

Characterization of Cucumber Fermentation Spoilage Bacteria by Enrichment Culture and 16S rDNA Cloning

Breidt, F., Medina, E., Wafa, D., Pérez-Díaz, I., Franco, W., Huang, H. Y., ... & Kim, J. H. (2013). Characterization of cucumber fermentation spoilage bacteria by enrichment culture and 16S rDNA cloning. *Journal of food science*, 78(3), M470-M476. <10.1111/1750-3841.12057> Accessed 27 Apr 2021.

Abstract

Commercial cucumber fermentations are typically carried out in 40000 L fermentation tanks. A secondary fermentation can occur after sugars are consumed that results in the formation of acetic, propionic, and butyric acids, concomitantly with the loss of lactic acid and an increase in pH. Spoilage fermentations can result in significant economic loss for industrial producers. The microbiota that result in spoilage remain incompletely defined. Previous studies have implicated yeasts, lactic acid bacteria, enterobacteriaceae, and Clostridia as having a role in spoilage fermentations. We report that *Propionibacterium* and *Pectinatus* isolates from cucumber fermentation spoilage converted lactic acid to propionic acid, increasing pH. The analysis of 16S rDNA cloning libraries confirmed and expanded the knowledge gained from previous studies using classical microbiological methods. Our data show that Gram-negative anaerobic bacteria supersede Gram-positive *Fermincutes* species after the pH rises from around 3.2 to pH 5, and propionic and butyric acids are produced. Characterization of the spoilage microbiota is an important first step in efforts to prevent cucumber fermentation spoilage. Practical Application An understanding of the microorganisms that cause commercial cucumber fermentation spoilage may aid in developing methods to prevent the spoilage from occurring..

Keywords

Pickled vegetables, *Pectinatus*, *Propionibacteria*, Secondary cucumber fermentation, Spoilage.