

Peningkatan aktivitas glukosidase pada penicillium sp id10 t065 dengan mutasi menggunakan sinar ultraviolet dan etil metil sulfonat serta analisis gen glukosidase 1 bgl1 pada mutan = Enhancement of glucosidase activity in penicillium sp id10 t065 through mutation using ultraviolet irradiation and ethyl methyl sulfonate and analysis of glucosidase 1 gene bgl1 in mutant

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Abstrak

[<b>ABSTRAK</b><br>

Isolat Penicillium sp. ID10-T065 dimutasi menggunakan sinar Ultraviolet (UV), Etil Metil Sulfonat (EMS), dan kombinasi UV-EMS. Hasil mutasi menunjukkan bahwa aktivitas enzim &#946;-glukosidase pada mutan lebih tinggi dibandingkan wild-type (1,78 U/ml), kecuali pada mutan UM23. Mutan UV13 mengalami peningkatan aktivitas &#946;-glukosidase tertinggi (1,88 U/ml pada selobiosa 0,1% dan 5,53 U/ml pada selobiosa 1%), sedangkan mutan UM23 menunjukkan aktivitas terendah (1,80 U/ml pada selobiosa 0,1% dan 1,75 U/ml pada selobiosa 1%). Aktivitas &#946;-glukosidase pada mutan EM31 sebesar 1,86 U/ml pada selobiosa 0,1% dan 4,26 U/ml pada selobiosa 1%. Hasil analisis sekuen gen &#946;-glukosidase 1 (bgl1) menunjukkan bahwa seluruh mutan mengalami mutasi substitusi ketika dibandingkan dengan sekuen wild-type. Mutan UV13 mengalami perubahan basa nukleotida paling banyak (7 basa) dibandingkan mutan EM31(5 basa) dan UM23 (2 basa). Perubahan basa juga mengakibatkan gen mengalami missense mutation sehingga terjadi kesalahan dalam penerjemahan kode asam amino, kecuali pada basa ke-2037 dari mutan UV13 dan basa ke-2034 serta 2037 mutan EM31. Perubahan basa pada posisi tersebut tidak mengubah translasi asam amino (silent mutation). Hasil analisis sekuen gen bgl1 dan aktivitas enzim menunjukkan bahwa sinar UV merupakan mutagen efektif untuk peningkatan aktivitas &#946;-glukosidase pada isolat Penicillium sp. ID10-T065. Hasil identifikasi secara molekuler dan analisis pohon filogenetik, isolat Penicillium sp. ID10-T065 memiliki kemiripan dan kekerabatan terdekat dengan spesies Penicillium oxalicum.

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<b>ABSTRACT</b><br>

The Penicillium sp. isolate ID10-T065 was mutated using Ultraviolet irradiation (UV), Ethyl Methyl Sulfonate (EMS), and combination of UV -EMS. The results showed that &#946;-glucosidase activity in the mutant was higher than that of wild-type (1,78 U/ml), except for the mutant UM23. The &#946;-glucosidase activity in mutant UV13 showed the highest activity (1,88 U/ml at cellobiose 0,1% and 5,53 U/ml at cellobiose 1%), while mutant UM23 showed the lowest activity (1,80

U/ml at cellobiose 0,1% and 1,75 U/ml at cellobiose 1%). The  $\alpha$ -glucosidase activity of EM31 was 1,86 U/ml at cellobiose 0,1% and 4,26 U/ml at cellobiose 1%. The results of the DNA sequence analysis of  $\alpha$ -glucosidase 1 (bgl1) showed that all mutants had substitution mutations when compared to the wild-type sequences. Mutant UV13 had the most base alteration (7 bases) compared to the mutant EM31 (5 bases) and UM23 (2 bases). The bases alteration was leading to missense mutation, except for the sequence of mutant UV13 at position 2037 and mutant EM31 at position 2034 and 2037. The base alteration of the sequence did not change the amino acid translation (silent mutation). The results of the DNA sequences analysis of bgl1 and enzyme activities showed that UV light is an effective mutagen to increase  $\alpha$ -glucosidase activity in *Penicillium* sp. ID10-T065. The molecular identification and phylogenetic analysis showed that *Penicillium* sp. ID10-T065 was closely related with *Penicillium oxalicum*., The *Penicillium* sp. isolate ID10-T065 was mutated using Ultraviolet irradiation (UV), Ethyl Methyl Sulfonate (EMS), and combination of UV -EMS. The results showed that  $\alpha$ -glucosidase activity in the mutant was higher than that of wild-type (1,78 U/ml), except for the mutant UM23. The  $\alpha$ -glucosidase activity in mutant UV13 showed the highest activity (1,88 U/ml at cellobiose 0,1% and 5,53 U/ml at cellobiose 1%), while mutant UM23 showed the lowest activity (1,80 U/ml at cellobiose 0,1% and 1,75 U/ml at cellobiose 1%). The  $\alpha$ -glucosidase activity of EM31 was 1,86 U/ml at cellobiose 0,1% and 4,26 U/ml at cellobiose 1%. The results of the DNA sequence analysis of  $\alpha$ -glucosidase 1 (bgl1) showed that all mutants had substitution mutations when compared to the wild-type sequences. Mutant UV13 had the most base alteration (7 bases) compared to the mutant EM31 (5 bases) and UM23 (2 bases). The bases alteration was leading to missense mutation, except for the sequence of mutant UV13 at position 2037 and mutant EM31 at position 2034 and 2037. The base alteration of the sequence did not change the amino acid translation (silent mutation). The results of the DNA sequences analysis of bgl1 and enzyme activities showed that UV light is an effective mutagen to increase  $\alpha$ -glucosidase activity in *Penicillium* sp. ID10-T065. The molecular identification and phylogenetic analysis showed that *Penicillium* sp. ID10-T065 was closely related with *Penicillium oxalicum*.]