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GENOME ANNOUNCEMENT

Genome Sequence of *Citrobacter* sp. Strain A1, a Dye-Degrading Bacterium

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***Citrobacter* sp. strain A1, isolated from a sewage oxidation pond, is a facultative aerobe and mesophilic dye-degrading bacterium. This organism degrades azo dyes efficiently via azo reduction and desulfonation, followed by the successive biotransformation of dye intermediates under an aerobic environment. Here we report the draft genome sequence of *Citrobacter* sp. A1.**

Citrobacter sp. is a ubiquitous Gram-negative enteric coccobacillus from the family of *Enterobacteriaceae*. Despite the pathogenicity of *Citrobacter* sp., biotechnological significance of the bacterium was reported mainly in dye decolorization, heavy metal precipitation, and biohydrogen production (1, 6, 7, 10). A local strain of *Citrobacter* sp., designated strain A1, was isolated from a sewage oxidation pond in the vicinity of Universiti Teknologi Malaysia in 1997 (N. A. A. Rashid, A. R. H. M. Yusoff, R. Ahmad, S. Misran, G. F. Chan, and P. Murugaiya, presented at the Simposium Kimia Analisis, Kuala Terengganu, Terengganu, Malaysia, 22 July 1999). Based on a carbon source utilization test (Biolog) and 16S rRNA gene sequences, strain A1 was closely related to *Citrobacter freundii* (2).

Strain A1 shows great potential in the decolorization of a broad range of azo dyes under microaerophilic conditions at 45°C. Strain A1 was found to possess a flavin reductase which is involved in the reduction of azo bond in various dyes (2, 11). Furthermore, the potential of strain A1 to operate as a bacterial consortium with other bacteria was explored. The syntropic interaction between strain A1, *Enterococcus casseliflavus* C1, and *Enterobacter cloacae* L17 enhanced the biodegradation of azo dye (3). Under microaerophilic conditions, the decolorization of amaranth by the consortium led to the production of hydrazo intermediate, followed by symmetric reductive cleavage to form aromatic amines, namely, 1-aminonaphthalene-4-sulfonic acid and 1-aminonaphthalene-2-hydroxy-3,6-disulfonic acid. The successive biotransformation of these dye intermediates via reductive deamination and desulfonation may be carried out by strain A1 (3). Further aerobic incubation led to the further catabolism of the dye intermediates to benzoyl-coenzyme A (CoA), protocatechuate, salicylate, gentisate, catechol, and cinnamic acid, which can be channeled into the beta-ketoadipate pathway (3). In addition, strain A1 can produce slimy extracellular polymeric substance (EPS) during azo dye decolorization which may serve as a protection for the bacterial consortium against harmful chemicals in the environment. In order to gain further insight into the versatility of strain A1 for future biotechnological applications, the genome of this bacterium was sequenced.

The draft genome sequence of *Citrobacter* sp. A1 was determined using Genome Analyzer IIx (100-bp paired-end reads). The paired-end reads were assembled *de novo* into 74 contigs (121× coverage) using CLC Genomics Workbench 4.8 (CLC bio, Denmark). The N_{50} length is 227,071 bp, and the longest contig is 719,223 bp. The open reading frames (ORFs), tRNAs, and rRNAs were determined using Prodigal 2.60, RNAmmer 1.2, and tRNAscan-SE 1.3, respectively (5, 8, 9). Subsequent annotation was performed using Blast2GO (4). The draft genome sequence contains 5,096,012 bp with an average GC content of 51.81%. A total of 4,853 ORFs, 63 tRNAs, and 4 rRNAs were identified.

Citrobacter sp. A1 possesses genes for azo reduction, deamination, and desulfonation, as well as for the degradation of benzoate, catechol, gentisate, and protocatechuate. In addition, the draft genome of the bacterium reveals its potential in heavy metal reduction, nitrate reduction, sulfate assimilation, quorum sensing, and biofilm formation. This reflects on the catabolic versatility of *Citrobacter* sp. A1, which holds promise in the biodegradation of various xenobiotics and the bioremediation of heavy metals.

Nucleotide sequence accession numbers. This whole-genome shotgun project of *Citrobacter* sp. A1 has been deposited at DDBJ/EMBL/GenBank under the accession number AKTT00000000. The version described in this paper is the first version, AKTT01000000.

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