ABSTRAK

IDENTIFIKASI SPESIES ISOLAT BAKTERI AKAR BAKAU (*Rhizophora* sp.) DARI LABUHAN MARINGGAI LAMPUNG TIMUR

Pencarian sumber daya mikroorganisme yang terdapat dalam jaringan tumbuhan mulai mendapat perhatian. Pada tumbuhan bakau terdapat beberapa jenis mikroorganisme salah satunya adalah bakteri. Pemanfaatan bakteri dalam berbagai bidang semakin meningkat contohnya pada produksi metabolit sekunder dan enzim. Penelitian ini bertujuan untuk mengidentifikasi spesies bakteri pada akar bakau secara fenotip dan genotip. Metode penapisan dilakukan untuk mendapatkan isolat bakteri akar bakau, kemudian dilakukan pengamatan morfologi isolat dan sel dengan pewarnaan gram. Uji biokimia dilakukan untuk menentukan genus dari isolat bakteri. Selanjutnya dilakukan sekuensing fragmen 16s rRNA untuk mengidentifikasi spesies organisme. DNA kromosom bakteri diisolasi dan diamplifikasi menggunakan instrumen *Polymerase Chain Reaction* (PCR) dengan primer *forward* BactF1 dan *reverse* UniB1 untuk memperoleh fragmen g en 16s rRNA. Hasil amplifikasi selanjutnya disekuensing untuk mengetahui urutan basa nukleotida dan dibandingkan dengan urutan basa 16s rRNA bakteri yang telah terdaftar di Bank Gen untuk diketahui homologinya dengan bakteri lain. Hasil pewarnaan gram menunjukkan isolat bakteri akar bakau T1, T2, T3, T5, T7, T8, T9, T10 merupakan bakteri gram positif dan isolat T4, T6 merupakan bakteri gram negatif. Dari uji biokimia didapatkan genus isolat T1, T9 adalah *Micrococcus*, isolat T2 *Clostridium*, Isolat T3 dan T7 *Vibrio*, isolat T4 dan T6 *Pseudomonas*, isolat T5 dan T8 *Staphylococcus*, dan isolat T10 *Bacillus*. . Hasil amplifikasi DNA kromosom isolat bakteri akar bakau T3 dan T7 menunjukkan pita DNA dengan ukuran ± 1.500 bp, sedangkan isolat bakteri T1,T2,T4,T5,T6,T8,T9, dan T10 tidak berhasil dilakukan amplifikasi fragmen gen 16s rRNA. Hasil analisis urutan basa 16s rRNA menunjukkan isolat T3 memiliki indeks kemiripan sebesar 87,39% dengan *Vibrio diazotrophicus* dan isolat T7 memiliki indeks kemiripian sebesar 87,80% dengan *Vibrio vulnificus*.

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Kata-kata kunci: bakteri akar bakau; pewarnaan gram; fragmen gen 16s rRNA; PCR, sekuensing.

ABSTRACT

IDENTIFICATION OF BACTERIAL ISOLATE SPECIES ON MANGROVE ROOTS (Rhizophora **sp.***) FROM LABUHAN MARINGGAI EAST LAMPUNG*

Research for the resources of microorganisms found in plant tissues began to get attention. In mangrove plants there are several types of microorganisms, one of them is bacteria. Utilization of bacteria in various fields is increasing, for example in the production of secondary metabolites and enzymes. This study aims to identify bacterial species in mangrove roots phenotypically and genotypically. Screening method was carried out to obtain mangrove root bacterial isolates, then morphological observations of isolates and cells were carried out by gram staining. Biochemical tests are carried out to determine the genus of bacterial isolates. Furthermore, the 16s rRNA fragment sequencing is subsequently to identify the species of organisms. Bacterial chromosome DNA was isolated and amplified using a Polymerase Chain Reaction (PCR) instrument with forward BactF1 and reverse UniB1 primers to obtain 16s rRNA gene fragments. The results of the amplification were then sequenced to determine the sequence of the nucleotide bases and compared with the 16s base sequence of bacterial rRNAs that had been registered at the Gen Bank for homology with other bacteria. The results of gram staining showed that mangrove root isolates T1, T2, T3, T5, T7, T8, T9, T10 were gram-positive and isolates T4, T6 were gram-negative bacteria. From the biochemical tests, the genus of T1, T9 isolates were Micrococcus, T2 Clostridium, T3 and T7 isolates were Vibrio, T4 and T6 isolates Pseudomonas, T5 and T8 Staphylococcus, T10 Bacillus. The results of T3 and T7 chromosome DNA amplification mangrove root showed that there was a band with a size of ± 1,500 bp, while the bacterial isolates of T1, T2, T4, T5, T6, T8, T9, and T10 did not succeed in the amplification of 16s rRNA gene fragments. The results of 16s rRNA base sequence analysis showed T3 isolates had a similarity index of 87.39% with Vibrio diazotrophicus and T7 isolates had a similarity index of 87.80% with Vibrio vulnificus.

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Keywords: Mangrove root bacteria; gram staining; gene fragment 16s rRNA; PCR; sequencing.