Intisari

KOMETABOLISME DIBUTYL PHTHALATE OLEH *Micrococcus luteus* 11A

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Di-*n*-butyl phthalate (DBP) merupakan salah satu anggota dari kelompok *ester phthalate* yang banyak digunakan sebagai *plasticizer*. DBP terdaftar sebagai polutan prioritas oleh *Environmental Protection Agency* (EPA) karena bersifat toksik dan terbukti berbahaya bagi manusia maupun lingkungan. *Micrococcus* berpotensi dalam kometabolisme pemecahan senyawa xenobiotik di lingkungan, termasuk di-*n*-butyl phthalate (DBP) karena kemampuan metabolisme yang luas. Penelitian ini bertujuan untuk menguji kemampuan bakteri *Micrococcus luteus* 11A dalam mendegradasi DBP. Untuk menstimulasi kemampuan *M. luteus* 11A dalam mendegradasi dibutyl phthalate, *M. luteus* 11A ditumbuhkan pada medium minimal yang ditambah dengan *phthalic acid* (PA) sebagai sumber karbon. Kultur yang tumbuh pada PA (11A-MP) kemudian ditumbuhkan pada medium minimal dengan DBP:PA (1:1), DBP:PA (3:1) sebagai sumber karbon dan DBP:YE (medium DBP dengan 0.05% ekstrak khamir). Koloni yang tumbuh dinamakan 11A-MAP, 11A-MAPP, dan 11A-MAY dan digunakan untuk penelitian selanjutnya. Pada penelitian ini diketahui bahwa 11A-MAPP dan 11A-MAY mampu mendegradasi senyawa dibutyl phthalate dengan laju sebesar $(1.16 \pm 0.14)x10^{-1}$ ppm/jam dan $(1.52 \pm 0.21)x10^{-1}$ ppm/jam. Studi molekuler dengan identifikasi gen yang bertanggung jawab dalam degradasi DBP, menunjukkan bahwa *Micrococcus luteus* 11A dikaitkan dengan gen pengkode ring-hydroxylating dioxygenase yang tergolong dalam *Rieske super family*.

Kata kunci: Degradasi dibutyl phthalate, *phthalate acid*, *Micrococcus luteus*, ring-hydroxylating dioxygenase, *Rieske super family*.

Abstract

DIBUTYL PHTHALATE COMETABOLISM BY *Micrococcus luteus* 11A

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Di-*n*-butyl phthalate (DBP) is a member of the Phthalic Acid Ester (PAEs) group widely used as a plasticizer. It has been considered as peril pollutant by Environmental Protection Agency (EPA), becuase of its toxicity and the evidence of human pervasive and environmental expossure to them. Becuse of its vast array metabolic capabilities, microorganisms are potentially to be explioted to breakdown xenobiotic compounds present in the environment, including the di-n-btyl phthalate (DBP). The objective of this work was to examine the capability of adapted *Micrococcus luteus* 11A to degrade DBP. To stimulate the capability of *M. luteus* 11A to degrade dibutyl phthalate, *M. luteus* 11A was grown in minimal medium supplemented with *phthalic acid* (PA) as a sole of carbon source. The culture that grew on PA (11A-MP) was then transfered into minimal medium with DBP:PA (1:1), DBP:PA (3:1) as sole carbon source and DBP:YE (DBP medium with 0.05% yeast extrcat). The growing colony was then designated as 11A-MAP, 11A-MAPP, and 11A-MAY, respectively and used for futher experiments. In this study, it was known that 11A-MAPP and 11A-MAY capable to degrade dibutyl phthalate with rate of (1.16 ± 0.14) $x10^{-1}$ $ppm.h^{-1}$ and (1.52 ± 0.21) $x10^{-1}$ $ppm.h^{-1}$, repectively. The molecular study by identification of responsible DBP degrading gene, indicated that *Micrococcus luteus* 11A was attributed by the ring-hydroxylating dioxygenase encoding gene belonging to the *Rieske super family*.

Key word : Dibutyl phthalate degradation, *phthalate acid*, *Micrococcus luteus*, ring-hydroxylating dioxygenase, *Rieske super family*.