

**ANALISIS PROFIL PROTEIN BAKTERI UBCR_12 DAN
UBCR_36 SELAMA INTERAKSINYA DENGAN *Colletotrichum
gloeosporioides*, *Fusarium oxysporum* DAN *Sclerotium rolfsii***

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**FAKULTAS PERTANIAN
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ANALISIS PROFIL PROTEIN BAKTERI UBCR_12 DAN UBCR_36 SELAMA INTERAKSINYA DENGAN *Colletotrichum gloeosporioides*, *Fusarium oxysporum* DAN *Sclerotium rolfsii*

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ABSTRAK

Bakteri rhizosfer banyak digunakan sebagai agen biokontrol untuk mengendalikan serangan jamur fitopatogen pada tanaman. Agar diperoleh agen biokontrol dengan aktivitas penekanan yang maksimal, diperlukan informasi menyeluruh terkait bagaimana mekanisme antagonis itu dihasilkan, sehingga menjadi acuan untuk menentukan modifikasi-modifikasi yang dapat mendorong peningkatan aktivitas penekanannya. Penelitian ini bertujuan untuk mengidentifikasi profil protein bakteri isolat UBCR_12 dan UBCR_36 yang terbentuk selama interaksinya dengan *C. gloeosporioides*, *F. oxysporum* dan *S. rolfsii*. Uji antagonis dilakukan pada dua jenis media yaitu media PDA basal dan media PDA modifikasi dengan penambahan 2% pepton. Selanjutnya dilakukan analisis dengan pendekatan proteomik menggunakan teknik SDS-PAGE untuk memvisualisasi pita protein spesifik yang diduga terlibat dalam mekanisme antagonis bakteri rhizosfer. Aktivitas penekanan tertinggi dari UBCR_12 dan UBCR_36 pada media PDA basal diperoleh terhadap *F. oxysporum* sebesar 53,6% dan 58,9% yang diduga diregulasi oleh penurunan ekspresi (*down-regulated*) pita protein berukuran 15 dan 37 kDa. Aktivitas penekanan tertinggi kedua isolat pada media PDA modifikasi diperoleh terhadap *S. rolfsii* sebesar 75,9% dan 62,9% masing-masingnya, dan diduga diregulasi oleh peningkatan ekspresi (*up-regulated*) pita protein berukuran 54 dan 60 kDa. Kedua isolat bakteri antagonis memperlihatkan profil ekspresi proteom ekstraseluler yang sama ketika berinteraksi dengan spesies jamur fitopatogen yang sama di media PDB basal. Sebaliknya, profil proteom ekstraseluler yang dihasilkan di media PDB dengan kandungan pepton menunjukkan variasi jumlah pita protein yang terekspresi dan perbedaan level ekspresi di masing-masing isolat selama interaksinya dengan jamur fitopatogen.

Kata kunci : antagonis, antijamur, jamur fitopatogen, proteomik, rhizobakteria

Skripsi ini telah dipertahankan di depan sidang penguji dan dinyatakan lulus tanggal 22 Januari 2018

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PROTEIN PROFILE ANALYSIS OF BACTERIA UBCR_12 AND UBCR_36 DURING THEIR INTERACTION WITH *Colletotrichum gloeosporioides*, *F. oxysporum* AND *S. rolfsii*

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ABSTRACT

Rhizosphere bacteria are widely used as biocontrol agents to control fungal phytopathogenic attacks on plants. In order to obtain a biocontrol agent with maximum antagonistic activity, thorough information is needed regarding how the antagonist mechanism is produced, thereby becoming a reference for determining the modifications that may encourage increased antagonistic activity. The objective of this study was to identify the protein profiles of bacteria isolates UBCR_12 and UBCR_36 formed during their interaction with *C. gloeosporioides*, *F. oxysporum* and *S. rolfsii*. An antagonistic test was performed on two types of medium namely basal PDA medium and modified PDA medium with the addition of 2% peptone. Furthermore, an analysis using proteomic approach using SDS-PAGE technique was used to visualize specific protein bands that were suspected to be involved in rhizosphere bacterial antagonist mechanisms. The highest antagonistic activity of UBCR_12 and UBCR_36 on basal PDA medium was obtained against *F. oxysporum* of 53.6% and 58.9% which was suspected to be regulated by the decreased expression (*down-regulated*) of protein bands of 15 and 37 kDa. The second highest pressure activity of the isolates on modified PDA media was obtained against *S. rolfsii* of 75.9% and 62.9%, respectively, and was suspected to be regulated by the increased expression (*up-regulated*) of protein bands of 54 and 60 kDa. Both antagonistic bacterial isolates exhibit the same extracellular proteom expression profile when interacting with the same phytopathogenic fungal species in basal PDB medium. In contrast, extracellular proteom profiles produced in PDB medium with peptone content showed variations in the number of expressed protein bands and differences in expression levels in each isolate during their interactions with phytopathogenic fungi.

Key words : antagonist, antifungal, phytopatogen fungi, proteomic, rhizobacteria

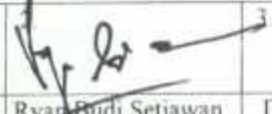
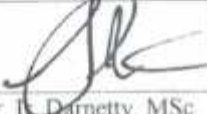
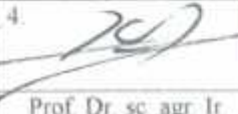

This thesis has been defended and was passed on January, 22nd 2018.

Abstract Editor

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