The Comparison of Bacterial Compositions on Seven Kinds of Fermented Tofu by High-throughput Sequencing

Jin, Linyi

This project aims at comparing bacterial composition and its effect on the nutrition and flavor of a traditional Chinese food, fermented tofu. Seven kinds of fermented tofu produced in different regions through distinguished production processes, were selected as experiment samples. Total DNA was extracted from each sample and proceeded to PCR to amplify the 16S rRNA V3 region. Subsequently, mixed PCR products were utilized for pyrosequencing. According to the sequence analysis, Firmicutes, Proteobacteria and Bacteroidetes are predominant in all samples, accounting for 95% out from the identified bacteria. Bacterial composition is complex at genus level, all samples contain more than 50 genus members. Besides, the composition of bacterial communities in fermented tofu correlates to geographic environment factors and production processes. Furthermore, Bacteroides and Clostridium, which also exist in normal human intestine and contribute to soy protein transformation and cellulose degradation, were detected in all samples. However, some pathogenic or opportunistic bacteria, such as Klebsiella and Salmonella, were noticed in some samples. These results suggest that the unique flavor of fermented tofu result from special bacterial flora, and fermented tofu might have food safety risks from pathogen contamination due to its open-to-air production process. Since the positive bacteria contains in fermented tofu make soybean more digestible, this project brings good news to those people who require more soybean protein, such as vegetarian. It is promising to isolate efficient bacteria strains to modify the production process of this tasty and nutritious traditional Chinese food, and popularize it all over the world.

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