Nucleotide sequences of 16S rRNA encoding genes from *Capnocytophaga ochracea* ATCC 33596, *Capnocytophaga sputigena* ATCC 33612 and *Capnocytophaga gingivalis* ATCC 33624

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Capnocytophaga (group DF-1) species (*C.ochracea, C.sputigena* and *C.gingivalis*) are thought to be associated with periodontal disease (1, 2). The clinically most important infections are seen in cases of localized juvenile periodontitis. Moreover, *Capnocytophaga* spp. are well-documented opportunistic pathogens, causing systemic infections primarily in granulocytopenic cancer patients with oral lesions (3).

Because of limitations of conventional methods for the sensitive detection and specific identification of these species in highly mixed samples such as subgingival plaque, the development of oligodeoxynucleotide probes directed against species-specifically conserved 16S rRNA target sequences may provide a more suitable tool.

For this reason the 16S rRNA encoding genes of *Capnocytophaga ochracea* ATCC 33596, *Capnocytophaga sputigena* ATCC 33612 and *Capnocytophaga gingivalis* ATCC 33624 were sequenced.

Amplification of the 16S rRNA gene was accomplished by PCR using universal primers designed from conserved regions of the 16S rRNA (4, 5). The amplicons were directly sequenced without cloning procedures by the dye terminator cycle-sequencing method using an ABI 373 A DNA-sequencer (Applied Biosystems, Weiterstadt, Germany). The PCR primers served also as sequencing primers. The results are shown in Figure 1 in an aligned form.

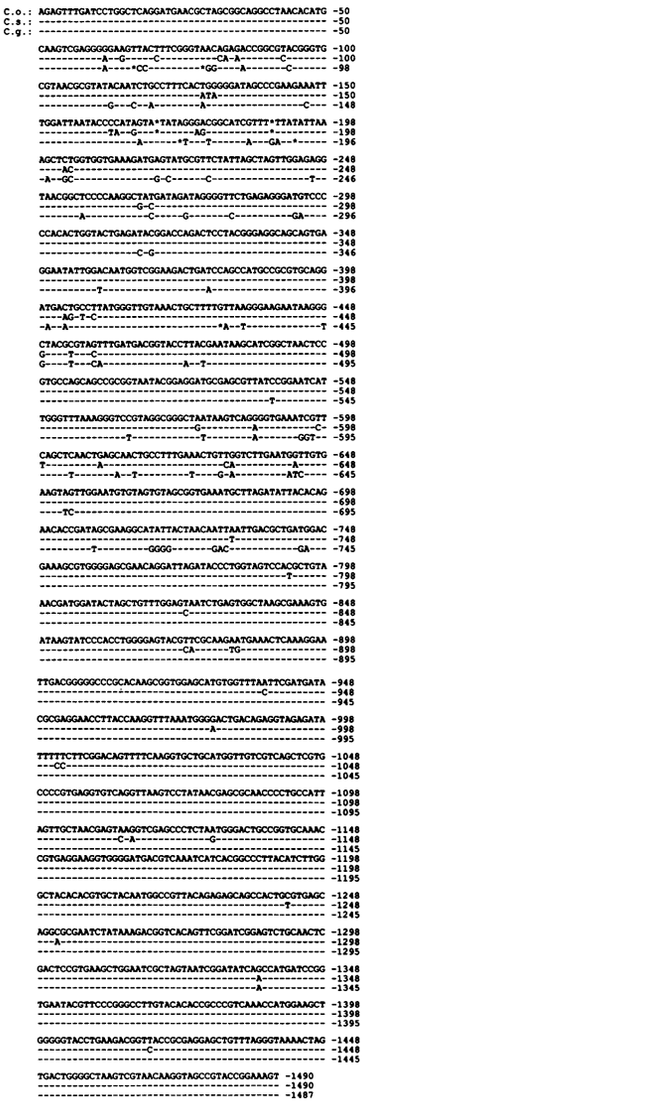

Figure 1. Sequences of 16S rRNA encoding genes from *Capnocytophaga ochracea* ATCC 33596 (C.o.), *Capnocytophaga sputigena* ATCC 33612 (C.s.) and *Capnocytophaga gingivalis* ATCC 33624 (C.g.) in an aligned form. Bars denote identical bases, asterisks indicate missing nucleotides at the given positions.

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