

Taxonomy and Diversity of the Class Ktedonobacteria from the Soil of Cisolok Geothermal Area = Taksonomi dan Keanekaragaman Kelas Ktedonobacteria dari Tanah di Kawasan Geotermal Cisolok

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Abstrak

Penelitian ini berfokus pada keanekaragaman taksonomi Class Ktedonobacteria, kemampuannya sebagai penghasil enzim, deskripsi takson baru, dan analisis whole genome. Tujuh belas isolat diperoleh dari sampel tanah di hutan dekat geysir, kawasan geotermal Cisolok, Jawa Barat. Sequence gen 16S rRNA dari semua isolat dibandingkan dengan spesies terdekat pada database EzBioCloud. Seluruh isolat memiliki nilai homologi yang rendah terhadap *Dictyobacter aurantiacus* S-27T (97,82-98,18%). Penapisan kemampuan enzimatik menunjukkan bahwa sebagian besar isolat (88,23%) menghasilkan amilase dan selulase. Komposisi bakteri dari enam sampel dianalisis dengan metode metabarcoding gen 16S rRNA pada daerah V1-V3 menggunakan Illumina Mi-Seq Next Generation Sequencing. Ktedonobacteria merupakan kelas yang paling mendominasi dalam Phylum Chloroflexota (17,74-89,49%) pada lima sampel; Namun, kelas tersebut tidak terdeteksi pada satu sampel (tanah di bawah batu besar). Empat puluh tujuh amplicon gen 16S rRNA dari taksa terdekat Ktedonobacteria berhasil diperoleh dari enam sampel yang mewakili garis keturunan baru pada tingkat takson yang tinggi. Strain S3.2.2.5 diisolasi dari tanah di dalam serasah batang bambu. Karakter fenotipik, genotipik, dan filogenetik menunjukkan bahwa strain tersebut mewakili spesies berbeda dari Genus *Dictyobacter*; sehingga diusulkan spesies baru *Dictyobacter halimunensis* sp. nov.This study focuses on the taxonomic diversity of the class Ktedonobacteria, their ability as enzyme producers, description of novel taxon, and whole genome analysis. Seventeen isolates were obtained from soil samples in the forest near geysir, Cisolok geothermal area, West Java. The 16S rRNA gene sequence of all isolates was compared with all related species in the EzBioCloud database. All isolates had low similarity values to *Dictyobacter aurantiacus* S-27T (97.82-98.18%). Primary screening of enzymatic abilities showed that most isolates (88.23%) were amylase- and cellulase-producing Ktedonobacteria. Bacterial composition analyses from six samples were performed based on the V1-V3 of 16S rRNA gene metabarcoding using Illumina Mi-Seq Next Generation Sequencing. Ktedonobacteria was the most dominating class within the phylum Chloroflexota (17.74-89.49%) in five samples; however, it was not detected in one sample (the soil under a big rock). Forty-seven 16S rRNA gene amplicons of Ktedonobacteria-related taxa were generated from six samples and represented the putative new lineages in high taxonomic rank. A strain S3.2.2.5 was isolated from soil inside a decayed bamboo stem. The phenotypic, genotypic, and phylogenetic data suggest this strain represents a distinct species of the *Dictyobacter* genera; hence, a new species, *Dictyobacter halimunensis* sp. nov. is proposed.