

**Analisis Metagenomik Komunitas Bakteri dan Jamur yang Berasosiasi dengan
Penyakit Moler pada Filosfer Bawang Merah di Lahan Pantai Kabupaten Bantul**

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Intisari

Fusarium spp., penyebab penyakit moler, menjadi salah satu alasan penurunan produktivitas bawang merah. Penyakit moler diketahui telah endemik di daerah Bantul. Penelitian ini bertujuan untuk mengetahui keragaman jamur dan bakteri pada filosfer bawang merah dengan menggunakan analisis metagenomik. Pengambilan sampel dilakukan pada minggu 2 dan 6 di 3 wilayah dengan jenis tanah berbeda: Sono (A, Grumusol Chromic), Samiran (B, Grumusol Chromic), dan Depok (C, Regosol Eutric). Analisis metagenomik dilakukan dengan kultur *independent* menggunakan gDNA pada sampel minggu ke 2 (2A, 2B, dan 2C) dan ke 6 (6A, 6B, dan 6C) dengan ITS pada region ITS1 untuk jamur dan 16S rRNA pada region V3-V4 untuk bakteri. *OTU cluster*, *taxonomic annotation*, keragaman alfa dan beta dianalisis menggunakan bioinformatika. Kultur *dependent* jamur dan bakteri ditumbuhkan pada media dan dilakukan analisis morfologi dan molekuler. Analisis metagenomik jamur ditemukan 35 genus dominan yang mayoritas berasal dari filum *Ascomycota*. Keragaman spesies jamur tertinggi ditemukan pada sampel 2A (Minggu ke 2, Sono). Analisis metagenomik bakteri ditemukan 35 genus bakteri dominan yang mayoritas berasal dari filum *Proteobacteria*. Keragaman spesies bakteri tertinggi ditemukan pada sampel 6B (Minggu ke 6, Samiran). Berdasarkan analisis metagenomik daun bawang merah di minggu 2 dan 6, tidak ada perbedaan yang signifikan pada komposisi komunitas jamur dan bakteri. Pada kultur *dependent*, tidak ditemukan jamur yang mampu tumbuh pada media. Sementara itu, bakteri patogen *Pseudomonas aeruginosa* ditemukan pada kultur bakteri, penyebab busuk lunak pada umbi bawang merah. Studi metagenomik mampu menjelaskan komunitas mikrob lebih baik dibandingkan teknik konvensional.

Kata kunci: *Fusarium* spp., komunitas mikrob, kultur *dependent*, kultur *independent*, metagenomik

Metagenomic Analysis of Bacterial and Fungal Communities Associated with Twisted Disease on Shallot Phyllosphere in Coastal Area of Bantul Regency

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Abstract

Fusarium spp., which causes twisted disease, is one of the reasons for the decreased shallots' productivity. The twisted disease is known to be endemic in the Bantul area. This study aims to determine the diversity of fungi and bacteria in the shallots' phyllosphere using metagenomic analysis. Sampling was carried out at weeks 2 and 6 in 3 areas with different soil types: Sono (A, Grumusol Chromic), Samiran (B, Grumusol Chromic), and Depok (C, Regosol Eutric). Metagenomic analysis was performed by independent culture using gDNA on weeks 2 (2A, 2B, and 2C) and 6 (6A, 6B, and 6C) with ITS in the ITS1 region for fungi and 16S rRNA in the V3-V4 region for bacteria. OTU cluster, taxonomic annotation, and alpha and beta diversity were analyzed using bioinformatics. Dependent cultures of fungi and bacteria were grown on the media, and morphological and molecular analyzes were performed. Metagenomic analysis of fungi found 35 dominant genera, most of which came from the phylum *Ascomycota*. The highest fungal species diversity was found in sample 2A (Week 2, Sono). Metagenomic analysis of bacteria found 35 dominant bacterial genera, most of which came from the phylum *Proteobacteria*. The highest bacterial species diversity was found in sample 6B (Week 6, Samiran). Based on the metagenomic analysis at weeks 2 and 6, there was no significant difference in the composition of the fungal and bacterial communities. In dependent culture, no fungi were found that were able to grow on the media. Meanwhile, pathogenic bacteria *Pseudomonas aeruginosa* was found in bacterial culture, which causes soft rot of shallot bulbs. Metagenomic studies can explain microbial communities better than conventional techniques.

Keywords: dependent culture, *Fusarium* spp., independent culture, metagenomics, microbial communities