RINGKASAN

Padi (*Oryza sativa* L.) merupakan salah satu tanaman pangan pokok masyarakat Indonesia. Kebutuhan beras dipasok dari padi sawah sekitar 95% dan padi gogo dari lahan kering hanya 5%. Produktivitas padi gogo masih rendah dibandingkan padi sawah, yaitu hanya 3,342 ton/hektar. Pemanfaatan lahan kering salah satunya lahan Ultisol yang luas di Indonesia, yaitu sekitar 45.794.000 Ha perlu dilakukan untuk meningkatkan jumlah produksi tanaman padi. Namun demikian, tanah Ultisol memiliki kendala, yang salah satunya adalah kandungan hara yang rendah. Salah satu upaya untuk mengatasi kendala tersebut adalah dengan pemupukan yang ramah lingkungan dan berkelanjutan. Pemupukan yang ramah lingkungan dan berkelanjutan salah satunya dengan penggunaan mikroorganisme PGPR (*Plant Growth Promoting Rhizobacteria*). Tujuan dari penelitian ini adalah: 1) menentukan identitas isolat bakteri TG-4 dan SR-2 hasil isolasi dari rizosfer tanaman singkong Desa Tanggeran dan Srowot, Banyumas melalui analisis bioinformatika sekuen 16S rRNA, 2) mengetahui hubungan kekerabatan dari isolat bakteri TG-4 dan SR-2 dengan bakteri lainnya yang telah terdata di *GenBank*, 3) untuk mengetahui kemampuan isolat bakteri TG-4 dan SR-2 dalam menghasilkan hormon IAA (*Indole Acetic Acid*), dan 4) menentukan isolat bakteri yang terbaik pengaruhnya terhadap pertumbuhan beberapa varietas padi lahan kering dalam skala laboratorium.

Penelitian ini dilakukan dengan beberapa tahapan, yaitu identifikasi molekuler dengan metode sekuensing gen 16S rRNA, pengujian IAA secara kualitatif, dan *bioassay*. Urutan nukleotida hasil sekuensing disejajarkan dengan sekuen dari *GenBank* menggunakan BLAST-N di *website* NCBI untuk mengetahui kemiripan antara isolat bakteri dengan strain referensi di *GenBank*. Hasil BLAST-N digunakan dalam membuat pohon filogenetik dengan menggunakan program MEGA X. Pengujian isolat bakteri penghasil IAA dilakukan dengan mengkultur isolat ke dalam media *Nutrient Broth* (NB) yang telah disuplementasi dengan L-triptofan 1000 ppm dan ditambahkan reagen salkowski. *Bioassay* dilakukan dengan perendaman benih padi gogo varietas INPAGO UNSOED 1 (V1), INPAGO UNSOED Parimas (V2), dan INPAGO 8 (V3) dengan isolat bakteri B0 (kontrol), B1 (isolat TG-4), B2 (isolat SR-2), dan B3(isolat TG-4 & SR-2) dan ditanam di dalam jar berisi tanah Ultisol steril.

Hasil dari analisis sekuensing gen 16S rRNA diperoleh bahwa urutan basa nukleotida isolat SR-2 berukuran 1398 bp dan TG-4 berukuran 1401 bp. Setelah dianalisis menggunakan BLAST-N, hasil menunjukkan bahwa isolat SR-2 memiliki homologi 100% dengan *Bacillus paramycoides* strain MCCC 1A04098 16S ribosomal RNA *partial sequence* dan isolat TG-4 memiliki homologi 98,77% dengan *Bacillus albus* strain MCCC 1A02146 16S ribosomal RNA *partial sequence*. Hasil analisis filogenetik pada program MEGA X menunjukkan bahwa isolat SR-2 dengan *Bacillus paramycoides* berkerabat dekat dengan jarak genetiknya, yaitu 0.000. Isolat TG-4 berkerabat dekat dengan *Bacillus albus* dengan jarak genetik 0.000. Hasil pengujian isolat bakteri TG-4 dan SR-2 dalam menghasilkan IAA menunjukkan bahwa kedua isolat mampu menghasilkan IAA.

Hasil analisis *bioassay* menggunakan uji F dengan taraf kesalahan 5% menunjukkan tidak adanya interaksi nyata antara perlakuan varietas dengan pemberian bakteri. Berdasarkan uji lanjut DMRT diperoleh bahwa perlakuan B3 (isolat TG-4 & SR-2) memberikan pengaruh lebih tinggi terhadap pertumbuhan padi gogo.

SUMMARY

Rice (Oryza sativa L.*) is one of the most important staple food commodities in Indonesia. The need for rice is supplied from 95% of wetland rice and 5% of upland rice. The productivity of upland rice is still low compared to wetland rice which is only 3,342 tons/ha. Utilization of dry land, mainly Ultisol soil type in Indonesia, which are around 45,794,000 hectares, needs to be undertaken to increase rice crop production. However, Ultisol soil has one main obstacle, which is low in nutrient content. One alternative effort could be done to overcome this obstacle is the application of environmentally friendly and sustainable fertilizers including the use of PGPR (Plant Growth Promoting Rhizobacteria) microorganisms. The purposes of this study were: 1) to identify TG-4 and SR-2 bacterial isolates previously isolated from the rhizosphere of cassava plants in Tanggeran and Srowot, Banyumas, through bioinformatics analysis of 16S rRNA sequences, 2) to determine the genetic kinship of TG-4 and SR-2 isolates with other bacteria that have been recorded in GenBank, 3) to determine the ability of TG-4 and SR-2 isolates in producing IAA (Indole Acetic Acid) hormones, and 4) to determine the best bacterial isolates for the growth of several upland rice varieties in Laboratory scale.*

This research was conducted in several stages, i.e. molecular identification with 16S rRNA gene sequencing methods, qualitative IAA testing, and bioassays. The sequence of nucleotides from sequencing work was aligned with the sequences from GenBank using BLAST-N on the NCBI website to determine the similarity between the bacterial isolates and reference strains available in GenBank. BLAST-N results were used in designing phylogenetic trees using the MEGA X program to determine the genetic kinship of the bacterial isolates with related strain collections in GenBank. Testing of IAA-producing bacterial isolates was carried out by culturing each isolate into NB (Nutrient Broth) media supplemented with 1000 ppm L-tryptophan and adding salkowski reagent. The bioassay was done by immersing upland rice seeds of INPAGO UNSOED 1 (V1), INPAGO UNSOED Parimas (V2), and INPAGO 8 (V3) with bacterial isolates which were B0 (control), B1 (TG-4 isolates), B2 (SR-2 isolates), and B3 (TG-4 & SR-2 isolates). The seeds were then planted in a jar containing sterile Ultisol soil.

The results of the 16S rRNA gene sequencing analysis showed that the nucleotide sequence of isolate SR-2 was 1398 bp in size and TG-4 was 1401 bp. After being analyzed using BLAST-N, the results showed that SR-2 isolate exhibited 100% homology with Bacillus paramycoides MCC 1A04098 16S ribosomal RNA partial sequence and TG-4 isolate revealed 98.77% homology with Bacillus albus strain MCCC 1A02146 16S ribosomal RNA partial sequences. The results of phylogenetic analysis using MEGA X program showed that the SR-2 isolate was closely related to Bacillus paramycoides with the genetic distance of 0,000. whereas TG-4 isolate was closely related to Bacillus albus with the genetic distance of 0,000. Both TG-4 and SR-2 bacterial isolates were confirmed to have the ability in producing IAA, which was indicated by the change in color from yellow to red in the samples following the addition of salkowski reagent. The

results of the bioassay analysis using the F test with an error level of 5% showed that there was no interaction between the treatment of varieties with the application of bacterial isolate. Based on further DMRT tests, B3 treatment gave a higher influence on the growth of upland rice.