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Abstract

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High-throughput sequencing analysis of the bacteria associated with a Chinese-reared population of *Dermatophagoides farinae* (Acari: Pyroglyphidae)*

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Dermatophagoides farinae Hughes is a widely distributed house dust mite (HDM) (Pyroglyphidae) and one of the major agents of HDM allergy in humans. Studies on the bacterial communities of *D. farinae* have focused on western populations, while there is a gap of knowledge about the bacterial communities associated with populations from East Asia. With this in mind, we aimed to investigate the diversity of bacteria in laboratory-reared *D. farinae* from Wuhu, Anhui Province, China.

The Illumina PE250 sequencing platform was used to amplify and sequence the V4 region of the bacterial 16S rRNA gene in laboratory-reared *D. farinae*. Each sample contained 80 *D. farinae*, regardless of sex and developmental stage, in eight replicates. For quality control of raw sequences, filtering and trimming were performed with FLASH, Trimmomatic, and UCHIME to remove chimeras and to obtain valid sequences. Analyses of Operational Taxonomic Units (OTUs), bacterial community composition and Alpah diversity were performed using Usearch algorithms, the Silva database for reference alignment, and MOTHUR. From the 187,616 valid sequences, 469 OTUs were clustered based on a sequence similarity greater than 97%. OTU annotation showed that the bacteria of Chinese-reared-*D. farinae* belong to 26 phyla, 43 classes, 100 orders, 167 families and 284 genera. At phylum level, bacteria were mainly annotated to five phyla: Proteobacteria, Firmicutes, Bacteroidota, Actinobacteriota, and Acidobacteriota. Among these phyla, Proteobacteria was the dominant phylum. At the generic taxonomic level, the predominant genera were *Ralstonia*, *Staphylococcus*, and *Sphingomonas*. Interestingly, the widely spread endosymbiont *Wolbachia* was rare. In addition, the Shannon, Simpson, Ace, and Chao indexes varied across the eight samples. This study demonstrated a high diversity of bacterial community composition in Chinese-reared-*D. farinae*, and showed differences in bacterial community diversity and abundance among individuals of Chinese-reared-*D. farinae*. Also, the dominant bacterial genus in Chinese-reared-*D. farinae* are significantly different from those of Western scholars.

Keywords: *Dermatophagoides farinae*, bacteria, diversity, high-throughput sequencing

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