

INTISARI

Komunitas bakteri tanah merupakan salah satu komponen penting pada tanaman pisang melalui interaksi antara akar tanaman, mikroorganisme antagonis, dan patogen tanah. Penelitian ini mengkaji bagaimana tekstur tanah berpengaruh terhadap struktur komunitas bakteri tanah pada perakaran Pisang Awak. Sampel tanah diambil dari tiga kabupaten dengan jenis tekstur tanah yang berbeda di Daerah Istimewa Yogyakarta yaitu Kulon Progo (lempung berliat), Bantul (lempung liat berpasir), dan Gunung Kidul (liat). *Plant* kultur jaringan Pisang Awak diaklimatisasi selama tiga bulan di *greenhouse* untuk kemudian *environmental* DNA (eDNA) diekstraksi dari dua zona perakaran untuk dilakukan analisis metagenomik amplicon pada daerah hipervariabel V5-V7 16S rRNA. Hasil analisis menunjukkan bahwa tekstur tanah mempengaruhi kondisi lingkungan tanah dan berperan dalam kelimpahan taksa bakteri tertentu. Genus bakteri yang berpotensi sebagai biomarker berdasarkan karakteristik khusus tekstur atau zona perakaran tanah adalah *Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium*, *MND1*, dan *Agromyces*. *Core microbiome* seluruh sampel pada tingkat genus adalah *Bacillus*, *Streptomyces*, *Nocardioideae*, *Sphingomonas*, *MND1*, dan *Gaiella*, sementara *Ectobacillus funiculus* merupakan *core microbiome* di tingkat spesies. Studi metagenomik diharapkan dapat menjadi landasan untuk penelitian terapan seperti eksplorasi agen biokontrol terhadap layu Fusarium pada tanaman pisang. Hal ini menyoroti bahwa mengidentifikasi komunitas tanah bakteri merupakan langkah krusial dalam mengembangkan strategi pengelolaan berbasis mikrobiom.

Kata kunci: ABB, Bioinformatika, Komunitas Bakteri, Metagenomik, Mikrobiom, Pisang

ABSTRACT

Soil bacterial community is one of the important components associated with the banana plant by mediating interactions between plant root-beneficial bacteria, antagonistic taxa, and soilborne pathogens. This research examines how soil texture shapes the soil bacterial community of Pisang Awak. Soil was sampled from three regencies with different soil texture types in the Daerah Istimewa Yogyakarta: Kulon Progo (clay loam), Bantul (sandy clay loam), and Gunung Kidul (clay). Pisang Awak plantlets were acclimatized for three months under greenhouse condition before environmental DNA (eDNA) was extracted from two soil compartments for amplicon metagenomic sequencing targeting the V5-V7 region of the 16S rRNA. The result showed that soil texture which formed by different proportion of constituent fractions, influences the soil environment and consequently alters the abundance of specific bacterial taxa. The genera that could potentially serve as biomarker based on particular characteristics of soil texture or the soil compartments are *Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium*, *MND1*, and *Agromyces*. The core bacterial microbes among all samples at genus level are *Bacillus*, *Streptomyces*, *Nocardioides*, *Sphingomonas*, *MND1*, and *Gaiella*, while *Ectobacillus funiculus* detected as the core bacterial species. Exploring the soil bacterial community establishes a key reference for applied research, including studies of ecological functions, crop production benefits, and biocontrol agents against Fusarium wilt in banana. This highlights that identifying core taxa is a critical step for developing microbiome-based management strategies.

Keywords: ABB, Amplicon Metagenomics, Banana, Bioinformatics, Microbiome, Microorganisms