Dechloromonas agitata gen. nov., sp. nov. and Dechlorosoma suillum gen. nov., sp. nov., two novel environmentally dominant (per)chlorate-reducing bacteria and their phylogenetic position

Laurie A. Achenbach, Urania Michaelidou, Royce A. Bruce, Johanna Fryman and John D. Coates

Author for correspondence: Laurie A. Achenbach. Tel: +1 618 453 7984. Fax: +1 618 453 8036. e-mail: laurie ! micro.siu.edu

Department of Microbiology and Center for Systematic Biology, Southern Illinois University, Carbondale, IL 62901, USA

Previous studies on the ubiquity and diversity of microbial (per)chlorate reduction resulted in the isolation of 20 new strains of dissimilatory (per)chlorate-reducing bacteria. Phylogenetic analysis revealed that all of the isolates were members of the Proteobacteria with representatives in the α-, β- and γ-subclasses. The majority of the new isolates were located in the β-subclass and were closely related to each other and to the phototrophic Rhodocyclus species. Here an in-depth analysis of these organisms which form two distinct monophyletic groups within the Rhodocyclus assemblage is presented. Two new genera, Dechloromonas and Dechlorosoma, are proposed for these β-subclass lineages which represent the predominant (per)chlorate-reducing bacteria in the environment. The type species and strains for these new genera are Dechloromonas agitata strain CKB' and Dechlorosoma suillum strain PS', respectively.

Keywords: Dechloromonas, Dechlorosoma, 16S rDNA, beta-Proteobacteria

INTRODUCTION

Recent concerns over the environmental contamination of ground waters and drinking waters with perchlorate has focused a significant amount of attention on the microbial metabolism of oxyanions of chlorine (Renner, 1998, 1999; Urbansky, 1998). Perchlorate contamination poses a significant health threat as preliminary toxicological studies have demonstrated that it has a direct effect on iodine uptake by the thyroid gland. In addition, at higher concentrations [6 mg (kg body wt) [d]−1] perchlorate can result in fatal bone marrow disease. Prior to 1997, perchlorate was an unregulated compound and its presence in the environment has been primarily associated with the manufacture, handling and dismantling of munitions, in which it is used as a major component of rocket propellants and explosives (Urbansky, 1998). In 1997, with the development of highly sensitive analytical techniques (Wirt et al., 1998), perchlorate contamination of drinking and recreational waters was identified throughout the US and particularly in the southwestern states of Utah, Nevada, Colorado and California. The California Environmental Protection Agency initiated a recommended maximum concentration limit (MCL) of 18 µg l−1 which, if exceeded, would require stoppage of water usage and remediation (Renner, 1998). Although the US Environmental Protection Agency recently increased this MCL to 32 µg l−1 (Renner, 1999), a value of 18 µg l−1 has been adhered to by several states throughout the US. In 1998, perchlorate was added to the US Environmental Protection Agency’s drinking water candidate contaminant list and a regulatory decision regarding an MCL value for this compound is to be made by August 2001 following an extensive toxicological study and identification of potential remediation technologies. In the meantime, due to
down-sizing and regular maintenance of the munitions inventory, the US military is expected to produce another 165 million pounds (approx. 75000 tonnes) of perchlorate requiring treatment in the next 5 years (Wallace et al., 1998).

Remediation efforts of perchlorate contamination have focused primarily on microbial processes because of the unique chemical stability and high solubility of perchlorate (Urbansky, 1998). Other physical/chemical technologies such as adsorption by activated charcoal, reverse osmosis or ion exchange have failed because of rapid saturation of active sites or the high cost, especially that associated with the processing of surface or groundwater contamination where excessively large volumes may require treatment. Although it has been recognized for more than 70 years that oxyanions of chlorine are suitable electron acceptors for microbial metabolism, this reductive process was originally identified with chlorate (Aslander, 1928) and was associated with nitrate-respiring organisms which simply used chlorate as a coincidental substrate for nitrate reductase (de Groot & Stouthamer, 1969; Hackenthal, 1965; Hackenthal et al., 1964). Growth was not associated with this metabolism and chlorite was formed as a toxic end product of this metabolism (de Groot & Stouthamer, 1969; Hackenthal, 1965; Hackenthal et al., 1964; Roldan et al., 1994). Similar studies have not been done with perchlorate.

In the last two decades, five organisms have been identified which can couple growth to the reduction of chlorine oxyanions (Malmqvist et al., 1994; Rikken et al., 1996; Romanenko et al., 1976; Stepanyuk et al., 1992; Wallace et al., 1996). Only two of these organisms have been characterized both phenotypically and genotypically (Malmqvist et al., 1994; Wallace et al., 1996). Although not demonstrated in all cases, it has been assumed that these organisms can couple growth to the reduction of both chlorate and perchlorate. However, the recent isolation of an organism that can grow by the reduction of chlorate but not perchlorate has indicated that this assumption may be incorrect (J. D. Coates, unpublished data). Recent studies in our laboratory have indicated that the ubiquity of microbial (per)chlorate respiration is much more extensive than was previously assumed (Coates et al., 1999b). Our studies resulted in the isolation and identification of more than 20 new dissimilatory (per)chlorate-reducing isolates (ClRB) from a broad diversity of environments, including both pristine and contaminated soils and sediments. The ClRB represented a broad phylogeny with members in the α-, β and γ-subclasses of the Proteobacteria; however, the majority were placed in the β-subclass. These organisms were closely related to each other and to the phototrophic Rhodocyclus species. Here we report on the identification of two novel groups of ClRB within the β-subclass of the Proteobacteria. The fact that members of these groups have been identified and isolated in nearly all environments screened in our laboratory suggest that members of these groups may represent the predominant (per)chlorate-reducing bacteria in the environment. In-depth descriptions of the phenotypic characteristics of these organisms have been published elsewhere (Bruce, 1999; Coates et al., 1999b; Michaelidou et al., 2000).

**METHODS**

**Sources of soils and sediments.** The organisms were isolated from samples collected from a broad diversity of environments as described previously (Coates et al., 1999b), including pristine and contaminated soils, sediments and waste sludges. The isolates were obtained using a standard shake-tube technique (Bruce, 1999) with acetate as the electron donor and chlorate as the electron acceptor. All cultures were maintained in both active liquid stocks as well as anaerobic frozen stocks in 10% glycerol at −70 °C.

**Medium and culturing conditions.** Standard anaerobic culturing techniques were used throughout (Hungate, 1969). The medium was boiled under N₂/CO₂ (80:20) to remove dissolved O₂ and then dispensed into anaerobic pressure tubes or serum bottles under N₂/CO₂ capped with thick butyl rubber stoppers and sterilized by autoclaving. The basal medium was bicarbonate-buffered freshwater medium that had been used previously for culturing strain CKB (Bruce, 1999). Sodium salts of acetate and chlorate (10 mM each) were used as the electron donor and acceptor, respectively, which were added from sterile anoxic stocks.

**16S rDNA sequencing and analysis.** PCR and sequencing of the 16S rRNA genes was performed as described previously (Coates et al., 1999b). Sequence entry and manipulation were performed with the MacVector 6.5 sequence analysis software program for the Macintosh (Oxford Molecular Group). Sequences of selected 16S rRNAs were downloaded from the Ribosomal Database Project (Maidak et al., 2000) and GenBank (Benson et al., 1998) into the computer program SeqApp (Gilbert, 1993). 16S rDNA sequences of ClRB were manually added to the alignment using secondary structure information for proper alignment (alignment available on request). Complete 16S rDNA sequences were generated for 14 ClRB strains. For the remaining six ClRB strains, partial 16S rDNA sequences were determined. Only those regions sequenced in all of the organisms (815 nt) were used in the subsequent phylogenetic analyses (included Escherichia coli positions 434–767, 807–1182 and 1266–1362). Distance, parsimony and maximum-likelihood analysis of the aligned sequences was performed on a Power Macintosh G3 using PAUP* 4.0 (Swofford, 1999). Bootstrap analysis was conducted on 100 replications using a heuristic search strategy to assess the confidence level of various clades. GenBank accession numbers for sequences represented in Fig. 1 are as follows: Treponema pallidum (M88726), Magnetospirillum gryphiswaldense (Y10109), isolate WD (AF170352), Azospirillum brasiliense (Z29617), isolate TTI (AF170353), Comamonas testosteronei (M11224), Ideonella dechloratans (X72724), isolate FL2 (AF288771), isolate FL8 (AF288772), isolate FL9 (AF288773), strain CKB* (AF047462), isolate CL (AF170354), isolate NM (AF170355), isolate CL24 + (AF288774), isolate CL24 (AF288775), Ferrribacterium linneticum (Y17060), isolate MissR (AF170357), isolate CCO (AF288776), isolate SIUL (AF170356), Rhodocyclus tenuis (D16209), Rhodocyclus purpureus (M34132), Azoarcus evansi (X77679), ‘Azoarcus denitrificans’ (L33689), Thauera...
selenatis (X68491), Azorarcus indigens (L15531), Dugannella zoogloeoides (previously Zoogloea ramigera; X74913), strain PS\(^T\) (AF170348), isolate SDGM (AF170349), isolate Isol (AF170350), isolate Iso2 (AF170351), Gill symbiont of Thysanorhabdus (L01575), isolate N8S (AF170359), Pseudomonas stutzeri (U26415), isolate PK (AF170358), isolate CFPBD (AF288777), Wolinella succinogenes ATCC 29543 (M26636) and Helicobacter pylori (M88157).

**G + C analysis.** Analysis of the G + C content of the chromosomal DNA was performed by the Identification Service of the Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ) using the HPLC method and conditions as described by Mesbah et al. (1989) and Tamaoka & Komagata (1984). Calibration of the method was performed with non-methylated \( \lambda \) DNA (Sigma) (Mesbah et al., 1989).

### RESULTS AND DISCUSSION

**Phylogenetic analysis**

Although ClRB representatives can be found throughout the Proteobacteria (Coates et al., 1999b; Michaelidou et al., 2000; Wallace et al., 1996), the current work demonstrates that the majority (15 strains) of the ClRB isolated to date for which 16S rDNA sequence data are available (22 strains) are closely related to each other and are classified within the *Rhodocyclus* assemblage in the \( \beta \)-subclass of the Proteobacteria (Fig. 1). Analyses of the 16S rDNA sequences indicated that these (per)chlorate-reducing isolates form two distinct monophyletic groups within the \( \beta \)-subclass (Fig. 1). One of these groups, represented by our previously published ClRB strain CKB\(^T\) (Bruce, 1999), contains 11 strains and is relatively diverse with 16S rDNA distances among this group ranging from 0 to 3.9%. The other group is represented by strain PS\(^T\) (Coates et al., 1999b; Michaelidou et al., 2000) and contains four isolates that are more phylogenetically compact than the members of the CKB group with distances only ranging from 0 to 0–12%. Representative ClRB from the CKB group are most closely related to the Fe(III)-reducer *Ferrribacterium limnicum* (Cummings et al., 1999), while PS group members are most closely related to the phototroph *Rhodocyclus tenuis*. Based on the unique phenotypic (Bruce, 1999; Coates et al., 1999b; Michaelidou et al., 2000) and genotypic characteristics of the organisms in this assemblage of ClRB, we propose that the two groups of ClRB within the \( \beta \)-subclass of the Proteobacteria represent two new genera within the *Rhodocyclus* assemblage. The names *Dechloromonas* gen. nov. and *Dechlorosoma* gen. nov. are proposed for the CKB and PS group members, respectively. *Dechloromonas* sp. strain CKB\(^T\) (Bruce, 1999) is the type strain for the *Dechloromonas* genus and *Dechlorosoma suillum* sp. nov. strain PS\(^T\) (Michaelidou et al., 2000) is the type strain for the *Dechlorosoma* genus. Unlike other members of the *Rhodocyclus* assemblage, these organisms are capable of dissimilatory (per)chlorate reduction and chlorite dismutation (Bruce, 1999; Coates et al., 1999b; Michaelidou et al., 2000). In addition, 16S rDNA sequences of the species of the two groups within this assemblage of ClRB shared no more than 94.1% similarity. For comparison, *Rhodococcus tenuis* shares 94.7% 16S rDNA sequence similarity to the most similar *Dechloromonas* species (strain CKB\(^T\)) and 94.0% similarity to the most similar *Dechlorosoma* species (strain Iso2). The G + C content for these two groups of ClRB is also distinct with *Dechloromonas agitata* CKB\(^T\) at 63.5±0.3 mol % and *Dechlorosoma suillum* PS\(^T\) at 65.8±0.2 mol % (mean±SD, \( n = 3 \)). *Rhodocyclus tenuis* has a G + C content of 64.8 mol % (Trüper & Imhoff, 1992).

All of the (per)chlorate-reducing *Dechloromonas* and *Dechlorosoma* species are heterotrophic facultative anaerobic respirers (Bruce, 1999; Coates et al., 1999b; Michaelidou et al., 2000). Other common features include the ability to couple growth to the complete oxidation of acetate with chloride or perchlorate as sole electron acceptor and the ability to dismute chlorite into chloride and \( \mathrm{O}_2 \). *Rhodocyclus tenuis* is a strict anaerobic respirer incapable of dismutating chlorite into chloride and \( \mathrm{O}_2 \). The ClRB strain GR-1 is also a member of the \( \beta \)-subclass of the Proteobacteria (Rikken et al., 1996), while PS group members are most closely related to the phototroph *Rhodocyclus tenuis*. Based on the unique phenotypic (Bruce, 1999; Coates et al., 1999b) and that washed whole-cell suspensions of this species were incapable of reducing (per)chlorate (Bruce, 1999) and that washed whole-cell suspensions of this species were incapable of dismutating chlorite into chloride and \( \mathrm{O}_2 \). None of the other close relatives to *Dechloromonas* and *Dechlorosoma* that were tested could grow and reduce (per)chlorate or dismute chloride in white whole-cell suspensions (data not shown; Coates et al., 1999b; Michaelidou et al., 2000).

Residing within the *Dechloromonas* group is a previously characterized Fe(III)-reducer, *Ferrribacterium limnicum* (Cummings et al., 1999), that shares 97.3% 16S rDNA sequence similarity to its closest relative, the ClRB strain MissR. Interestingly, *Ferrribacterium limnicum* is a strict anaerobic respirer unable to reduce (per)chlorate (data not shown). None of the ClRB isolated in this study were able to reduce ferric iron (Coates et al., 1999b). In addition, similarly to *Rhodocyclus tenuis* and in contrast to all tested
(per)chlorate-reducing bacteria, washed whole-cell suspensions of *Ferribacterium limneticum* did not dismutate chlorite into chloride and $\text{O}_2$. This is in contrast to all known CIRB, including the isolates described in this study, which are facultative anaerobes capable of coupling growth to the dissimilation of either perchlorate or chlorate (Coates *et al.*, 1999b). The distinct physiological differences between *Ferribacterium limneticum* and the closely related CIRB imply that *Ferribacterium limneticum* is in fact a member of a separate genus.

Although the CIRB *Wolinella succinogenes* strain HAP-1 was originally thought to be a strict anaerobe, a recent study indicated that it is, in fact, a micro-aerophile (Wallace *et al.*, 1998). This is similar to one of our isolates, ‘*Dechlorosporillum anomolous*’ strain WD, a member of the $\alpha$-subclass of the Proteobacteria...
closely related to a magnetotactic Magnetospirillum sp. (Michaelidou et al., 2000) which also grows preferentially under microaerophilic conditions.

Significance

To date, very little is known about microorganisms capable of dissipatory (per)chlorate reduction and until recently only three organisms had been described both phenotypically and genotypically which are capable of this metabolism (Bruce, 1999; Malmqvist et al., 1994; Wallace et al., 1996). Here and in previous work we describe several new (per)chlorate-reducing organisms that were isolated from a broad diversity of environments (Coates et al., 1999b; Michaelidou et al., 2000). Sequence analyses of the 16S rDNAs from the isolates indicated that all were members of three (α, β and γ) of the five subclasses of the Proteobacteria (Coates et al., 1999b). A previously described (per)chlorate-reducing bacterium, Wolinella succinogena strain HAP-1 (Wallace et al., 1996), was shown to be a member of the ε-subclass. These results demonstrate that the phylogenetic diversity of dissipatory (per)chlorate-reducing bacteria is far greater than was previously considered. Most proteobacterial subclasses contain only a few ClRB; however, the majority of the ClRB isolated to date reside in the β-subclass. The fact that the majority of the known (per)chlorate-reducing isolates are either Dechloromonas or Dechlorosoma species suggests that these groups are likely to represent the predominant (per)chlorate-reducing bacteria in the environment. This is further supported by the fact that, in almost every environment screened in our studies, members of these two groups were either isolated or their presence was identified by molecular analyses (Bruce, 1999; Coates et al., 1999a, b; Michaelidou et al., 2000).

In addition to the treatment of chlorate and perchlorate contamination, previous studies in our lab have demonstrated that the unique metabolic capabilities of (per)chlorate-reducing bacteria can alternatively be used for the treatment of other contaminants, including heavy metals, radionuclides (J. G. Lack, S. Chaudhuri & J. D. Coates, unpublished data) and hydrocarbons (Coates et al., 1998, 1999a). The only known natural source of (per)chlorate is from mineral deposits in Chile (Ericksen, 1983; Schilt, 1979) and the presence of (per)chlorate in the environment is the result of anthropogenic contamination over the last 100 years. It is thus surprising that such a phylogenetically diverse set of organisms should have evolved the ability to grow by dissipatory (per)chlorate reduction in such a short time frame and suggests that the metabolic capability to grow by the dissimilation of (per)chlorate is the result of a horizontal gene transfer event in the environment. This hypothesis is further supported by the fact that some ClRB are almost identical phenotypically and genotypically to organisms not capable of (per)chlorate reduction. For example, the γ-Proteobacteria strain PK is 99.8% similar to Pseudomonas stutzeri based on 16S rDNA sequence analysis and phenotypically shares many characteristics of a pseudomonad; yet, strain PK is able to grow by dissipatory (per)chlorate reduction while Pseudomonas stutzeri cannot (Coates et al., 1999b). The specific genetic mechanisms that confer (per)chlorate reduction and the true role of ClRB in the environment have yet to be identified.

Description of Dechloromonas gen. nov.

Dechloromonas [De.chlo.ro.mo’nas. L. pref. de from; Gr. adj. chloros green (chlorine); Gr. fem. n. monas unit, monad; N.L. fem. n. Dechloromonas a dechlorinating monad].

Rod-shaped, Gram-negative cells, 0.5×2 μm, non-spore-forming, non-fermenting, facultative anaerobe. Cells are motile by a single polar flagellum and occur singly or in chains of two to three cells. A strictly respiring, complete oxidizer that oxidizes acetate with O2, ClO3−, ClO4− or NO3− as alternative electron acceptors. Perchlorate and chloride are completely reduced to chloride. Cells contain c-type cytochrome(s). Type species is Dechloromonas agitata.

Description of Dechloromonas agitata sp. nov.

Dechloromonas agitata (a.gi.ta’ta. L. fem. part. adj. agitata agitated, highly active).

Cells can grow with O2, ClO3− or ClO4− as alternative electron acceptors. Organics used as alternative electron donors include propionate, butyrate, lactate, succinate, yeast extract, fumarate and malate. The reduced form of the humic substances analogue 2,6-anthrahydroquinone disulfonate, Fe(II) or sulfide can also serve as alternative electron donors coupled to the reduction of chlorate. Fe(II) is oxidized to insoluble amorphous Fe(III) oxide while sulfide is oxidized to elemental sulfur. Cells contain c-type cytochrome(s). Optimum growth is observed at 35 °C, pH 7.5 and 1% NaCl with acetate (10 mM) as electron donor and chlorate (10 mM) as electron acceptor. G+C content is 63.5 mol %, Type strain, CKB7, has been deposited in the American Type Culture Collection under ATCC 700666T and in the Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH under DSM 13637T.

Description of Dechlorosoma gen. nov.

Dechlorosoma [De.chlo.ro.so’ma. L. pref. de from; Gr. adj. chloros green (chlorine); Gr. neut. n. soma body; N.L. neut. n. Dechlorosoma dechlorinating body].
Cells are Gram-negative, facultative anaerobic, non-spore-forming, non-fermentative rods, 1.0 × 0.3 μm. Cells are motile by a single polar flagellum and occur singly or in chains. Simple organic fatty acids are used as electron donors with O₂, ClO₄⁻, ClO₃⁻ or NO₃⁻ as alternative electron acceptors. Organic electron donors are completely oxidized and perchlorate or chlorate are completely reduced to chloride. Cells contain c-type cytochrome(s). Type species is Dechlorosoma suillum.

**Description of Dechlorosoma suillum sp. nov.**

*Dechloromonas suillum* [su.ill’um; L. neut. adj. suillum pertaining to swine (Michaelidou *et al.*, 2000)].

Cells use acetate, propionate, butyrate, Casamino acids, lactate and ethanol as alternative electron donors with O₂, (per)chlorate or nitrate as electron acceptor. Nitrate is reduced to N₂ gas. Optimum growth is observed at 37 °C and pH 6.5 in freshwater medium (0% NaCl). G+C content is 65.8 mol%. Type strain, PS², has been deposited in the American Type Culture Collection under ATCC BAA-33³ and in the Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH under DSM 13638⁴.

**Habitat**

*Dechloromonas agitata* was obtained from (per)chlorate-reducing enrichments from samples collected from a pulp and paper plant waste pulp sludge in Pennsylvania. *Dechlorosoma suillum* was obtained from (per)chlorate-reducing enrichments from samples collected from a primary treatment lagoon of swine waste at the Agricultural Research Facility at Southern Illinois University, Carbondale campus. Acetate (10 mM) was used as the electron donor in the enrichment and isolation cultures for both organisms.

**ACKNOWLEDGEMENTS**

The authors wish to acknowledge the guidance of Dr H. G. Trüper in the development of the correct etymology. Support for this research was in part from grant DE-FG02-98ER62689 from the Department of Energy to J. D. C and L. A. A. and from the 1998 Oak Ridge Associated Universities Junior Faculty award to J. D. C.

**REFERENCES**


Gilbert, D. G. (1993). SeqApp, 1.9a157 ed. Biocomputing Office, Biology Department, Indiana University, Bloomington, IN, USA.


