

ABSTRAK

Teresia Junetti Rajagukguk, NIM 4212520007 (2025), Identifikasi Bakteri Asam Laktat Makanan Fermentasi Tradisional Naniura Menggunakan Metode *Next Generation Sequencing* (Ngs).

Naniura merupakan makanan fermentasi tradisional khas Batak yang diolah melalui fermentasi spontan tanpa proses pemanasan, sehingga memungkinkan pertumbuhan berbagai mikroorganisme, terutama bakteri asam laktat (BAL). Penelitian ini bertujuan untuk mengidentifikasi serta menganalisis keberagaman spesies BAL pada naniura berbahan dasar ikan mas (*Cyprinus carpio*) dan ikan mujair (*Oreochromis mossambicus*) menggunakan pendekatan metagenomik berbasis *Next Generation Sequencing* (NGS). Tahapan penelitian meliputi ekstraksi DNA total, pengujian kualitas DNA, serta sekuensing gen 16S rRNA untuk memperoleh profil komunitas mikroba secara menyeluruh. Hasil analisis menunjukkan bahwa bakteri asam laktat yang ditemukan pada naniura berbahan dasar ikan mas (*Cyprinus carpio*) dan ikan mujair (*Oreochromis mossambicus*) memiliki kesamaan spesies meliputi *Enterococcus casseliflavus*, *Lactiplantibacillus pentosus*, *Lactiplantibacillus plantarum*, *Lactobacillus acetotolerans*, *Lactobacillus kitasatonis*, *Lactococcus lactis*, *Leuconostoc citreum*, *Leuconostoc mesenteroides*, *Levilactobacillus brevis*, *Limosilactobacillus vaginalis*, dan *Weissella confusa*. Perbedaan spesifik ditemukan pada keberadaan *Tetragenococcus halophilus* dan *uncultured Vagococcus sp.* yang hanya teridentifikasi pada naniura ikan mas, serta *Marinilactibacillus piezotolerans* yang hanya ditemukan pada naniura ikan mujair.

Kata Kunci: Bakteri asam laktat, metagenomik, naniura, NGS.

ABSTRACT

Teresia Junetti Rajagukguk, NIM 4212520007 (2025), Identification of Lactic Acid Bacteria from the Traditional Fermented Food Naniura Using the Next Generation Sequencing (NGS) Method.

Naniura is a traditional Batak fermented food processed through spontaneous fermentation without heat treatment, allowing the growth of various microorganisms, particularly lactic acid bacteria (LAB). This study aimed to identify and analyze the diversity of LAB species in naniura made from common carp (*Cyprinus carpio*) and tilapia (*Oreochromis mossambicus*) using a metagenomic approach based on Next Generation Sequencing (NGS). The research stages included total DNA extraction, DNA quality assessment, and 16S rRNA gene sequencing to obtain a comprehensive profile of the microbial community. The results showed that the lactic acid bacteria found in naniura made from both common carp and tilapia shared several species, namely *Enterococcus casseliflavus*, *Lactiplantibacillus pentosus*, *Lactiplantibacillus plantarum*, *Lactobacillus acetotolerans*, *Lactobacillus kitasatonis*, *Lactococcus lactis*, *Leuconostoc citreum*, *Leuconostoc mesenteroides*, *Levilactobacillus brevis*, *Limosilactobacillus vaginalis*, and *Weissella confusa*. Specific differences were observed in the presence of *Tetragenococcus halophilus* and uncultured *Vagococcus* sp., which were only identified in carp-based naniura, whereas *Marinilactibacillus piezotolerans* was exclusively detected in tilapia-based naniura.

Keywords: Lactic acid bacteria, metagenomics, naniura, NGS.

