**Clostridium sardiniense** Prévot 1938 and **Clostridium absonum** Nakamura *et al.* 1973 are heterotypic synonyms: evidence from phylogenetic analyses of phospholipase C and 16S rRNA sequences, and DNA relatedness

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**Clostridium sardiniense** Prévot 1938 and **Clostridium absonum** Nakamura *et al.* 1973 have long been considered similar in terms of their biological and biochemical properties, but their taxonomic positions have not been clarified by DNA–DNA hybridization studies or rigorous analysis of 16S rRNA genes. In the present study, DNA–DNA hybridization analysis revealed that *C. absonum* strains DSM 599<sup>T</sup>, DSM 600 and KZ 1544 shared 83–0.0–86.3 % DNA relatedness with *C. sardiniense* DSM 2632<sup>T</sup>. 16S rRNA gene sequence analysis showed that the *C. absonum* strains also shared high identity with *C. sardiniense* DSM 2632<sup>T</sup> (99–7, 99–3 and 99.8 % for DSM 599<sup>T</sup>, DSM 600 and KZ 1544, respectively), implying that *C. absonum* and *C. sardiniense* are synonyms. In addition, alignment of the inferred amino acid sequences for phospholipase C (PLC) indicated 96.5 % identity between PLCs from *C. sardiniense* and *C. absonum*, but relatively low identity with other clostridial species. These results strongly suggest that the species *C. sardiniense* and *C. absonum* should be united, with the name *C. sardiniense* having priority.

Clostridia produce lecinthinases known as phospholipase C (PLC) (Titball, 1999; Jepson & Titball, 2000). The best characterized clostridial PLC is produced by *Clostridium perfringens*. Because *C. perfringens* PLC is toxic to mammals, it is termed an alpha-toxin and considered a major virulence factor. However, there are still many PLCs expressed by other clostridial species. Previous results suggest that these PLCs are similar but retain species-specific structure and function (Clark *et al.*, 2003; Karasawa *et al.*, 2003). *Clostridium absonum* was first described by Nakamura *et al.* (1973) and, unlike *C. perfringens*, is primarily isolated from soil and animal faeces. Later, this species was also identified as a causative agent of gas gangrene (Nakamura *et al.*, 1979; Masaki *et al.*, 1988). Although the morphological and biochemical properties of *C. absonum* are similar to those of *C. perfringens* (Nakamura *et al.*, 1973; Hayase *et al.*, 1974), *C. absonum* is easily differentiated from *C. perfringens* by the lecinthinase (PLC) neutralization test. In this assay, PLC produced by *C. absonum* on half-antitoxin egg-yolk agar cannot be completely neutralized by *C. perfringens* type A antitoxin as is the *C. perfringens* PLC (Nakamura *et al.*, 1973). Recently, our research group isolated the PLC gene (*caa*) from *C. absonum* and characterized the crystal structure of the expressed protein (*Caa*) (Clark *et al.*, 2003). In the course of these studies, particular attention was paid to *Clostridium sardiniense* since this species is similar to *C. absonum* in biological and biochemical properties (Cato *et al.*, 1986). *C. sardiniense* was initially described by Prévot in 1938 as a PLC-producing clostridial species. It is
frequently isolated from soil samples (Rodriguez et al., 1993) and the faces of infants (Borriello, 1980), although no association with gas gangrene has been reported. We isolated the PLC gene from C. sardiniense and found it to be highly homologous to caa, suggesting both genes may derive from the same species. Based on 16S rRNA gene sequence data, C. sardiniense has been classified relatively far from C. absonum in Clostridium 16S rRNA Cluster I (Collins et al., 1994). However, no DNA–DNA hybridization studies have been performed to confirm this phylogenetic relationship. Therefore, to clarify the taxonomic relationship between three strains of C. absonum (DSM 599T, DSM 600 and KZ 1544) and C. sardiniense DSM 2632T, we compared inferred amino acids for the respective PLCs and 16S rRNA genes, and performed DNA–DNA hybridization analyses.

C. sardiniense DSM 2632T (= ATCC 33455T = VPI 2971T), C. absonum DSM 599T (= ATCC 27555T = NCTC 10984T = CIP 104302T = JCM 1381T) (Clark et al., 2003), C. absonum DSM 600, C. absonum KZ 1544 (Nakamura et al., 1979), C. perfringens KZ 221 (Tsutsui et al., 1995; Karasawa et al., 2003), Clostridium bifermens KZ 1012 (Karasawa et al., 2003) and Clostridium sordellii NCIMB 10717T (= ATCC 9714T) (Karasawa et al., 2003) were used in this study. For extraction of whole-cell DNA, bacterial strains were cultured in 40 ml of GAM broth (Nissui Pharmaceutical) at 37°C for 16 h. Extraction and purification of whole-cell DNA was performed as described previously (Wang et al., 2000; Karasawa et al., 2003). As a preliminary experiment, a 900 bp fragment of the plc gene of C. sardiniense was amplified by using the KAG209 (5'-TGGATGAAAAAGATTGATGAAAGG-3') and KAG210 (5'-TTCTCTTTTCTATCCACATATCTGG-TATATC-3') primer set for highly conserved regions of clostridial plc genes (Karasawa et al., 2003). The sequence of the 900 bp fragment showed high identity with the C. sardiniense plc gene.

Of a PLC-positive transformant was extracted with a QIAprep Spin Miniprep kit (Qiagen), sequenced in both directions using a BigDye® Terminator Cycle Sequencing Ready Reaction kit (Applied Biosystems) with synthetic primers and electrophoresed on an ABI Prism 310 Genetic Analyser (Applied Biosystems). A 1519 bp fragment of the 16S rRNA gene was amplified by using KAG268 (5'-TTTAAATTTCTATGATGATGCTC-3') and KAG269 (5'-AGAAAGGAGGTGATCCGCA-3') as a primer set, designed from conserved sequences identified by comparing several clostridial 16S rRNA genes. The amplification, cloning and sequencing of the 16S rRNA genes was the same as described for the C. sardiniense plc gene except PCR was carried out using a two-step procedure of 30 cycles at 94°C for 20 s and 72°C for 40 s, after pre-heating at 94°C for 1 min. To prepare DNA probes for DNA–DNA hybridization analysis, chromosomal DNA was labelled by random priming using digoxigenin–dUTP according to the manufacturer’s instructions for the DIG High Prime DNA Labelling and Detection Starter Kit II (Roche Molecular Biochemicals). DNA–DNA hybridization was carried out as described by Ezaki et al. (1989) with some modifications. Purified chromosomal DNA was diluted to 100 μg ml⁻¹ with H₂O and denatured by boiling for 10 min at 100°C. Denatured DNA was diluted to 20 μg ml⁻¹ with PBS (8 mM Na₂HPO₄, 1.5 mM KH₂PO₄, pH 7–7.2, 137 mM NaCl, 2–7 mM KCl) containing 0–1 M MgCl₂ and aliquots (100 μl) were immobilized onto NUNC-immuno microplates (Nalge Nunc International) by incubation at 37°C for 3 h. Duplicate controls were made for each DNA sample. After aspirating the coating solution, 200 μl of pre-hybridization solution [2 x SSC (1 x SSC is 0.15 M NaCl/0.015 M sodium citrate), 5 x Denhardt’s solution, 25% formamide, 200 μg salmon sperm DNA ml⁻¹] was added to wells and incubated at 37°C for 3 h. Before hybridization with labelled DNA probe, wells were washed three times with 2 x SSC. One-hundred microlitres of hybridization solution (2 x SSC, 5 x Denhardt’s solution, 3% dextran sulfate, 25% formamide, 50 μg denatured salmon sperm DNA ml⁻¹, 0.5 μg denatured digoxigenin–dUTP labelled probe ml⁻¹) was added to wells and incubated at 37°C overnight. The wells were washed three times with 300 μl of 2 x SSC and once with 300 μl of washing buffer (0.1 M maleic acid, 0.15 M NaCl, pH 7.5, 0.3% Tween 20). Detection of dsDNA was done by using an anti-digoxigenin–alkaline phosphatase conjugate included in the kit. Finally, 100 μl of p-nitrophenyl phosphate disodium (mg ml⁻¹) (in 0.05 M Tris/NaCl, pH 10–0, 0.1 M NaCl, 0.5 mM MgCl₂) was dispensed into the wells, with a 30 min incubation at 37°C, and the reaction was stopped by adding 100 μl of 3 M NaOH. Absorbance was measured with a microplate reader EAR 340 AT (Tecan) at 405 nm with a reference wavelength of 620 nm. The assay was repeated at least three times for all strains with results shown as the mean ± SD. Multiple alignments of sequences were created by using the CLUSTAL W method and phylogenetic trees were calculated by using the neighbour-joining method.
contained within an online software package (http://www.ddbj.nig.ac.jp/search/clustalw-e.html). Unrooted phylogenetic trees were constructed with TreeView (version 1.6.6 for Windows) software.

The plc gene of C. sardiniense DSM 2632T consisted of 1197 nt encoding 398 aa residues. The inferred protein had a molecular mass of 45.7 kDa and a pl of 5.26. Between the plc gene of C. sardiniense and the caa gene of C. absonum DSM 599T (Clark et al., 2003), nucleotide differences were found at 57 positions, resulting in coding changes for 14 aa. Alignment of amino acid sequences revealed that the C. sardiniense PLC had 96.5% identity with Caa and showed relatively low identity with PLCs from C. perfringens (Cpa), C. bifermentans (Cbp) and C. sordellii (Csp) (Karasawa et al., 2003). A phylogenetic tree based on the amino acid sequences of PLCs from related clostridial species is shown in Fig. 1. The PLC of C. sardiniense was closely related to that of C. absonum. Not surprisingly, since Cbp and Csp, however, were only loosely related to Cpa, Caa and the C. sardiniense PLC.

As mentioned above, Caa could not be completely neutralized with antiserum to Cpa (Nakamura et al., 1973). When the half-antitoxin egg-yolk agar test (Willis & Hobbs, 1958) was used to compare PLCs of C. sardiniense and C. absonum, the C. sardiniense DSM 2632T PLC was also incompletely neutralized by antiserum to C. perfringens PLC (data not shown).

The 16S rRNA genes from C. sardiniense DSM 2632T and C. absonum DSM 599T, DSM 600 and KZ 1544 were sequenced. Alignment of the 16S rRNA gene sequences revealed that the C. absonum strains shared extremely high identity with the sequence of C. sardiniense DSM 2632T (99.3–99.9%). A phylogenetic tree based on 16S rRNA gene sequences is shown in Fig. 2. C. absonum strains DSM 599T, DSM 600 and KZ 1544 appeared closely related to C. sardiniense DSM 2632T. According to Collins et al. (1994), although C. sardiniense, as well as C. absonum, is classified in Clostridium 16S rRNA cluster I, C. sardiniense is only loosely associated with C. absonum. Of note is that

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**Fig. 1.** Unrooted phylogenetic tree based on PLC amino acid sequences. Bar, 0.1 substitution per site.

**Fig. 2.** Unrooted phylogenetic tree based on 16S rRNA gene sequences. Bar, 0.1 substitution per site. The microheterogeneity of the 16S rRNA gene from C. absonum and C. sardiniense strains did not affect the phylogenetic tree.

Clostridium absonum and C. sardiniense are synonyms.
the 16S rRNA gene sequences for both C. absonum and C. sardiniense in GenBank/EMBL/DDBJ (accession nos X77842 and X73446, respectively) contain several undetermined nucleotide residues, probably resulting in the loose association reported by Collins et al. (1994). Indeed, we also found a few undetermined nucleotide residues in preliminary sequences for these 16S rRNA genes when we used a direct method with PCR products. Therefore, the PCR products of the 16S rRNA genes were cloned into a plasmid vector and three to six clones were sequenced per strain. Our results indicated two kinds of 16S rRNA gene with microheterogeneity in every strain tested. The two different clones found in C. sardiniense DSM 2632T were defined as DSM 2632C1 (four of six sequenced clones) and DSM 2632C2 (two of six sequenced clones). Differences found at six nucleotide positions between DSM 2632C1 and DSM 2632C2 were: G819, C880, C1001, T1003, G1010 and G1489 in DSM 2632C1 substituted by A819, T880, T1001, C1003, A1010 and A1489 in DSM 2632C2. Microheterogeneities were also found in three strains of C. absonum with C1001 and G1010 in DSM 599C1 (two of three clones) substituted by T1001 and A1010 in DSM 599C2 (one of three clones); C225, C359, C442, A819, C821 and C982 in DSM 600C1 (two of three clones) substituted by T225, T359, T442, G819, T821 and T982 in DSM 600C2 (two of three clones); and T1001, T1003 and G1010 in KZ 1544C1 (two of three clones) substituted by C1001, C1003 and A1010 in KZ 1544C2 (one of three clones). Microheterogeneities have been reported in the 16S rRNA operon of E. coli (Carbon et al., 1979), the 23S rRNA operon of Clostridium botulinum type A (East et al., 1992) and the 5S rRNA operon of Bacillus species (Raue et al., 1977). Although microheterogeneity does not pose a problem for phylogenetically distant organisms, such considerations become increasingly important when close genealogical relationships exist (East et al., 1992). However, despite the microheterogeneity, the phylogenetic analysis of 16S rRNA gene sequences implies that C. absonum and C. sardiniense can be classified at equal taxonomic positions.

High levels of DNA relatedness were detected between C. sardiniense DSM 2632T and the three strains of C. absonum: (83-0, 84-7 and 86-3 % for DSM 599T, DSM 600 and KZ 1544, respectively) (results of DNA–DNA hybridizations are available as supplementary material in IJSEM Online). However, relatively low levels of DNA relatedness (18-2–28-0 %) were detected between C. perfringens KZ 221 and all strains of C. absonum and C. sardiniense. A relatively high level of DNA relatedness (64-6 %) was found for C. bifermentans and C. sordellii, which are considered closely related based on data from 16S rRNA gene sequences (Collins et al., 1994) and DNA–DNA hybridization analyses (Nakamura et al., 1975). However, C. bifermentans and C. sordellii showed low level DNA relatedness to C. absonum, C. sardiniense and C. perfringens. DNA–DNA hybridization also indicated that C. absonum is equal to C. sardiniense in its phylogenetic position.

Interestingly, phylogenetic trees exhibited excellent correlation whether based on the inferred amino acid sequences of PLCs, 16S rRNA genes or degree of DNA relatedness in hybridization experiments. Our results suggest that the evolution of PLC closely parallels that of 16S rRNA genes in PLC-producing clostridia. Genes encoding PLC could be as useful for phylogenetic analysis of PLC-producing clostridia as 16S rRNA genes. Similarly, the phylogenetic tree based on 16S rRNA gene sequences of PLC-producing clostridia should provide good clues for analysing the primary structure and function of clostridial PLCs.

C. sardiniense and C. absonum were first described by Prévot (1938) and Nakamura et al. (1973), respectively. Cato et al. (1986) recognized that C. sardiniense was similar to C. absonum in its biological and biochemical properties, and further noted that 'C. sardiniense is differentiated from C. absonum by motility but since some strains labeled C. absonum have been found to be motile, clear separation of the species must await DNA homology studies'. However, until this study, the taxonomic position of both species had not been clarified. DNA hybridization studies had not been conducted, and the 16S rRNA gene sequences for C. absonum DSM 599T and C. sardiniense DSM 2632T in GenBank/EMBL/DDBJ (accession nos X77842 and X73446, respectively) contained undetermined nucleotides, resulting in a reportedly loose association between these species (Collins et al., 1994). The present study has demonstrated that C. absonum strains DSM 599T, DSM 600 and KZ 1544 share 83-0–86-3 % DNA relatedness with C. sardiniense strain DSM 2632T. Moreover, 16S rRNA gene sequence analysis showed that all C. absonum strains in this study shared high identity with C. sardiniense DSM 2632T (99-7, 99-3 and 99-8 % for DSM 599T, DSM 600 and KZ 1544, respectively), implying that C. absonum and C. sardiniense can now be classified at equal taxonomic positions. In addition, alignment of inferred amino acids for PLCs indicated 96-5 % identity between the C. sardiniense and C. absonum proteins, but relatively low identity to other clostridial species. These results strongly suggest that the names C. sardiniense and C. absonum are synonyms. Therefore, according to Rule 24b of the International Code of Nomenclature of Bacteria, we propose that C. absonum be recognized as a later synonym of C. sardiniense, and that the species C. sardiniense and C. absonum should be united, with the name C. sardiniense having priority.

**Emended description of Clostridium sardiniense Prévot 1938**


The description of the species is as given by Cato et al. (1986), based mainly on the studies of Nakamura et al. (1973) and Holdeman et al. (1977).

The type strain is DSM 2632T (= ATCC 33455T = VPI 2971T).
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References


