Analysis of the 16S rRNA gene of microorganism WSU 86-1044 from an aborted bovine foetus reveals that it is a member of the order Chlamydiales: proposal of Waddliaceae fam. nov., Waddlia chondrophila gen. nov., sp. nov.

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The structural gene encoding the 16S rRNA of the new obligate intracellular organism presently designated WSU 86-1044T was sequenced and analysed to establish its phylogenetic relationships. The 16S rDNA sequence was most closely related to those of chlamydial species, having 84.7-85.3% sequence similarity, while it had 72.4-73.2% similarity with rickettsia-like organisms. When the sequences of the four species of chlamydiae (Chlamydophila psittaci, Chlamydia trachomatis, Chlamydophila pneumoniae and Chlamydophila pecorum) were compared, they had > 93% sequence similarity indicating that WSU 86-1044T was not close enough to be in the same family as current Chlamydiaceae members. However, based on the 84.7-85.3% 16S rDNA sequence similarity of WSU 86-1044T and other previously described characteristics, WSU 86-1044T belongs to a novel family within the order Chlamydiales; hence, the proposal of Waddliaceae fam. nov., Waddlia chondrophila gen. nov., sp. nov.

Keywords: chlamydia, phylogeny, 16S rRNA, 16S rDNA sequence, abortion

INTRODUCTION

The organism WSU 86-1044T, was originally isolated from tissues of a first-trimester aborted bovine foetus at the Washington Animal Disease Diagnostic Laboratory (Dilbeck et al., 1990). A cytopathic effect was observed within 2-3 d after the initial inoculation of bovine turbinate (BT) cell cultures with pooled spleen and liver homogenates. The organism was serially passaged numerous times and consistently induced cytopathic effect. It replicated rapidly to high levels, reaching peak titres exceeding $10^5$ 50% tissue-culture-infective doses (TCID$_{50}$) per ml within 3 d (Dilbeck et al., 1990). Replication was inhibited by tetracycline, but not by penicillin or gentamicin (Dilbeck et al., 1990). Light microscopy revealed organisms within cytoplasmic inclusions that ranged in size from 0.2 to 0.4 μm (Dilbeck et al., 1990). Electron microscopy confirmed that the organisms multiplied within a cytoplasmic vacuole with a developmental life cycle resembling that of erlichiae and chlamydiae (Dilbeck et al., 1990; Kocan et al., 1990). The organisms occurred in two forms; a reticulated form found within a cytoplasmic vacuole, and a dense infective form that was released from the cells.

Presently, WSU 86-1044T is characterized as an obligate intracellular organism, which replicates within cytoplasmic vacuoles, exhibiting structural characteristics compatible with those of rickettsiae and chlamydiae (Dilbeck et al., 1990; Kocan et al., 1990). Serological identification of WSU 86-1044T was not successful as the organism did not react with monoclonal or polyclonal antisera to a variety of Rickettsia, Coxiella, Wolbachia, Anaplasma or Chlamydia spp. (Dilbeck et al., 1990). However, it did react weakly with antisera to Cowdria ruminantium. Thus, WSU 86-1044T has not been taxonomically classified.
Progress in molecular biology using PCR and sequencing of DNA encoding 16S rRNA has enabled determination of the precise phylogenetic position of each bacterial species, particularly obligate intracellular bacteria which express few phenotypic characters (Hills et al., 1996; Roux & Raoult, 1995). The primers are chosen from sequences that are highly conserved among the phylogenetic group referred to as the eubacteria (Wilson et al., 1990; Woese, 1987), but which are not found in eukaryotes, archaea or mitochonndria. It is therefore possible to amplify only sequences that are not found in eukaryotes, archaea or mitoebacteria (Wilson, 1990) among the phylogenetic group referred to as the closely related genealogical relationships of bac-

In an effort to classify the agent WSU 86-1044T, the DNA encoding the 16S rRNA was PCR-amplified and sequenced. Comparison of the 16S rDNA sequence with other 16S rDNA sequences in GenBank indicated that WSU 86-1044T belonged to the order Chlamydiales. However, the similarity was not sufficient to allow its classification in any of the families within the order.

In a recent paper by Everett et al. (1999) on a revised classification scheme for the order Chlamydiales, Chlamydia pneumoniae, Chlamydia psittaci and Chlamydia psittaci were reclassified to Chlamydothila gen. nov. as Chlamydothila pneumoniae comb. nov., Chlamydothila psittaci comb. nov. and Chlamydothila psittaci comb. nov., respectively. Their new names will be used throughout this paper.

METHODS

WSU 86-1044T. The isolation of the organism from pooled foetal liver/lung homogenate has been described previously (Dilbeck et al., 1990). The organism was cloned at the 8th passage by three serial limiting dilutions in 96-well plates of bovine turbinate (BT) cells (ATCC CRL-1390) (Dilbeck et al., 1990). Cloned organisms at the 13th passage in BT cells with a titre of 1 x 10^6 TCID50 were used in these studies.

DNA extraction. Genomic DNA was prepared from WSU 86-1044T passages in bovine turbinate cells. The supernatants were harvested when the cytopathic effect was advanced and stored at -70 °C. For use, the fluid was thawed and clarified at 500 g for 10 min, and the organisms pelleted at 20000 g for 30 min. DNA was prepared from the sedimented WSU 86-1044T organisms using Puregene DNA Isolation Kit (Gentra Systems).

PCR amplification. The DNA encoding the 16S rRNA was amplified in vitro via PCR (White, 1993) by using a primer set (forward 5' AGA GTT TGA TCC TGG 3' and reverse 5' TAC CTT GTT ACG ACT T 3') selected from the conserved sequences at the beginning and the end of the eubacterial kingdom 16S rDNA (Wilson et al., 1990; Woese, 1987). PCR amplification was done in 100 μl reaction mixture and Taq DNA polymerase from Gibco-BRL. Typically, a tube contained 10 μl 10 x PCR buffer made of 200 mM Tris/HC1 (pH 8.4) and 500 mM KCl, 5 μl 50 mM MgCl2, 2 μl 10 mM dinucleotide mix (Invitrogen), 0.5 μl 50 mM of the reverse and forward primers, 79.5 μl of double-distilled water, the primer- containing 0.25 μg target DNA and 0.5 μl (2.5 U) Taq DNA Polymerase. Before addition of the target DNA and Taq polymerase a wax gem (Perker-Elmer) was added to the tube and heated at 75 °C for 5 min and then allowed to cool to room temperature. Amplification was performed in a GeneAmp PCR System 9600 Thermal Cycler (Perkin-Elmer) in which the target DNA was denatured by incubation at 95 °C for 1 min followed by 35 cycles of denaturation (94 °C for 1 min), primer annealing (55 °C for 3 min) and primer extension (72 °C for 3 min). At the end of the cycling, the reaction mixture was held at 72 °C for 7 min and cooled to 4 °C. The size of the PCR product was verified by agarose gel electrophoresis of 10 μl reaction mixture (Sambrook et al., 1989).

Cloning, sequencing and sequence analysis. The amplified fragment was ligated into the EcoRI site of vector pCR 2.1 (Invitrogen) and used to transform Esherichia coli (one-shot cell INVaxF Competent Cells; Invitrogen). Individual, transformed colonies were grown in Luria Broth, DNA was isolated and then digested with EcoRI. DNA fragments were separated in 1.5% agarose gel and stained with ethidium bromide to verify the size of the fragment ligated into the plasmid. Nucleotide sequencing of the recombinant inserts from selected colonies was performed by the Laboratory for Biotechnology and Bioanalysis, Washington State University, using the Perkin Elmer Applied Biosystems Prism Dye Terminator Kit and analysed on an ABI 373 DNA Sequencer. Cloning the amplified fragment into pCR 2.1 enabled sequencing of the whole amplicon, initially using M13 forward and reverse primers (Invitrogen) approximately 100 bases up- and downstream from the EcoRI cloning site, and subsequently with commercially synthesized specific primers (Life Technologies) selected as sequence information was obtained. Table 1 shows the primers used to sequence through the entire 16S rDNA amplicon of the WSU 86-1044T. Sequence analysis programs REFORMAT, GAP, REVERSE, PILEUP, DISTANCES, NEIGHBOR and GROWTREE in the University of Wisconsin Genetics Computer Group (GCG), version 8 (1994), were used for DNA analyses (Devereux et al., 1984). GenBank search for similarities was accomplished using BLAST and FASTA programs on-line (Pearson & Lipman, 1988). Comparison of the WSU 86-1044T 16S rDNA sequence with published sequences of other organisms, most of which were obligate intracellular bacteria, was performed both by PILEUP and by DISTANCES analysis to calculate the Kimura two-parameter distances. Sequences of the following micro-organisms (GenBank accession no. and strain designation in parentheses) were compared: Chlamydococci (formerly Chlamydia) psittaci (M13769, strain 6BC3), Chlamydia trachomatis (M59178, strain 434C), Chlamydococci (formerly Chlamydia) pneumoniae (Z49873, strain TW-183), Chlamydococci (formerly Chlamydia) pecorum (U737782), Simkania negevensis (L27666, strain Z'), Parachlamydia acanthamoebae (Y07556, strain Bn9), Rickettsia rickettii (M21293, strain R), Cowdria ruminantium [X61659, strain Crystal Springs (Zimbabwe) isolate], Anaplasma marginale (M60313), Ehrlichia phagocytophila (M73220, strain OS') and Esherichia coli (M24996).

The neighbour-joining method and tree construction were
performed by using the NEIGHBOR and GROWTREE programs, respectively. All sequences were aligned using the PILEUP multiple-sequence alignment program.

RESULTS

PCR product

Conserved eubacterial rDNA primers amplified a major WSU 86-1044T fragment slightly above 1.5 kb. When the plasmid with the insert was isolated and digested with EcoRI endonuclease, three fragments resulted comprising the vector pCR 2.1 (3-9 kb), one insert fragment slightly longer than 0.8 kb, and a second insert fragment of approximately 0.7 kb, indicating an internal EcoRI site in the amplicon. An EcoRI site at nucleotide positions 679–685 from the 5' of WSU 86-1044T was confirmed by sequence analysis. An EcoRI site was also reported approximately 680 nucleotides from the 5' end of rDNA for Chlamydo-

Species The sequences of the Simkaniaceae and Chlamydiales Chlamydiales, Chlamydia trachomatis, Chlamydo-

phylla (formerly Chlamydia) psittaci (Weisburg et al., 1986). The sequence of Chlamydo-

Phylogenetic analyses

A new classification of the order Chlamydiales has been proposed in which the currently known strains with > 90% 16S rRNA similarity form the Chlamydiales family. The chlamydia-like organisms which have 80–90% 16S rRNA similarity form two new families: Simkaniaceae and Parachlamydiaceae (Everett et al., 1999). We compared 16S rDNA sequences of some members of the Chlamydiaceae, Simkaniaceae and Parachlamydiaceae (Everett et al., 1999), WSU 86-1044T, and some intracellular parasites from the Rickettsiaceae to assess their percentage sequence similarity. WSU 86-1044T exhibited the greatest similarity to members of the order Chlamy-

DISCUSSION

Analysis of 16S rDNA of WSU 86-1044T indicated that the abortion agent was closely related to the members of the order Chlamydiales, having 84.5–85.3% sequence similarity. The relatively high degree of similarity of WSU 86-1044T 16S rDNA to 16S rDNA from the members of the order Chla-

mydiales provided justification for its inclusion in this group/order. However, when the rDNA sequences of four members from the family Chlamydiaceae were aligned they had sequence similarities of 93.8–96.7%. Therefore the lower level of sequence similarity between WSU 86-1044T and the members of the Chla-

mydiales family did not justify inclusion of WSU 86-

1044T into this family (Kahane et al., 1995; Everett & Andersen, 1997; Everett et al., 1999; Takahashi et al., 1997).

It has been shown that WSU 86-1044T is morpho-

logically similar to rickettsiae and chlamydiae but is biochemically and antigenically distinct (Dilbeck et al., 1990; Kocan et al., 1990). Two developmental forms (dense bodies and reticulate bodies) of WSU 86-1044T organisms were observed in intracytoplasmic vacuoles by electron microscopy. WSU 86-1044T was completely resistant to penicillin in vitro, whereas all known

Fig. 1. Dendogram (based on the distances calculated by PILEUP analysis) showing relationship between WSU 86-1044T, chlamydiae and rickettsiae. Bar indicates 10 nucleotide substitutions.
Table 1. Primers for sequencing the rDNA amplicon of WSU 86-1044T

<table>
<thead>
<tr>
<th>Primer</th>
<th>Sequence (position/source)</th>
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<tbody>
<tr>
<td>Forward</td>
<td></td>
</tr>
<tr>
<td>F1 (M13)</td>
<td>5' GTTTCCCCAGTCACGAGCTTGA (Invitrogen)</td>
</tr>
<tr>
<td>F2</td>
<td>5' GCTCAGAAGGCTAAGACGGC (277-298)</td>
</tr>
<tr>
<td>F3</td>
<td>5' CTAGCTTTGACCTGACGCTGT (752-774)</td>
</tr>
<tr>
<td>F4</td>
<td>5' GAATCTGCAACTCGGCTTCCAT (1323-1345)</td>
</tr>
<tr>
<td>Reverse</td>
<td></td>
</tr>
<tr>
<td>R1 (M13)</td>
<td>5' TTGTGACCGGATAAACATTTG (Invitrogen)</td>
</tr>
<tr>
<td>R1</td>
<td>5' CACTCTAAATGCTGGCAAC (392-373)</td>
</tr>
<tr>
<td>R2</td>
<td>5' CACCGCTACATGTTGGAATCC (843-822)</td>
</tr>
<tr>
<td>R4</td>
<td>5' GATCCTCTCTAGCACCATA (1358-1336)</td>
</tr>
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</table>

Chlamydia are sensitive (Moulder, 1991). Furthermore, WSU 86-1044T did not react with either polyclonal or monoclonal antibodies used to type chlamydia, although there was some reactivity with antibodies to Chlamydia ruminantium (Dilbeck et al., 1990).

Evolutionary distance values calculated using distances were used to construct the phylogenetic tree shown in Fig. 1. The tree shows the distinctions between chlamydiae and rickettsiae. Although WSU 86-1044T, Simkania negevensis and Parachlamydiae acanthamoebae formed a cluster, the three are as far apart from one another (84-6-87-2% sequence similarity) as they are from the chlamydiae.

The genetic data described herein, and the morphological similarity (Kocan et al., 1990), are consistent with a close relationship between WSU 86-1044T and the chlamydiae. However, since rDNA sequence similarity of >90% has been suggested as a criterion for classifying chlamydia-like organisms within the same family of the order Chlamydiaceae (Everett et al., 1999), WSU 86-1044T having <90% similarity does not fit into any of the present families in the order Chlamydiaceae. Therefore, we propose that WSU 86-1044T be classified as Waddlia chondrophila gen. nov., sp. nov.

Description of Waddlia gen. nov.

Waddlia [Wadd'li.a. N.L. fem. n. Waddlia arbitrary name derived from the abbreviation WADDL (Washington Animal Disease Diagnostic-Laboratory)]. Members of the genus Waddlia have 16S rDNA that is >90% similar to that of the type species, Waddlia chondrophila strain WSU 86-1044T.

Description of Waddlia chondrophila sp. nov.

Waddlia chondrophila (chon.drophi.la. Gr. n. chondros clump; Gr. adj. philos, -a friendly to; M.L. chondrophila liking clumps, in reference to the association of the organism with cellular mitochondria).

The species Waddlia chondrophila currently includes only the type strain, WSU 86-1044T (= ATCC VR 1470T). Waddlia chondrophila was isolated from the tissues of a first-trimester aborted bovine foetus. The description of this species is identical to that of 'micro-organism WSU 86-1044' (Dilbeck et al., 1990; Kocan et al., 1990) which are obligate intracellular organisms resistant to penicillin. They grow well in BT producing multiple cytoplasmic vacuoles and Gram-negative, periodic acid–Schiff negative and non-acid-fast inclusions. The inclusions contain coccolid organisms ranging from 0.2 to 0.5 μm in size. The BT infectivity is abolished by tetracycline and/or chloroform treatment. The organism multiplies by binary fission and has two developmental forms: the dense form which is infective, and the reticulated form, usually associated with mitochondria, which undergoes binary fission. These organisms do not react with antisera used for typing chlamydiae or rickettsiae. The 16S rDNA of the Waddliaceae strains are >90% similar to ribosomal genes in WSU 86-1044T. The family Waddliaceae belongs to the order Chlamydiaceae and is a sister taxon of the Chlamydiaceae because the ribosomal genes are 80–90% similar to ribosomal genes in the Chlamydiaceae. Phylogenetic analyses of the Waddliaceae 16S rDNA sequence is presented here. At present this family comprises a single genus, the type genus Waddlia.

Description of Waddliaceae fam. nov.

Waddliaceae (Wadd'li.a.ceae. M.L. fem. n. Waddlia the type genus of the family; -aceae ending to denote a family; M.L. fem. pl. Waddliaceae the Waddlia family).

Waddliaceae currently includes the type genus, Waddlia. The description of this family is identical at present to that of 'micro-organism WSU 86-1044' (Dilbeck et al., 1990; Kocan et al., 1990) which are obligate intracellular organisms resistant to penicillin. They grow well in BT producing multiple cytoplasmic vacuoles and Gram-negative, periodic acid–Schiff negative and non-acid-fast inclusions. The inclusions containcoccolid organisms ranging from 0.2 to 0.5 μm in size. The BT infectivity is abolished by tetracycline and/or chloroform treatment. The organism multiplies by binary fission and has two developmental forms: the dense form which is infective, and the reticulated form, usually associated with mitochondria, which undergoes binary fission. These organisms do not react with antisera used for typing chlamydiae or rickettsiae. The 16S rDNA of the Waddliaceae strains are >90% similar to ribosomal genes in WSU 86-1044T. The family Waddliaceae belongs to the order Chlamydiaceae and is a sister taxon of the Chlamydiaceae because the ribosomal genes are 80–90% similar to ribosomal genes in the Chlamydiaceae. Phylogenetic analyses of the Waddliaceae 16S rDNA sequence is presented here. At present this family comprises a single genus, the type genus Waddlia.
containing one monotypic genus, revised taxonomy of the family Chlamydiaceae description of the order Chlamydiales (Everett et al., 1999). For a newly identified strain to be described as a member of Waddliaceae, a nearly full-length rDNA of the new strain may only differ from Waddlia chondrophila 16S rDNA by < 10%.

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REFERENCES


