

ABSTRAK

PERBANDINGAN PROFIL METABOLIT SEKUNDER JAMUR *Xylaria* sp. PENYEBAB PENYAKIT BUSUK AKAR DAN PANGKAL BATANG TEBU *WILD TYPE* DAN TERADAPTASI FUNGISIDA FLUTRIAFOL MENGUNAKAN GC-MS

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SIFA PERMATASARI

Penyakit busuk akar dan pangkal batang pada tebu yang disebabkan oleh *Xylaria* sp. merupakan penyakit utama dengan kerugian signifikan. Salah satu alternatif pengendalian penyakit ini adalah aplikasi fungisida dari golongan *Demethylation Inhibitors* (DMI) seperti flutriafol. Penggunaan fungisida secara terus-menerus berisiko menyebabkan resistensi pada jamur patogen. Penelitian ini bertujuan untuk mengidentifikasi dan membandingkan profil metabolit *Xylaria* sp. *wild type* dan teradaptasi fungisida flutriafol menggunakan GC-MS. Penelitian dilakukan melalui tahapan isolasi jamur dari tanaman tebu sakit, pembuatan *Xylaria* sp. teradaptasi fungisida flutriafol melalui seleksi bertingkat dengan peningkatan konsentrasi flutriafol, uji sensitivitas untuk menentukan nilai EC_{50} , produksi metabolit sekunder, serta analisis profil metabolit menggunakan GC-MS yang dilanjutkan dengan perhitungan *fold change*. Hasil penelitian menunjukkan nilai EC_{50} isolat *Xylaria* sp. *wild type* sebesar 1,96 $\mu\text{g/mL}$ dan *Xylaria* sp. teradaptasi fungisida flutriafol sebesar 2,5 $\mu\text{g/mL}$, yang menandakan penurunan sensitivitas pada *Xylaria* sp. teradaptasi fungisida flutriafol. Analisis GC-MS berhasil mengidentifikasi 27 metabolit sekunder, dengan 16 metabolit sekunder yang sama pada kedua isolat. Beberapa metabolit sekunder meningkat pada *Xylaria* sp. teradaptasi fungisida flutriafol, sedangkan sebagian lainnya menurun atau hanya muncul pada salah satu isolat. Berdasarkan penelitian ini dapat diketahui bahwa adaptasi pada fungisida flutriafol berkaitan dengan perubahan profil metabolit sekunder sebagai bentuk penyesuaian metabolisme jamur terhadap tekanan fungisida.

Kata kunci: *Demethylation Inhibitors* (DMI), flutriafol, GC-MS, metabolit sekunder, resistensi fungisida, *Xylaria* sp.

ABSTRAK

COMPARISON OF SECONDARY METABOLITE PROFILES OF XYLARIA SP. CAUSING SUGARCANE ROOT ROT AND BASAL STEM ROT IN WILD TYPE AND FLUTRIAFOL-ADAPTED ISOLATES USING GC-MS

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Root rot and basal stem rot disease in sugarcane caused by *Xylaria* sp. is a major disease with significant losses. One alternative for controlling this disease is the application of fungicides from the Demethylation Inhibitors (DMI) group such as flutriafol. Continuous use of fungicides carries the risk of causing resistance in pathogenic fungi. This study aims to identify and compare the metabolite profiles of *Xylaria* sp. wild type and flutriafol-adapted isolates using GC-MS. The research was conducted through several stages, including fungal isolation from diseased sugarcane plants, development of flutriafol-adapted *Xylaria* sp. through stepwise selection with increasing concentrations of flutriafol, sensitivity testing to determine EC₅₀ values, production of secondary metabolites, and metabolite profiling analysis using GC-MS followed by fold change calculation. The results showed that the EC₅₀ value of the *Xylaria* sp. wild type isolate was 1.96 µg/mL, while that of the flutriafol-adapted *Xylaria* sp. isolate was 2.5 µg/mL, indicating decreased sensitivity in the flutriafol-adapted isolate. GC-MS analysis successfully identified 27 secondary metabolites, with 16 metabolites shared by both isolates. Some secondary metabolites increased in the flutriafol-adapted *Xylaria* sp., while others decreased or were present only in one isolate. Based on this study, it can be concluded that adaptation to flutriafol is associated with changes in the secondary metabolite profile as a form of fungal metabolic adjustment to fungicide pressure.

Keywords: Demethylation Inhibitors (DMI), flutriafol, fungicide resistance, GC-MS, secondary metabolites, *Xylaria* sp.