

# HOUSEKEEPING GENE SEQUENCE ANALYSIS IS A REQUIRED PROCEDURE FOR EXPLORING NOVEL LAB STRAIN FROM TRADITIONAL FERMENTED FOODS

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Traditional fermented foods have a close relationship with the culture, tradition and climate of their localities of origin, and are produced by local techniques with different kinds of materials. Lactic Acid Bacteria (LAB) that are comprised a large bacterial group containing of about 370 species in 33 genera, are closely involved in the production of fermented foods. To reveal the distinctive features of traditional fermented foods, and to explore novel LAB strains in terms of their possible application as probiotics, it is very important to investigate the LAB diversity associated with the fermentation.

The 16S rRNA-based method has become a mainstream for classification and identification of bacteria, and it is now used as an alternative gold standard to DNA-DNA hybridization test. However, in many cases, members of a group of closely related species are impossible to discriminate on the basis of their 16S rRNA gene sequences alone, because the similarity values in these species are considerably higher than the recommended value for species differentiation (>97%).

During a study of biodiversity of LAB in stinky tofu brines and fu-tsai (fermented mustard) in Taiwan, we found the novel LAB strains which could not be clearly placed within any recognized species by means of 16S rRNA gene sequencing. On the basis of housekeeping genes (such as *pheS* and *rpoA*) similarities, these strains were clearly discriminated from the known validated species. From the results of the phenotypic and genotypic features, we have proposed that these strains represent the novel *Lactobacillus* species, as *Lactobacillus odoratitofui* sp. nov. and *Lactobacillus futsaii* sp. nov., respectively.

In conclusion, we confirmed that the analysis based on housekeeping gene sequences is a required procedure which enabled the detailed identification of LAB strains in species groups for which the identification by 16S rRNA-based methods is impossible.

**keywords:** housekeeping genes, Lactic acid bacteria, taxonomy