ABSTRAK

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ANALISIS RESISTENSI ANTIBIOTIK PADA *Bacillus subtilis* G8 DAN *Bacillus velezensis* SS3.4
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Probiotik digunakan secara luas baik pada manusia maupun hewan karena memiliki manfaat kesehatan. *Bacillus* spp. memiliki keunggulan sebagai probiotik karena menghasilkan endospora sehingga lebih tahan terhadap pemrosesan industri dan kondisi ekstrem pada saluran pencernaan inang. Namun, sejumlah produk probiotik komersial diketahui memiliki gen resistensi antibiotik sehingga dikhawatirkan dapat menyebarkan resistensi antibiotik ke lingkungan. Informasi mengenai resistensi antibiotik pada *Bacillus* spp. masih terbatas, sehingga penelitian ini dilakukan untuk mempelajari kemampuan resistensi antibiotik pada *B. subtilis* G8 dan *B. velezensis* SS3.4. Uji kerentanan antibiotik secara fenotipik dilakukan dengan metode difusi disk. Kedua isolat resisten terhadap *oxacillin*, *lincomycin*, dan *tiamulin*, serta cukup resisten terhadap *streptomycin*. SS3.4 juga resisten terhadap *amoxicillin*, *ampicillin*, *methicillin*, *tetracycline*, dan *clindamycin*. Analisis bioinformatika menemukan gen yang berperan dalam resistensi antibiotik terkait, yaitu *ybxI* (*oxacillin*), *aadK* (*streptomycin*), dan *vmlR* (*lincomycin* dan *tiamulin*) pada G8, serta *bla1* (*amoxicillin* dan *ampicillin*), *BcII* (*methicillin* dan *oxacillin*), *aadK* (*streptomycin*), *tet*(45) (*tetracycline*), *clbA* (*clindamycin*, *lincomycin*, dan *tiamulin*), dan *vmlR* (*lincomycin* dan *tiamulin*) pada SS3.4. Seluruh gen dikodekan di kromosom. Ditemukan sembilan sekuens yang diduga berasal dari plasmid pada SS3.4. Tidak ada gen resistensi antibiotik yang ditemukan pada plasmid. Sejauh ini G8 dan SS3.4 diperkirakan aman sebagai kandidat probiotik, namun dibutuhkan penelitian lebih lanjut untuk memeriksa keberadaan elemen genetik yang dapat berpindah.

Kata Kunci : *Bacillus*, bioinformatika, probiotik, resistensi antibiotik

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ANALYSIS OF ANTIBIOTIC RESISTANCE IN *Bacillus subtilis* G8 AND *Bacillus velezensis* SS3.4
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Probiotics are widely used in both humans and animals due to their health benefits. As probiotics, *Bacillus* spp. are beneficial because their endospores provide better resistance against industrial processing and extreme conditions in the host digestive tract. However, some commercial probiotic products had been discovered to harbor antibiotic resistance genes that pose risks of spreading antibiotic resistance to the environment. Information regarding antibiotic resistance in *Bacillus* spp. is still limited, thus this research was conducted to study the antibiotic resistance pattern in *B. subtilis* G8 and *B. velezensis* SS3.4. Phenotypic antibiotic susceptibility test was performed using the disk diffusion method. Both isolates were resistant to oxacillin, lincomycin and tiamulin, while were moderately resistant to streptomycin. SS3.4 was also resistant to amoxicillin, ampicillin, methicillin, tetracycline and clindamycin. Bioinformatics analysis showed genes that are responsible in those antibiotic resistance, namely *ybxI* (oxacillin), *aadK* (streptomycin) and *vmlR* (lincomycin and tiamulin) in G8, as well as *bla1* (amoxicillin and ampicillin), *BcII* (methicillin and oxacillin), *aadK* (streptomycin), *tet*(45) (tetracycline), *clbA* (clindamycin, lincomycin and tiamulin) and *vmlR* (lincomycin and tiamulin) in SS3.4. All genes were encoded on chromosomes. Nine sequences presumably to be derived from plasmid were found in SS3.4. No antibiotic resistance gene was found on the plasmid. In conclusion, G8 and SS3.4 were considered safe as probiotic candidates, but further research will be needed to examine the presence of mobile genetic elements.

Keywords : *Bacillus*, bioinformatics, probiotics, antibiotic resistance

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