

# Fungal and bacterial community composition and structure in fermented ‘hairy’ tofu (Mao tofu)

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## Abstract

The process of fermenting tofu extends thousands of years. Despite a resurgent interest in microbial communities and fermented foods, little knowledge exists concerning microbial diversity of communities of fermented ‘hairy’ tofu known in China as Mao tofu. We used high-throughput metagenomic sequencing of the ITS, LSU and 16S rDNA marker genes to disentangle the Mao tofu fungal and bacterial community composition and diversity across the four most important markets in the Yunnan region of China. We show that hairy tofu in this region consists of around 170 fungal and 365 bacterial taxa. Significant differences in community structure were found between markets and niches. Machine learning random forest models were able to accurately classify both market and niche of sample origin. An over-abundance of yeast taxa were detected, and Geotrichum were the most abundant fungal taxa, followed by Torulaspora, Trichosporon, and Pichia. Mucor (Mucormycota) was also abundant in the LSU data and especially in the outside niche (rind), which consists of the visible ‘hairy’ mycelium. The majority of the bacterial OTUs belonged to Proteobacteria, Firmicutes, and Bacteroidota, with Acinetobacter, Lactobacillus, Sphingobacterium and Flavobacterium the most abundant members. Of interest, putative fungal pathogens of plants (e.g. Cercospora, Diaporthe, Fusarium) and animal (e.g. Metarhizium, Entomopathogenella, Pyxidiophora, Candida, Clavispora), as well as bacterial (e.g. Legionella) pathogens, were detected. Non-target eukaryotic taxa detected in by LSU amplicon sequencing included soybean (*Glycine max*), Protozoa, Metazoa (e.g. Nematoda and Platyhelminthes), Rhizaria and Chromista, providing evidence of additional biocomplexity and diversity in the tofu microbiome.

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