06
Day 1	1.60 ± 1.07*	0.22 ± 0.23*	0.11 ± 0.11	0.48 ± 0.61	2.41 ± 2.02*
Day 3	2.43 ± 0.44*	0.10 ± 0.03*	0.02 ± 0.03*	0.82 ± 0.30	3.37 ± 0.75*
Day 7	2.35 ± 0.31*	0.18 ± 0.06*	0.02 ± 0.01*	0.79 ± 0.33	3.349 ± 0.59*
Day 11	2.92 ± 0.38*	0.12 ± 0.12*	0.03 ± 0.04*	0.75 ± 0.20	3.82 ± 0.38*
Day 19	2.58 ± 0.40*	0.17 ± 0.10*	0.17 ± 0.01	0.82 ± 0.07	3.75 ± 0.57*
Day 25	3.14 ± 0.41	0.20 ± 0.10*	0.12 ± 0.10	0.75 ± 0.24	4.21 ± 0.66*
Day 33	2.10 ± 0.28*	0.45 ± 0.10*	0.03 ± 0.01*	0.33 ± 0.11*	2.91 ± 0.48*

*Significant difference from day 0 samples ($P < 0.05$).

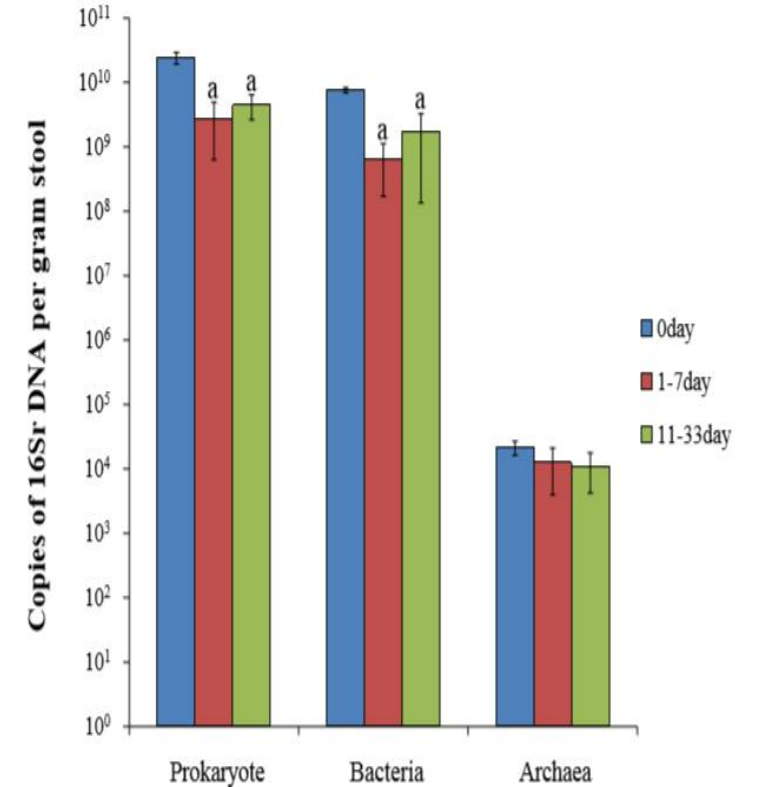


Figure S5: The 16S rDNA copies of prokaryote, bacteria and archaea quantified by qPCR. Error bars represent the standard error of the medians. Student T-test was used to analyze the differences between different stages of dietary shift. "a" means a significant difference between day 0 and plant-based samples, $P < 0.05$.

RESULT

Functions of Microbial Communities Inferred by Predictive COGs

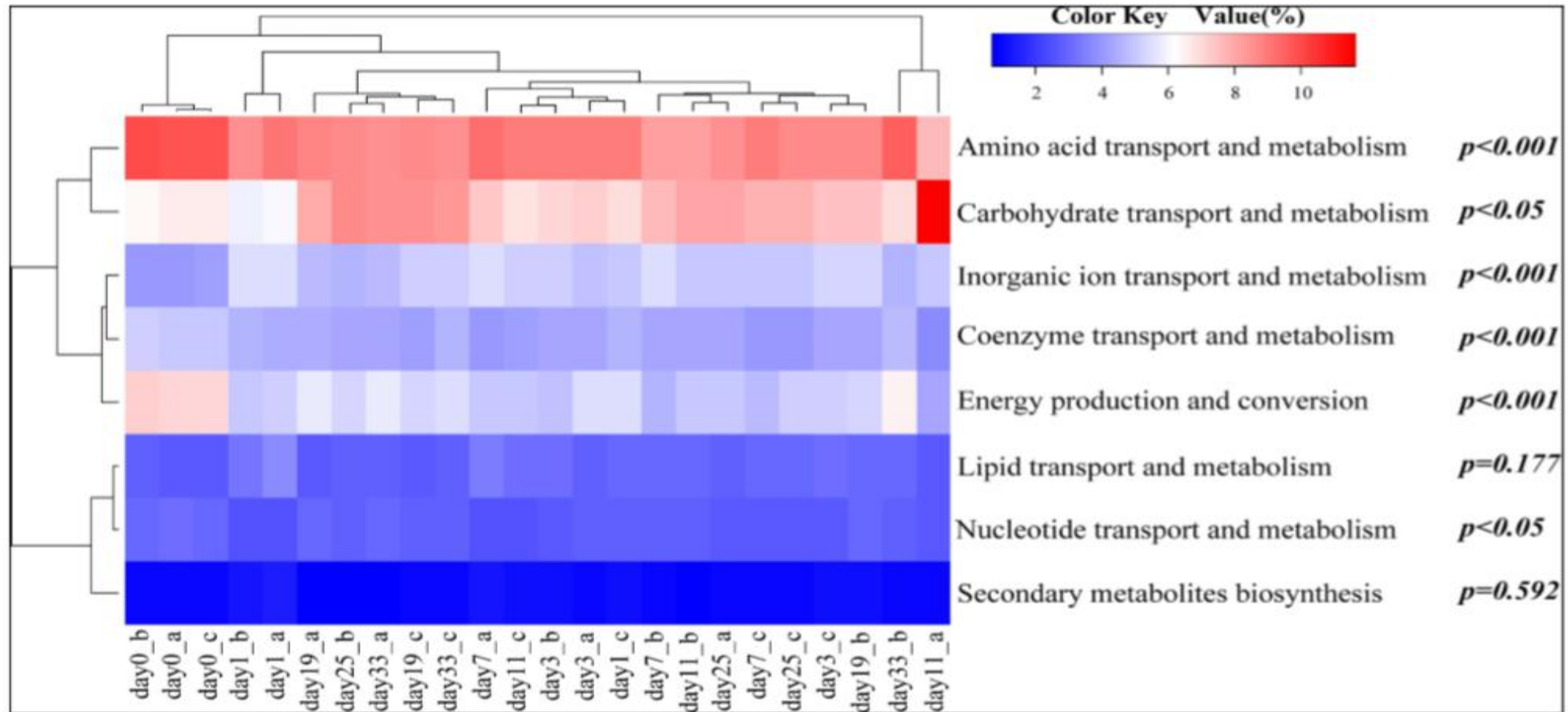
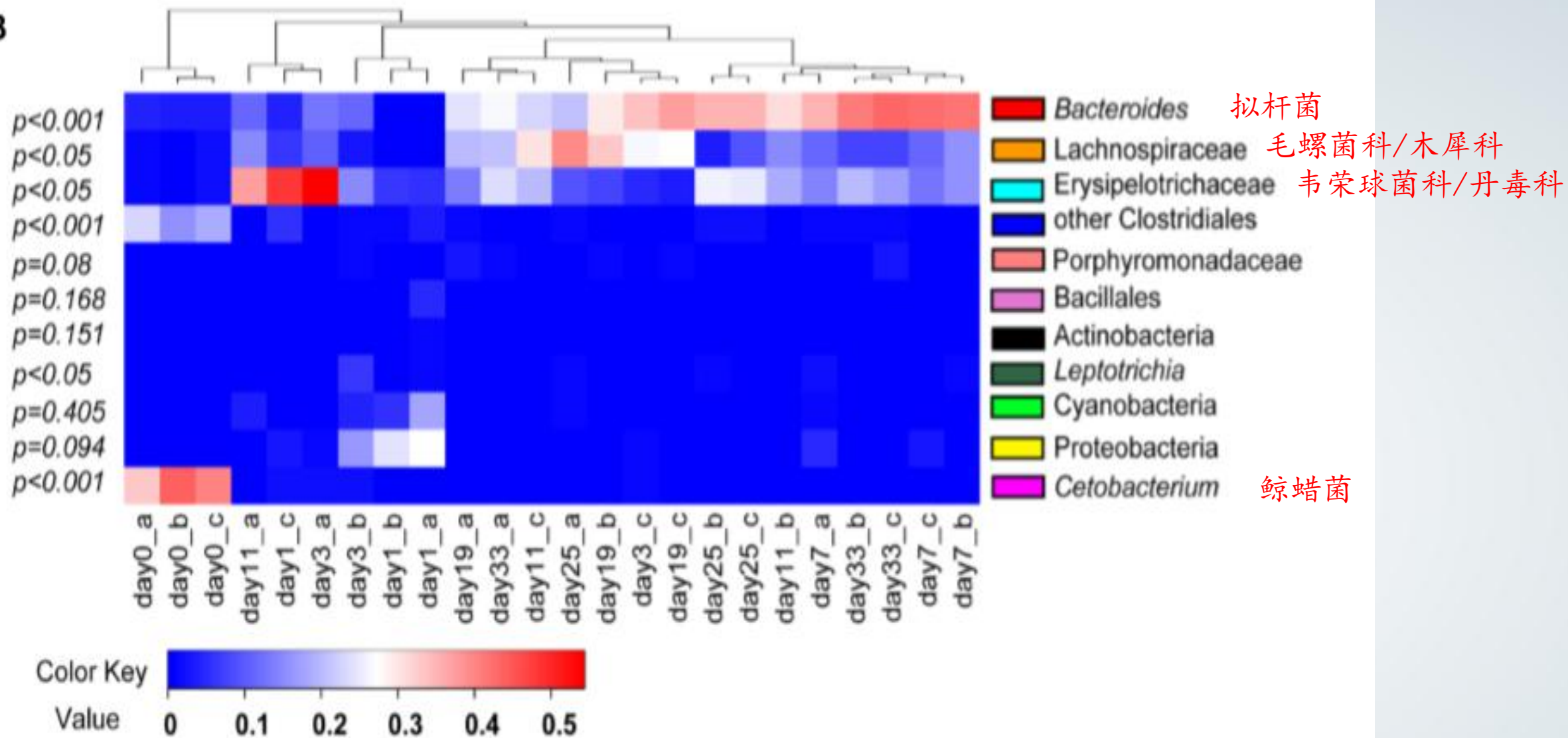


FIGURE 3 | Heat map showing relative abundances of clusters of orthologous group (COG) categories predicted by PICRUSt. The relationship among specimens is determined by the complete clustering method with Bray-Curtis distance. In the heat map, the red and blue colors indicate high and low relative abundance, respectively. The P -values exhibit statistical differences in relative abundances of COG categories between animal-diet samples and day 11–33 plant-diet samples, where $P < 0.05$ was chosen as statistically difference. a, b, and c represent different samples on the same day.

RESULT

B



DISCUSSION

- 1、 Gut microbial communities changed rapidly when the diet shifted. *Cetobacterium*, underwent a short period of high instability, and then began to stabilize again.
- 2、 A significant increase in species richness from animal diet samples to plant-diet samples. The intestinal microbiome structure changes associated with the adaptation to the switch from a high protein/low fiber diet to a low protein/high fiber diet.
- 3、 Short chain fatty acid levels decreased significantly after the dietary shift, the lower accessibility (and even indigestibility in some cases) of nutrients in Sudan grass in comparison to fish meal resulted in a decline in prokaryote and bacteria counts, leading to a decrease in SCFA levels.

致谢

THANKS

语大义之方，论万物之理。受益终身！

