ABSTRAK

PERBANDINGAN PROFIL METABOLIT JAMUR *Xylaria* sp. PENYEBAB BUSUK AKAR DAN PANGKAL BATANG TEBU YANG SENSITIF DAN RESISTEN TERHADAP FUNGISIDA CARBENDAZIM MENGGUNAKAN GC-MS

Oleh

NI MADE RIA PRATEKA

Penyakit busuk akar dan pangkal batang (BAPB) yang disebabkan oleh jamur *Xylaria* sp. merupakan salah satu penyakit utama pada tanaman tebu di Lampung. Tingkat serangan 25–26% dapat menyebabkan penurunan produktivitas tebu hingga 12,3%. Penggunaan fungisida sebagai salah satu alternatif pengendalian berpotensi memicu resistensi pada patogen. Penelitian ini bertujuan untuk mengidentifikasi dan membandingkan profil metabolit *Xylaria* sp. yang resisten dan sensitif terhadap fungisida carbendazim menggunakan *Gas Chromatography–Mass Spectrometry* (GC-MS). Penelitian dilaksanakan dari Agustus 2025 sampai Februari 2026 di Laboratorium Penyakit Tumbuhan, Fakultas Pertanian, Universitas Lampung. Analisis GC-MS dilakukan di Laboratorium Sentral, Universitas Padjadjaran. Mutan tahan carbendazim diperoleh melalui pemaparan bertingkat pada media PSA mengandung carbendazim dengan konsentrasi 1,0–4,0 µg/mL. Sensitivitas isolat ditentukan berdasarkan nilai EC_{50}, dan profil metabolit dianalisis menggunakan GC-MS. Hasil penelitian menunjukkan bahwa nilai EC_{50} isolat *wild type* sebesar 0,711 µg/mL dan mutan sebesar 1,007 µg/mL, yang mengkonfirmasi keberhasilan pembentukan mutan resisten. Analisis GC-MS didapatkan 25 senyawa, dengan 12 senyawa ditemukan pada kedua isolat, 9 senyawa spesifik pada *wild type*, dan 4 senyawa spesifik pada mutan. Isolat mutan menunjukkan kandungan lebih tinggi pada furfural (15,16%) dan acetic acid (3,51%) dibandingkan *wild type* (8,80% dan 2,22%), sementara L-lactic acid lebih tinggi pada *wild type* (14,12%) dibandingkan mutan (10,25%). Perbedaan profil metabolit secara kuantitatif dan kualitatif mengindikasikan adanya reorganisasi metabolisme sebagai bentuk adaptasi fisiologis *Xylaria* sp. terhadap tekanan fungisida carbendazim.

Kata kunci: busuk akar dan pangkal batang, carbendazim, GC-MS, metabolomik, *Xylaria* sp.

ABSTRACT

COMPARISON OF METABOLITE PROFILES OF Xylaria sp. CAUSING ROOT AND BASAL STEM ROT IN SUGARCANE BETWEEN CARBENDAZIM-SENSITIVE AND CARBENDAZIM-RESISTANT ISOLATES USING GC-MS

By

NI MADE RIA PRATEKA

Root and basal stem rot disease (RBSR) caused by Xylaria sp. is one of the major diseases affecting sugarcane in Lampung. Disease incidence of 25–26% can result in a reduction in sugarcane productivity of up to 12.3%. The use of fungicides as one of the control alternatives has the potential to induce resistance in the pathogen. This study aimed to identify and compare the metabolite profiles of carbendazim-resistant and carbendazim-sensitive isolates of Xylaria sp. using Gas Chromatography–Mass Spectrometry (GC-MS). The research was conducted from August 2025 to February 2026 at the Plant Disease Laboratory, Faculty of Agriculture, University of Lampung. GC-MS analysis was performed at the Central Laboratory, Universitas Padjadjaran. Carbendazim-resistant mutants were generated through stepwise exposure on PSA medium containing carbendazim at concentrations of 1.0–4.0 µg/mL. Isolate sensitivity was determined based on EC_{50} values, and metabolite profiles were analyzed using GC-MS. The results showed that the EC_{50} value of the wild-type isolate was 0.711 µg/mL and that of the mutant was 1.007 µg/mL, confirming the successful development of resistant mutants. GC-MS analysis detected a total of 25 compounds, of which 12 were present in both isolates, 9 were specific to the wild type, and 4 were specific to the mutant. The mutant isolate exhibited higher levels of furfural (15.16%) and acetic acid (3.51%) compared to the wild type (8.80% and 2.22%, respectively), whereas L-lactic acid was more abundant in the wild type (14.12%) than in the mutant (10.25%). Quantitative and qualitative differences in metabolite profiles indicate a reorganization of metabolism as a form of physiological adaptation of Xylaria sp. to carbendazim fungicide pressure.

Keywords: *carbendazim, GC-MS, metabolomics, root and stalk base rot , Xylaria sp.*