

INTISARI

Bakteri *B. amyloliquefaciens* GMEKP1 telah diketahui mampu menghasilkan metabolit sekunder beragam dan memiliki aktifitas antifungi. Penelitian dengan pendekatan metabologenomik dapat membantu prediksi metabolit sekunder lebih mudah dan cepat. Disisi lain penggunaan fungisida sintesis secara terus-menerus dapat menyebabkan resistensi pada jamur patogen tanaman, sehingga diperlukan penelitian ini dengan tujuan untuk mendapatkan informasi senyawa metabolit sekunder dari GMEKP1 yang berpotensi menjadi antifungi jamur patogen tanaman khususnya pada *Fusarium vanettenii* dan *Ganoderma boninense*. Metode yang dilakukan pada penelitian ini meliputi analisis genomik melalui platform antiSMASH 7.0 dan BAGEL4; produksi metabolit sekunder GMEKP1; ekstraksi metabolit sekunder dengan pelarut etil-asetat; karakterisasi metabolit sekunder menggunakan *targeted* dan *untargeted* LC-HRMS; serta uji *in-silico molecular docking* terhadap protein target kutinase (PDB ID: 1OXM) dari jamur *F. vanettenii* dan protein lakase (UniProtKB ID: A0A5K1JSJ0) dari jamur *G. boninense*. Hasil penelitian pada studi ini ditemukan 12 BGCs yang didominasi oleh senyawa poliketida. Sejumlah 3 dari 8 senyawa yang sebelumnya sudah diprediksi oleh AntiSMASH 7.0 terdeteksi oleh *targeted* LC-HRMS yaitu tetain-basilisin, difisidin dan bacillaene. Sedangkan pada *untargeted* LC-HRMS menunjukkan bahwa senyawa antifungi dominan yang terdeteksi adalah *Cyclo(leucylprolyl)*, betain dan piperidin. Berdasarkan uji *in-silico molecular docking* senyawa metabolit sekunder yang berpotensi sebagai anti-fungi adalah tetain-basilisin (BGCs-2); bacillaene (BGCs-8), difisidin (BGCs-12) dan *Cyclo(leucyl-prolyl)*. Keempat senyawa tersebut berpotensi menghambat protein kutinase dari jamur *F. vanettenii* melalui ikatan hidrogen dan alkyl. Sedangkan senyawa tetain-basilisin, difisidin dan *Cyclo(leucyl-prolyl)* cukup berpotensi menghambat protein lakase dari jamur *G. boninense* melalui ikatan hidrogen. Hasil analisis metabologenomik pada studi ini diharapkan dapat digunakan sebagai acuan uji lanjut terhadap efektifitas metabolit sekunder secara *in-vitro* dan aplikasi biofungisida.

Kata kunci: genomik, metabolomik, *Bacillus amyloliquefaciens* GMEKP1, metabolit sekunder, anti-fungi, *in-silico molecular docking*, kutinase, lakase

ABSTRACT

The *Bacillus amyloliquefaciens* GMEKP1 has been known to produce various secondary metabolites and has antifungal activity. Metabologenomic approach research can help predict secondary metabolites more easily and quickly. On the other hand, the continuous use of synthetic fungicides can caused plant pathogenic fungi resistance, so this research is needed with the aim of obtaining information on secondary metabolites of GMEKP1 which have the potential to become antifungal plant pathogenic fungi, especially on *Fusarium vanettenii* and *Ganoderma boninense*. The methods used in this study were genomic analysis using the antiSMASH 7.0 and BAGEL4 platforms; GMEKP1 secondary metabolite production; extraction of secondary metabolites with ethyl-acetate solvent; characterization of secondary metabolites using targeted and untargeted LC-HRMS; in-silico molecular docking of cutinase protein (PDB ID: 1OXM) from *F. vanettenii* and Laccase protein (UniProtKB ID: A0A5K1JSJ0) from *G. boninense*. The research results in this study was found 12 BGCs which were dominated by polyketide compounds. Three of the eight compounds previously predicted by AntiSMASH 7.0 were detected by the LC-HRMS target (tetain-basilicin, difficidin and bacillaene). Untargeted LC-HRMS showed that the dominant antifungal compounds detected were Cyclo(leucylprolyl), betaine and piperidine. Based on the in-silico molecular docking test, the secondary metabolites that have potential as antifungals are tetain-basilicin (BGCs-2); bacillaene (BGCs-8), difficidin (BGCs-12) and Cyclo(leucylprolyl). These four compounds have the potential to inhibit Cutinase from *F. vanettenii* through hydrogen and alkyl bonds. While the compounds tetain-basilicin, difficidin and Cyclo(leucylprolyl) have the potential to inhibit Laccase from the *G. boninense* through hydrogen bonding. The results of the metabologenomics analysis in this study can be used as a reference for further testing the effectiveness of secondary metabolites in vitro and application of biofungicides.

Keywords: genomics, metabolomics, *Bacillus amyloliquefaciens* GMEKP1, secondary metabolite, antifungal, in-silico molecular docking, cutinase, laccase