# Isolation and Characterization of Pure Cultures from Commercially Produced Sato Loog-Pang in four Regions of Thailand

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## Abstract

Sato Loog-Pang, a traditional Thai fermentation starter, relies on a complex microbial community of molds and yeasts for its amylolytic and ethanol-producing capabilities. This research examined key mold and yeast isolates from Loog Pang Sato samples collected across four distinct regions of Thailand. Six samples per region (North, Northeast, Central, and South) were analyzed, resulting in the isolation of 13 molds and 12 yeasts, which were assessed for amylase and ethanol production, respectively. The dominant microorganisms varied significantly by region. In the North, *Amylomyces rouxii* (syn. *Mucor indicus*) and *Saccharomyces malanga* were prevalent. For the Northeast, *Aspergillus niger* and *Saccharomyces cerevisiae* were identified as key players. The Central region's Loog Pang Sato was characterized by Mucor indicus and *Saccharomycopsis fibuligera*. Finally, *Rhizopus arrhizus* and *Saccharomycopsis fibuligera* were found to be the primary mold and yeast species in the Southern region.

***Keywords*** *: Loog-Pang, Sato, Thai rice wine, Pure culture, alcoholic beverage*