Full Paper

Aerobic degradation of cis-dichloroethene by the marine bacterium Marinobacter salsuginis strain 5N-3

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An aerobic bacterium, designated strain 5N-3 (NBRC 113055), that degrades cis-dichloroethene (cDCE) was isolated from a sea sediment in Japan. Strain 5N-3 was able to degrade a certain amount of cDCE in the presence of pyruvate without the action of inducers. In the presence of inducers, such as phenol and benzene, the strain completely removed cDCE. By the application of 16S ribosomal RNA (16S rRNA) gene sequencing and average nucleotide identity analyses, the strain 5N-3 was identified as Marinobacter salsuginis. On the other hand, identified species of Marinobacter are not known to degrade cDCE at all. A draft genome sequence analysis of the strain 5N-3 suggested that the dmp-homologous operon (operon for phenol degradation) may be contributing to the aerobic degradation of cDCE. This is the first report on an aerobic marine bacterium that has been found to degrade cDCE.

Key Words: aerobic degradation; cDCE; cis-dichloroethene; marine bacterium; Marinobacter

Introduction

Chloroethylenes (perchloroethene (PCE), trichloroethene (TCE), cis-1,2-dichloroethene (cDCE), trans-1,2-dichloroethene (tDCE), 1,1-dichloroethene and vinyl chloride (VCM)) are common environmental contaminants. PCE and TCE have been used as dry cleaning solvents and metal degreasing agents around the world. Lesser chlorinated ethenes, such as cDCE and VCM, are formed by the reductive dechlorination of PCE, TCE, and chlorinated ethanes. cDCE and VCM exhibit properties of low biodegradability and high toxicity. It is generally agreed that the presence of microorganisms capable of degrading chloroethenes is one of the important factors that can completely remove these compounds from their environments.

Many aerobic/anaerobic chloroethene-degrading bacteria have been isolated from terrestrial environments. It has been reported that, under aerobic conditions, many bacteria isolated from terrestrial environments, such as soils and rivers, are capable of degrading TCE, DCEs and VCM by co-metabolic oxidation (Mattes et al., 2010). On the other hand, a few species of Mycobacterium, Pseudomonas, Nocardioides, Ochrobactrum, and Ralstonia are known as VCM-assimilating bacteria (Mattes et al., 2010), and Polaromonas sp. strain JS666 is the only known cDCE-assimilating bacterium isolated from terrestrial environments (Coleman et al., 2002).

A few reports are available on chloroethene-degrading anaerobic bacteria found in marine environments. Reductive-dehalogenase-homologous (rdhA) genes were detected from the anaerobic marine subsurface sediments in the Pacific Ocean and their sequences were found to be similar to those of known anaerobic dehalorespiring bacteria, such as Dehalococcoides (Futagami et al., 2009). Additionally, Futagami reported that the enrichments of samples sourced from the subseafloor sediments of the Nankai Trough degraded TCE (Futagami et al., 2009, 2013). These reports suggested that anaerobic dehalorespiring bacteria inhabit marine, as well as terrestrial, environments. On the other hand, chloroethene-degrading aerobic bacteria have never been isolated from sea samples. In the current study, we report a cDCE-degrading aerobic bacterium belonging to the genus Marinobacter that was isolated from a sea sediment.

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Materials and Methods

Enrichment and isolation of chloroethene-degrading bacteria. Sea sediments were collected from the Kawasaki bay in Japan in February, 2011. To enrich and isolate aerobic bacteria degrading TCE, cDCE and VCM, 10 mg of the sediment was inoculated into 10 ml of modified SN medium (Waterbury et al., 1986) with a tenfold increase in vitamin concentration (SNv medium) supplemented with 20 mg/l of chloroethene in a 100-ml vial sealed with Teflon-coated butyl rubber stoppers and aluminum caps, and cultivated at 25°C under conditions of shaking at 150 rpm. Cultures that decreased the levels of chloroethenes were further subcultured in 1 ml of SNv medium supplemented with 5 mg/l of chloroethenes and various energy and carbon sources. As supplemental carbon sources, a sugar mix (consisting of 100 mg/l of glucose, arabinose, fructose and fucose) and 100–500 mg/l of yeast extract, glucose, arabinose, fructose, fucose or pyruvate were used. To isolate cDCE-degrading bacteria, the streak plate method was used to obtain single, isolated bacterial colonies on the plates of SNv agar containing 1,000 mg/l of pyruvate. To estimate their cDCE-degrading activities, each isolate was cultured separately in SNv medium supplemented with 5 mg/l of cDCE and 500 mg/l of pyruvate. Cell growth was measured by turbidity at 660 nm.

Bacterial strains, culture conditions, and chemicals. Strains 5N-1, 5N-3 and 5N-13 were isolated in the study and strain 5N-3 was submitted to the Biological Resource Center, NITE (illustrated as NBRC) under the number NBRC 113055. Marinobacter adhaerens DSM 23420\textsuperscript{T}, Marinobacter flavimaris DSM 16070, Marinobacter hydrocarbonoclasticus DSM 8798\textsuperscript{T}, Marinobacter koreensis NBRC 106396\textsuperscript{T}, Marinobacter sedimentalis DSM 15400, Arthrobacter pascens NBRC 12139, Ferrimonas kyonanesis NBRC 101286 and Oceanobacter kriegii NBRC 15467 were procured from the NBRC and DSMZ (Deutsche Sammlung von Mikroorganismen und Zellkulturen) culture collections. Modified SNv medium was used as the basal medium in this study. Cultures of the strains were maintained by routine subculturing on SNv medium supplemented with 1,000 mg/l of pyruvate, or on Marine Agar 2216 (MA; Becton Dickinson), at 25°C. 200 mg/l of cDCE and TCE in water, 700 mg/l of cDCE in DMSO and 1,000 mg/l of VCM in ethanol were used as stock solutions.

Measurement of TCE, cDCE and VCM by gas chromatography. Concentrations of TCE, cDCE and VCM were measured by applying the technique of headspace gas chromatography with flame ionization detection (GC-FID) using an Agilent 6890N GC (Agilent, Palo Alto, CA, USA) equipped with a GC sampler 80 (Agilent) and a DB-624 capillary column (30 m-by-0.32 mm, J&W Scientific, Folsom, CA, USA). The headspace gas (250 µl) was injected. The temperature of the oven was held for 5 min at 35°C, then increased to 165°C at a rate of 30°C/min and held constant at 165°C for 1 min (total runtime: 10.3 min). The injection and detection temperatures were 200°C and 250°C, respectively. Except for the enrichment and isola-
Aerobic degradation of cis-dichloroethene by the marine bacterium *Marinobacter salsuginis* strain 5N-3

**Degradation activity by resting cells.** Cells grown for 4 days on plates of SNv agar containing 1,000 mg/l of pyruvate were washed thrice with artificial seawater and then suspended in it. The optical density (OD600) was adjusted to 10. cDCE (10 mg/l) was added into 1 ml of the cell suspension in a vial and the concentration of cDCE in the gas phase of the vial was monitored with a GC-FID.

**Sequence analysis.** The 16S rRNA gene sequence of the isolate was amplified by conducting a polymerase chain reaction (PCR) using the universal primer pair (Fukunaga et al., 2006). The draft genome was sequenced using a combined strategy of shotgun sequencing with 454 GS-FLX Titanium (Roche Diagnostics, Branford, CT, USA) and paired-end sequencing with MiSeq (Illumina, Inc., San Diego, CA, USA). The data obtained from these analyses were assembled using Newbler version 2.6. The assembled contig was submitted to the RAST (Rapid Annotations using Subsystems Technology) server (https://rast.nmpdr.org/) for automatic annotation. Average nucleotide identity (ANI) values based on the genome sequences were calculated as a substitute for DNA-DNA hybridization (Goris et al., 2007) using JSpecies (Richter and Rossello-Mora, 2009). The GenBank/EMBL/DDBJ accession numbers for the draft genomes of strains 5N-3 and NBRC 109114 are BGZH01000001-BGZH01000010 and BGZI01000001-BGZI01000084, respectively.

**Results and Discussion**

**Enrichment, isolation, and phylogenetic analysis of the cDCE-degrading bacterium**

To obtain enrichment cultures with aerobic chloroethene-degrading activities, the sea sediment samples were inoculated in SNv media supplemented with TCE, cDCE and VCM along with various energy and carbon sources under aerobic conditions. Consequently, cDCE-degrading enrichment was obtained, but TCE- and VCM-decreases were not observed. Therefore, we focused on a cDCE-degrading enrichment sample designated 5N that was cultivated in SNv medium containing 5 mg/l of cDCE and 500 mg/l of pyruvate. The 5N enrichment was monitored constantly and a decrease in the concentration of cDCE was observed within 2 weeks (data not shown). Pure strains designated 5N-1, 5N-3, 5N-6 and 5N-13 were isolated from the 5N enrichment sample and similarities in their 16S rRNA gene sequences were found to match with *Azoarcus buckelii* (94.2%), *Marinobacter salsuginis* (99.9%), *Marinobacter hydrocarbonoclasticus* (100%) and *Thalassospira profundimaris* (99.3%), respectively. Among the 4 strains, only strain 5N-3 could degrade cDCE. Strain 5N-3 grew on 200–1,000 mg/l of pyruvate, 1,000 mg/l of succinate, 200 mg/l of phenol, 200 mg/l of benzene, 1,000 mg/l of pristane and 200 mg/l of benzene in 4 ml of SN medium and also in 4 ml of Marine Broth. Each value is the average ± standard deviation (error bars) based on three independent experiments.
cDCE-degradation activity of strain 5N-3 in liquid culture

The time courses of cDCE degradation in the control and cultures of the isolates along with some Marinobacter species and other marine bacteria are shown in Fig. 1. All strains of the bacteria grew in SNv medium containing 500 mg/l of pyruvate and 5 mg/l of cDCE, but only strain 5N-3 clearly demonstrated approximately 60% of cDCE degradation. The demonstration of the phenotypic characteristic of cDCE degradation in Marinobacter is strain-specific and not species-specific or genus-specific. The rate of cDCE degradation by strain 5N-3 under liquid culture conditions in the presence of inducers and carbon sources is shown in Fig. 2. Strain 5N-3 could decrease cDCE by 50% in the medium containing 1,000 mg/l of pyruvate as the sole source of carbon and energy. On the other hand, strain 5N-3 was found to grow on 1,000 mg/l of succinate and 200 mg/l of pristane, as well as in Marine Broth, but these cultures demonstrated a low degradation of cDCE. Strain 5N-3 grew well on Marine Broth rather than on 1,000 mg/l of pyruvate, but the cDCE degradation rate was more rapid on pyruvate than on Marine Broth. cDCE degradation activity may depend on the kind of substrate but not on the cell concentration. When 200 mg/l of phenol was used as a carbon and energy source, the strain removed cDCE completely. Additionally, when 200 mg/l of benzene was added as an inducer, strain 5N-3 completely removed cDCE from the culture supplemented with 1,000 mg/l of pyruvate. The highest capacity for degradation of cDCE by strain 5N-3 was observed under the conditions in which inducers such as benzene and phenol were present. Meanwhile, the strain could clearly degrade cDCE even in the absence of inducers. It is not clear why the culture system with pyruvate demonstrated a better cDCE-degradation activity than those with succinate, pristane, or Marine Broth.

Activity of cDCE-degradation by resting cells of strain 5N-3

It has been reported that aerobic bacteria degrading...
cDCE in terrestrial environments use oxidizing enzymes such as monooxygenase or dioxygenase to oxidize chloroethenes (Mattes et al., 2010). To confirm the activity of oxidizing enzymes in strain 5N-3, the ability of resting cells to degrade cDCE was tested (Fig. 3). The heat-killed cells and resting cells under anaerobic conditions did not exhibit cDCE degradation, while the resting cells under aerobic conditions degraded more than 60% of cDCE within 29 hours. Because terrestrial cDCE degradation has been reported to require inducers (Ensign et al., 1992), the ability of the resting cells to degrade cDCE suggested that the strain 5N-3 might be degrading cDCE using oxidizing enzymes similar to the other cDCE-degrading aerobic bacteria and constantly expresses the required genes, unlike the other aerobic bacteria that are known to degrade cDCE.

**Genomic analysis**

The draft genome sequencing of strain 5N-3 and *M. salsuginis* NBRC 109114T was performed. The genomes of both the strains, 5N-3 and NBRC 109114T, consisted of chromosomes that were 4.7 Mbp in size. Their ANIb value was found to be 99.9% and this result led to the conclusion that they are the same species. The two strains commonly possessed more than 96% of the predicted protein-coding genes, such that strain 5N-3 and NBRC 109114T have 63 and 79 unique predicted protein-coding genes, respectively. Both the strains also have the operon homologous to dmp operon (operon for phenol degradation) that codes for phenol hydroxylase, catechol 2,3-dioxygenase, ferredoxin-like protein, putative 5-carboxymethyl-2-hydroxymuconic semialdehyde dehydrogenase oxidoreductase protein, 2-hydroxymuconic-semialdehyde dehydrogenase, 4-hydroxy-2-oxovalerate aldolase, 4-oxalocrotonate decarboxylase, and 4-oxalocrotonate tautomerase (Table 1). The strain 5N-3 demonstrated a low capacity for cDCE degradation when grown on pyruvate without an inducing substrate and a high degradation capacity when grown on media containing phenol. It is suggested that the strain 5N-3 uses phenol hydroxylase for cDCE degradation like many terrestrial bacteria that degrade cDCE using aromatic hydrocarbon monoxygenase. On the other hand, it is not clear why *M. salsuginis* NBRC 109114T could not degrade cDCE in the presence of pyruvate. There are reports that the expression of the dmp operon is regulated by the activator and sensor protein DmpR (Shingler et al., 1993). DmpR consists of four domains as follows: domain A is a sensor for inducing substrates like phenol, domain B is a linker between domain A and C, domain C is a transcriptional activator, and domain D is the DNA binding region. The amino acid sequence of DmpR in both the strains showed 100% similarity in domain B, domain C and domain D and a difference of 4 residues was observed in domain A. The difference in the amino acid residues in domain A of DmpR may be responsible for the expression of the dmp-homologous operon and cDCE degradation. Or the difference in the amino acid sequence of other proteins in the dmp operon in both the strains (Table 1) may be concerned with cDCE degradation activity. Alternatively, the hypothetical proteins predicted to be present only in the genome of the strain 5N-3 may be involved in the degradation of cDCE. Further analyses are necessary to elucidate the mechanism of cDCE degradation in strain 5N-3.

**Conclusion**

First, a marine cDCE-degrading strain 5N-3 was isolated from a sea sediment and identified to be *M. salsuginis*. The strain could degrade cDCE with pyruvate, as well as with phenol and benzene as inducers. While many terrestrial bacteria need inducing substrates, such as phenol or toluene, to degrade chlorinated ethylenes (Mattes et al., 2010), this strain could degrade cDCE without the addition of such inducing substrates. Additionally, the genome analyses inferred that strain 5N-3 uses phenol hydroxylase for the degradation of cDCE, but we could not decipher its unique mechanism in the genome. These findings suggest that the natural decomposition of cDCE may occur in non-polluted marine environments. Further research on bacterial degradation of chlorinated ethylenes in the marine environment may provide new evidence of microbial functions in the marine ecosystem.

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