UNIVERSITAS
GADJAH MADA

Diversitas Komunitas Bakteri Usus pada Benih Ikan Lele (Clarias sp.) yang Sehat dan Sakit
Farida Zaqiyah, Dr. Ir. Triyanto, M.Si.; Dr. Senny Helmiati, S.Pi., M.Sc.
Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/

INTISARI

Diversitas Komunitas Bakteri Usus pada Benih Ikan Lele (*Clarias* sp.) yang Sehat dan Sakit

Penelitian ini mengkaji komunitas bakteri usus pada benih ikan lele (*Clarias* sp.) sehat dan sakit yang dikumpulkan dari dua fasilitas budidaya di Kapanewon Karangmojo dan Cangkringan, Yogyakarta, Indonesia. Sampel usus dikelompokkan berdasarkan status kesehatan dan dianalisis menggunakan sekuensing amplikon gen 16S rRNA *full-length* pada *platform Oxford Nanopore Technologies PromethION,* dilanjutkan dengan klasifikasi taksonomi menggunakan Kraken2 dan Bracken. Analisis diversitas alfa mengungkap *richness, evenness,* dan *Shannon diversity index* yang lebih tinggi pada benih ikan lele sehat dibandingkan ikan sakit dari dua lokasi, sedangkan Simpson diversity index bernilai sama antarsampel. Secara taksonomi, ikan lele sehat didominasi Filum Fusobacteriota (45,14%) dengan genus Cetobacterium sebagai genus dominan, diikuti Bacillota (14,94%, terutama genus Clostridium) dan Cyanobacteriota (14,59%). Pada ikan lele sakit, Fusobacteriota tetap dominan (39,12%) namun diikuti peningkatan tajam Bacteroidota (38,08%, didominasi genus Bacteroides 34,07%) dan Pseudomonadota (10,18%), sementara Cyanobacteriota dan Bacillota menurun tajam. Genus Cetobacterium menjadi *biomarker* utama komunitas usus ikan sehat, sedangkan genus Bacteroides menjadi *biomarker* utama ikan sakit, disertai peningkatan genus minor Dysgonomonas, Plesiomonas, dan Akkermansia. Selain itu, ditemukan kehadiran genus patogen oportunistik yang dikenal luas pada ikan lele, yakni Edwardsiella (0,65%), Pseudomonas (0,44%), dan Aeromonas (0,33%), yang hanya terdeteksi pada ikan sakit meski dengan kelimpahan sangat rendah, namun tetap relevan sebagai indikator kualitatif penciri kondisi sakit mengingat perannya sebagai agen penyakit sistemik pada ikan lele. Hasil ini menyoroti adanya pergeseran mikrobiota usus yang berkaitan dengan status kesehatan ikan dan memberikan dasar bagi penelitian lanjutan dengan jumlah sampel yang lebih besar.

Kata Kunci : microbiota usus, status kesehatan, LEfSe *biomarker*, *long-read sequencing*, keragaman taksonomi

UNIVERSITAS
GADJAH MADA

Diversitas Komunitas Bakteri Usus pada Benih Ikan Lele (Clarias sp.) yang Sehat dan Sakit
Farida Zaqiyah, Dr. Ir. Triyanto, M.Si.; Dr. Senny Helmiati, S.Pi., M.Sc.
Universitas Gadjah Mada, 2026 | Diunduh dari http://etd.repository.ugm.ac.id/

ABSTRACT

Diversity of Gut Bacterial Communities in Healthy and Diseased Catfish (*Clarias* sp.) Fingerlings

This study investigated the gut bacterial community of healthy and diseased African catfish (*Clarias* sp.) juveniles collected from two aquaculture facilities in Karangmojo and Cangkringan Districts, Yogyakarta, Indonesia. Gut samples were grouped according to health status and analysed using full-length 16S rRNA gene amplicon sequencing on the Oxford *Nanopore* Technologies PromethION platform, followed by taxonomic classification with Kraken2 and Bracken. Alpha diversity analysis revealed higher *richness*, *evenness*, and Shannon diversity index values in healthy juveniles than in diseased juveniles from both locations, whereas the Simpson diversity index remained identical across samples. Taxonomic analysis showed that the gut microbiota of healthy catfish was dominated by the phylum Fusobacteriota (45.14%), with *Cetobacterium* as the predominant genus, followed by Bacillota (14.94%), represented mainly by *Clostridium*, and Cyanobacteriota (14.59%). In diseased fish, Fusobacteriota remained the dominant phylum (39.12%) but was accompanied by a marked increase in Bacteroidota (38.08%), predominantly represented by *Bacteroides* (34.07%), and Pseudomonadota (10.18%), while the relative abundances of Cyanobacteriota and Bacillota declined substantially. *Cetobacterium* was identified as the principal biomarker of the healthy gut microbiota, whereas *Bacteroides* emerged as the primary biomarker of diseased fish, together with increased abundances of the minor genera *Dysgonomonas*, *Plesiomonas*, and *Akkermansia*. In addition, the opportunistic pathogenic genera *Edwardsiella* (0.65%), *Pseudomonas* (0.44%), and *Aeromonas* (0.33%), which are widely recognised as pathogens of African catfish, were detected exclusively in diseased fish. Although present at very low relative abundances, their occurrence remains relevant as a qualitative indicator of disease status because of their established roles as causative agents of systemic infections in catfish. These findings demonstrate a shift in the gut microbiota associated with fish health status and provide a foundation for future studies involving larger sample sizes.

Keywords : *Clarias* sp., gut microbiota, health status, LEfSe biomarker, long-*read* sequencing, taxonomic diversity.