The diet conditions of dung beetles influence the changes in gut microbes

Yue Mao[1], Xingjian Yang[2], Hui Yuan[1], Chunmei Zou[3], and Tao Xiong[1]

[1]Yangtze University
[2]Grinnell College
[3]Hubei Geshuo Biotechnology Co., Ltd

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Abstract

Using 16S rRNA sequencing, we investigated the gut microbial diversity, variability, and functional prediction of gut microbes in dung beetles in starvation and heavy diet states. The results showed that the gut microflora was richer in the re-eating state than in the starving state. The dominant flora at the phylum level for the starvation and re-diet states are Firmicutes, Proteobacteria, but the proportions are not the same. At the genus level, the dominant flora in the starvation group was Vagococcus, while the dominant flora in the rediet group was Romboutsia. In terms of functional prediction, 27 metabolic pathways in 6 areas of Metabolism, Genetic Information Processing, Environmental Information Processing, Cellular Processes, Organismal Systems, and Human Diseases were significantly different. The study shows that status affects the diversity of the gut microbes of the Chinese dung beetle, and the results may provide the necessary data for the study and development of the gut microbes of the Chinese dung beetle.

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Table.1 Specimen diversity index

Group	Chao1	ACE	shannon	simpson	coverage
HG	289.8637333	289.5066933	3.060659667	0.169788108	0.999857867
HF	849.2214333	847.98982	5.228211333	0.021782827	0.999414033

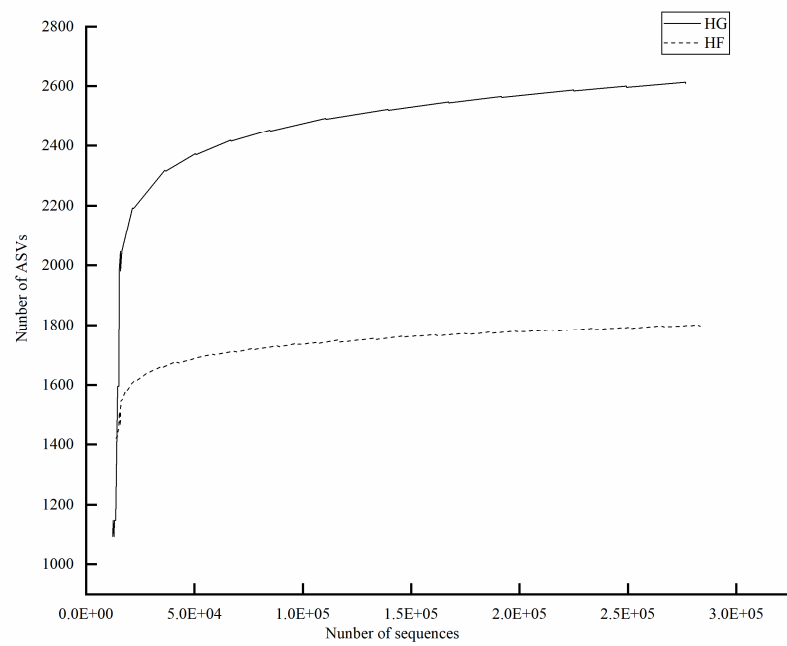Fig.1 Venn diagram of Microbial species composition
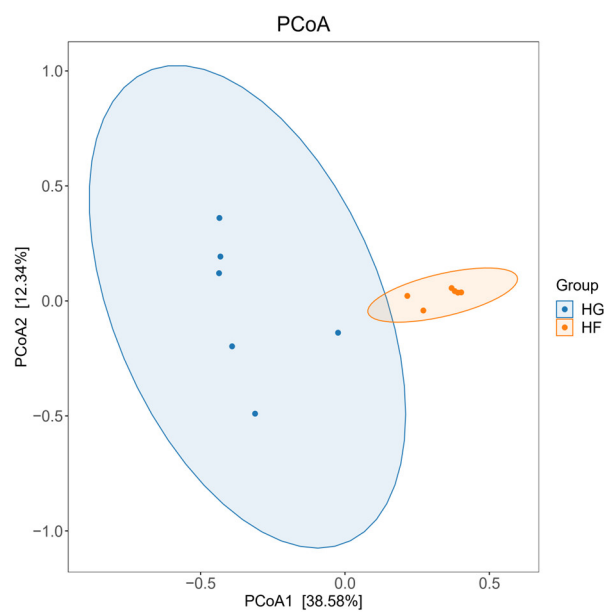

Fig.2 Rarefaction curve of all specimen
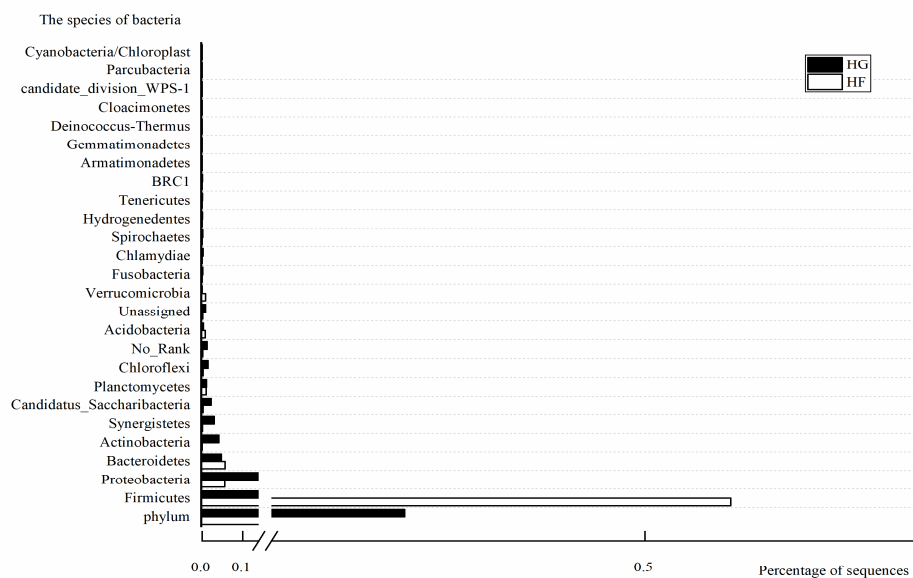
Fig.3 PCoA analysis

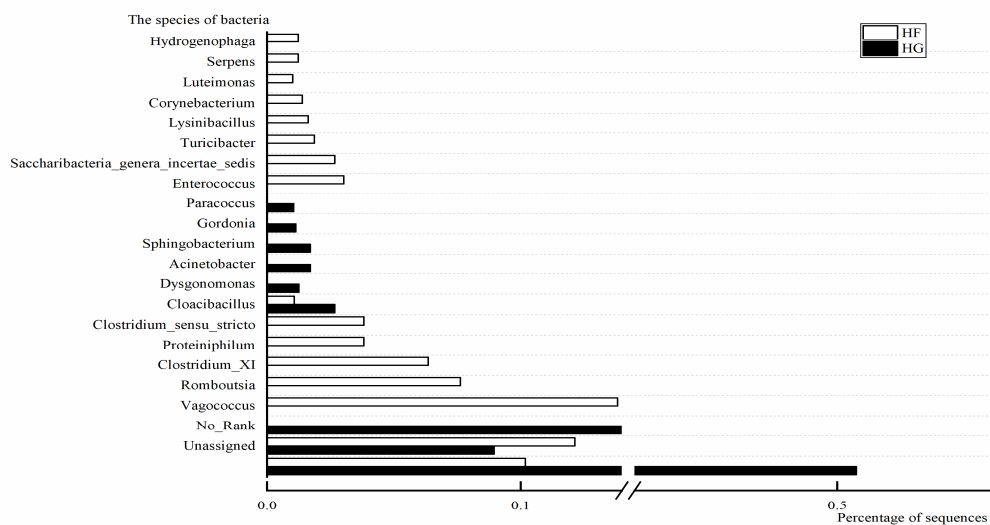Fig.4 The composition of gut flora at the phylum level
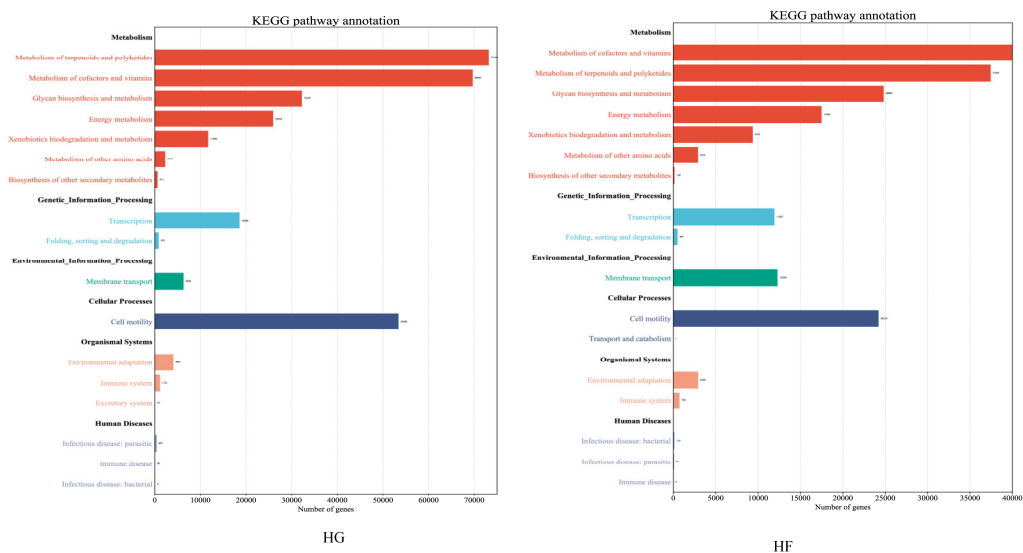
Fig.5 The composition of gut flora at the genus level

Fig 6 Kegg pathyway relative abundance