



DEMETILASI METILMERKURI OLEH BAKTERI YANG DIISOLASI DARI SEDIMEN SUNGAI SANGON

Suheryanto

ABSTRAK

Penelitian tentang "demetilasi metilmekuri oleh bakteri yang diisolasi dari sedimen Sungai Sangon" telah dilakukan. Penelitian ini bertujuan untuk mempelajari keberadaan spesies merkuri di sedimen Sungai Sangon dan transformasi metilmekuri oleh aktivitas bakteri *indigenous*. Tujuan spesifik penelitian adalah (1) menentukan tingkat pencemaran total merkuri dan metilmekuri di sedimen Sungai Sangon, (2) mendapatkan bakteri *indigenous* yang resisten terhadap metilmekuri dan berperan aktif dalam demetilasi metilmekuri, (3) mengkaji mekanisme demetilasi metilmekuri oleh isolat bakteri *indigenous*. Penelitian diawali dengan menganalisis total merkuri dan metilmekuri di sedimen Sungai Sangon menggunakan metode *CV-AAS (Cold Vapour Atomic Absorption Spectrometry)* dan *Gas Liquid Chromatography (GLC)*. Hasil penelitian menunjukkan bahwa konsentrasi total merkuri dan metilmekuri bervariasi. Konsentrasi total merkuri daerah hulu adalah 236,67 ng/g, tengah 154,25 ng/g, dan hilir 70,25 ng/g. Sementara itu, konsentrasi metilmekuri daerah hulu adalah 48,50 ng/g, tengah 96,25 ng/g, dan hilir 55,00 ng/g.

Isolasi bakteri dilakukan secara langsung dan tidak langsung melalui teknik kultur diperkaya. Penelitian ini menemukan 82 isolat bakteri pengguna metilmekuri. Setelah melalui seleksi, hanya 6 isolat bakteri yang resisten dan tumbuh menggunakan metilmekuri. Isolat tersebut adalah strain SDM 41, SDM 78, SDM 81, SDPM 8a, SDPM 8b, dan SDPM 24.

Uji kemampuan demetilasi metilmekuri dilakukan melalui percobaan pertumbuhan. Kemampuan demetilasi metilmekuri bakteri ditunjukkan dengan penurunan konsentrasi metilmekuri pada fasa eksponensial akhir pertumbuhan. Kemampuan demetilasi tertinggi ditunjukkan oleh strain SDM 81 dan SDPM 8a. Mekanisme demetilasi metilmekuri diawali dengan terlepasnya gugus metil ($-CH_3$) dan dihasilkan ion merkuri (Hg^{+2}). Hasil aktivitas protein spesifik pada Elektroforesis gel *PAGE* dan *NATIVE* menunjukkan pelepasan ion Hg^{+2} akibat aktivitas enzim organomerkuriliasa dengan berat molekul 19 – 27 kDa.

Keenam isolat bakteri berhasil diidentifikasi dengan alat BD Phoenix dan mempunyai karakter yang spesifik dalam demetilasi metilmekuri. Keenam isolat bakteri mempunyai kemiripan dengan *Brevundimonas diminuta* (strain SDM 41), *Bacillus cereus* (strain SDM 78), *Empedobacter brevis* (strain SDM 81), *Klebsiella pneumoniae* (strain SDPM 8a), *Pseudomonas aeruginosa* (strain SDPM 8b) dan *Spingomonas paucimobilis* (strain SDPM 24).

Kata kunci : demetilasi, metilmekuri, isolat bakteri, sedimen, Sungai Sangon



DEMETHYLATION METHYLMERCURY BY BACTERIA ISOLATED FROM SEDIMENT SANGON RIVER

Suheryanto

ABSTRACT

Research about “demethylation methylmercury by bacteria isolated from sediment Sangon River has been done. The aim of this research was to reveal the fate of the methylmercury in the sediment of Sangon River and the transformation of methylmercury by indigenous bacteria activities. Specifically, this research consisted of (1) determination of total mercury and methyl mercury contamination in River Sangon sediment, (2) isolation of indigenous bacteria, which had resistant to methylmercury and had active role in methylmercury demethylation, (3) learning mechanism of methylmercury demethylation by indigenous isolated bacteria. At the beginning, total mercury and methylmercury in Sangon River sediment were analyzed using Cold Vapour Atomic Absorption Spectrometry (CV-AAS) and Gas Liquid Chromatography (GLC) methods. Results indicated that contamination of total mercury and methylmercury varied. The concentrations of total mercury in upstream were 236.67 ng/g, middle 154.25 ng/g, downstream 70.25 ng/g, while the concentrations of methylmercury in upstream were 48.50 ng/g, middle 96.25 ng/g downstream 55.00 ng/g.

Based on the growing ability in methylmercury contamination, the isolation of bacteria was conducted using direct and indirect methods, by means of culture technique with the once harvest systems. This research found 82 isolated from Sangon River sediment which were able to tolerate the methylmercury. However, only 6 bacteria isolated exhibited resistance to methylmercury. These were strain SDM 41, SDM 78, SDM 81, SDPM 8a, SDPM 8b, and SDPM 24.

The demethylation ability of the strains towards methylmercury was investigated by growth test. The demethylation ability of bacteria was indicated by the decrease in methylmercury concentration at final exponential phase of growth. The highest decrease of methylmercury concentration was shown by SDM 81 and SDPM 8a strain. The demethylation mechanism was begun with realising $-CH_3$ group and producing mercury ion (Hg^+). The specific protein activity at gel of PAGE and NATIVE Electrophoresis showed the release of Hg^{+2} was caused by organomercurylase enzyme activity. It had 19 - 27 kDa molecular weight.

These six isolated bacteria had been successfully identified using BD Phoenix method and showed the specific character in methylmercury demethylation. These six isolates were similar to *Brevundimonas diminuta* (strain SDM 41), *Bacillus cereus* (strain SDM 78), *Empedobacter brevis* (strain SDM 81), *Klebsiella pneumoniae* (strain SDPM 8a), *Pseudomonas aeruginosa* (strain SDPM 8b) and *Spingomonas paucimobilis* (strain SDPM 24).

Keyword : *demethylation, methylmercury, bacteria isolated, sediment, Sangon River*