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Comparative Genomic Analysis of Microbial Community Diversity in Soybeans Cultivated from Korea and Japan Soils

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Soybeans (*Glycine max*) are a vital crop in both Korea and Japan, extensively used in fermented products that play an essential role in their respective cuisines. The microbial communities involved in fermentation greatly influence the flavor and nutritional profile of these products. This study aims to compare the microbial diversity of soybeans grown in Korean and Japanese soils. Using Kraken 2 metagenomic analysis, the microbial taxa associated with soybeans from both regions were identified. Results showed significant differences in both bacterial and eukaryotic communities, with Korean soybeans displaying higher microbial diversity compared to Japanese soybeans. Alpha and beta diversity analyses revealed distinct microbial species driven by geographic and environmental factors, which may explain regional variations in fermentation characteristics. Understanding these microbial dynamics can enhance fermentation techniques and optimize the sensory qualities of soy-based foods. Future research aims to explore the functional roles of specific microorganisms in soybean fermentation and their broader applications in food innovation.