

DIVERSITAS BAKTERI ENDOFIT PADA DAUN BAWANG PUTIH (*Allium sativum* L.) TERINFEKSI *POTYVIRUS* BERDASARKAN METABARKODING

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Intisari

Bawang putih (*Allium sativum* L.) merupakan salah satu komoditas hortikultura penting secara global, namun produktivitasnya masih rendah karena beberapa faktor, termasuk infeksi virus. Selain memengaruhi kesehatan tanaman secara langsung, infeksi virus juga berpotensi memengaruhi komunitas mikroorganisme yang berperan penting dalam mendukung pertumbuhan tanaman. Penelitian ini bertujuan untuk menganalisis diversitas, komposisi komunitas, dan potensi fungsional bakteri endofit pada daun bawang putih sehat dan terinfeksi virus dari berbagai lokasi geografis menggunakan metabarkoding. Penilaian infeksi virus dilakukan melalui skoring keparahan infeksi dan deteksi molekuler menggunakan RT-PCR dengan primer universal dan spesifik *Potyvirus*. Analisis bakteri endofit dilakukan melalui metabarkoding gen 16S rRNA menggunakan *Oxford nanopore technologies*, diikuti dengan analisis bioinformatika untuk identifikasi taksonomi, analisis diversitas, serta prediksi fungsional komunitas bakteri endofit. Hasil skoring infeksi menunjukkan penyebaran infeksi virus tiap lokasi berada pada tingkat keparahan (VI) sedang (55-58%) dengan distribusi infeksi (PDI) pada kategori *Widespread* ($\geq 75\%$). Deteksi RT-PCR mengonfirmasi keberadaan *Potyvirus* dengan beberapa infeksi campuran pada sampel terinfeksi. Profil taksonomi menunjukkan adanya kecenderungan pergeseran dominansi beberapa taksa akibat kondisi infeksi yang diduga memengaruhi kondisi endosfer. Analisis diversitas alfa menunjukkan tidak ada perbedaan signifikan antar kelompok, sedangkan analisis diversitas beta mengindikasikan pergeseran komposisi komunitas bakteri yang signifikan. Prediksi fungsional menunjukkan perbedaan yang tidak signifikan pada kapasitas metabolik global, yang mencerminkan adanya redundansi dan resiliensi fungsional komunitas mikroba. Meskipun demikian, beberapa fungsi spesifik terkait metabolisme, transpor nutrisi, dan respons stres menunjukkan perbedaan antar kondisi. Hasil ini menunjukkan bahwa infeksi virus memengaruhi komposisi bakteri endofit tanpa mengubah kekayaan dan kelimpahan taksa serta potensi fungsional globalnya.

Kata kunci: *Allium sativum* L., diversitas bakteri, interaksi tanaman–mikroba, metabarkoding, *Potyvirus*

DIVERSITY OF ENDOPHYTIC BACTERIA IN GARLIC LEAVES (*Allium sativum* L.) INFECTED WITH POTYVIRUS BASED ON METABARCODING

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Abstract

Garlic (*Allium sativum* L.) is one of the globally important horticultural commodities, however, its productivity remains low due to several factors, including viral infections. In addition to directly affecting plant health, viral infections may also influence microbial communities that play an important role in supporting plant growth. This study aimed to analyze the diversity, community composition, and functional potential of endophytic bacteria in healthy and virus-infected garlic leaves from various geographical locations using a metabarcoding approach. Assessment of viral infection was conducted through infection severity scoring and molecular detection using RT-PCR with universal and specific primers for *Potyvirus*. Endophytic bacterial analysis was performed through 16S rRNA gene metabarcoding using Oxford Nanopore Technologies, followed by bioinformatic analyses for taxonomic identification, diversity analysis, and functional prediction of endophytic bacterial communities. Infection scoring results showed that viral infection at each location was at a moderate severity level (VI) of 55–58%, with infection distribution (PDI) in the widespread category ($\geq 75\%$). RT-PCR detection confirmed the presence of *Potyvirus* with several mixed infections in infected samples. The taxonomic profile indicates a tendency toward shifts in the dominance of certain taxa under infected conditions, which are presumed to affect the endosphere environment. Alpha diversity analysis showed no significant differences between groups, whereas beta diversity analysis revealed significant shifts in bacterial community composition. Functional prediction showed no significant differences in global metabolic capacity, reflecting functional redundancy and resilience of the microbial community. Nevertheless, several specific functions related to metabolism, nutrient transport, and stress response showed differences between conditions. These results indicate that viral infection affects the composition of endophytic bacteria without altering taxon richness and abundance or their global functional potential.

Keywords: *Allium sativum* L., bacterial diversity, metabarcoding, plant–microbe interaction, *Potyvirus*