Members of the genus *Prevotella* are among the most commonly isolated organisms among the human oral microbiota. Although a number of novel species have been proposed in recent years (Downes et al., 2005, 2007; Sakamoto et al., 2004, 2005a, b), molecular identification techniques such as 16S rRNA gene sequence analysis continue to reveal additional un-named taxa. The aim of this study was to characterize four strains isolated from the human mouth by means of a range of microscopic, biochemical and molecular techniques.

Strain E7.56\(^T\) was obtained from necrotic pulp, strain 4D22 from subgingival plaque in a deep periodontal pocket and strains AHN 8723 and AHN 8376 from the gingival crevices of two children. Strains were grown at 37 °C on fastidious anaerobe agar (FAA; LabM) supplemented with 5% horse blood under anaerobic conditions (80% N\(_2\), 10% H\(_2\), 10% CO\(_2\)) in an anaerobic workstation (Don Whitley Scientific). Colony morphologies were viewed by means of a dissecting microscope and recorded after incubation for 5 days. Cellular morphology was recorded after Gram-staining of smears prepared from 2 day FAA plate cultures. Hanging-drop preparations of 18 h cultures of peptone-yeast extract-glucose (PYG) broth were examined by phase-contrast microscopy for cellular motility. Transmission electron microscopy was used to examine the cell-wall ultrastructure as described previously (Downes et al., 2002).

Biochemical and physiological tests were performed using standard methods (Holdeman et al., 1977; Jousimies-Somer et al., 2002). Fermentation tests were performed using pre-reduced, anaerobically sterilized (PRAS) sugars prepared in an anaerobic workstation (Holdeman et al., 1977). Susceptibility to special-potency antibiotic discs [vancomycin (5 μg), kanamycin (1 mg) and colistin (10 μg)] was determined on FAA (Jousimies-Somer et al., 2002). The presence and amounts of volatile and non-volatile fatty acids produced as metabolic end products were determined by gas chromatography of PYG broth cultures (Holdeman et al., 1977). Enzyme profiles were generated with the Rapid ID 32A anaerobe identification kit (bioMérieux) using bacteria harvested from Columbia agar plates (LabM) supplemented with 5% horse blood, according to the manufacturer’s instructions.

The G+C content of the DNA of strain E7.56\(^T\) was determined by HPLC as described previously (Wade et al., 1999). The 16S rRNA genes of the strains were sequenced as described previously (Downes et al., 2005). Sequences were assembled using the BioEdit program (Hall, 2007) and their closest relatives identified by BLAST interrogation of the GenBank database (Altschul et al., 1990). Sequences were aligned by CLUSTAL W within BioEdit and phylogenetic trees were constructed using MEGA version 4 (Tamura et al., 2007), by the neighbour-joining method from distance matrices prepared using the Jukes–Cantor correction.
Virtually complete sequences of the 16S rRNA gene were obtained for all four strains. Pairwise comparisons over 1451 aligned bases showed that the sequences of the four strains did not differ by more than three bases from each other. The group clustered within the genus *Prevotella* and were grouped in a loose cluster bounded by *Prevotella buccalis* and *Prevotella shahii* (Fig. 1). The generally low bootstrap values for the branches in this cluster indicated that little confidence should be placed in the branch topology. Indeed, the 16S rRNA gene sequence identity between strain E7.56<sup>T</sup> and the other strains in this cluster shown in Fig. 1 was very similar in all cases, ranging from 88% for *P. buccalis*, *Prevotella enoeca*, *Prevotella pleuritidis* and *Prevotella stercorea* to 91% for *Prevotella marshii*.

The four strains were obligately anaerobic, non-motile, pigmenting Gram-negative bacilli that were 0.7 μm wide by 1.5–5.0 μm long, arranged singularly and as end-to-end pairs. Transmission electron microscope examination of an ultrathin section of strain E7.56<sup>T</sup> showed a typical Gram-negative cell wall, including a thin peptidoglycan layer and an outer membrane (Fig. 2). When viewed under a plate microscope after 5 days of incubation on FAA plates, colonies were 1.2–1.8 mm in diameter, circular, entire, convex and iridescent with a mottled internal appearance with bright pink to reddish brown colours in the centre and a cream-coloured periphery (Fig. 3). Colony colour could be variable, with some dull brown-coloured colonies also present, especially in older cultures. Overall, pigmentation varied from brown on FAA with 5% horse blood to dark brown/black on FAA with 5% rabbit blood. Strains were resistant to the special-potency vancomycin and kanamycin discs and sensitive to colistin. Growth of all strains in peptone-yeast extract (PY) broth produced a moderately turbid suspension (2 to 3+ on a scale of 0 to 4+). Growth was enhanced (to 4+) by the addition of 1% fermentable carbohydrates. Strains were saccharolytic (see species description), and moderate to major amounts of acetic, isovaleric and succinic acids and minor to trace amounts of isobutyric acid were produced as end products of metabolism. Indole was produced and gelatin was hydrolysed but other biochemical tests were negative (see species description). The G+C content of the DNA of strain E7.56<sup>T</sup> was 46 mol%.

The addition of 1% ferric ammonium citrate solution to actively growing cultures in PRAS PY aesculin broth resulted in black colour development. However, exposure of the broth to UV light revealed bright fluorescence comparable with uninoculated aesculin broth, indicating the presence of aesculin and, therefore, a negative test result for aesculin hydrolysis (Jousimies-Somer et al., 2002).

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**Fig. 1.** Phylogenetic tree based on 16S rRNA gene sequence comparisons over 1361 aligned bases showing relationships between strain E7.56<sup>T</sup> and related species. The tree was constructed using the neighbour-joining method from a distance matrix constructed from aligned sequences using the Jukes–Cantor correction. Numbers represent bootstrap values for each branch based on data for 100 trees. Accession numbers for 16S rRNA sequences are given for each strain. Bar, 0.02 nucleotide substitutions per site.

**Fig. 2.** Transmission electron micrograph of an ultrathin transverse section of a cell of strain E7.56<sup>T</sup>. Bar, 100 nm.

**Fig. 3.** Colony morphology of strain E7.56<sup>T</sup> grown on FAA plus 5% horse blood agar after 5 days incubation. Bar, 1 mm.
All four strains were positive for \( \alpha \)-galactosidase, \( \beta \)-galactosidase, \( \alpha \)-glucosidase, N-acetyl-\( \beta \)-glucosaminidase, \( \alpha \)-fucosidase, alkaline phosphatase, leucyl glycine arylamidase, alanine arylamidase and indole production in the Rapid ID32A identification panel, while reactions to \( \beta \)-glucosidase and glutamyl glutamic acid arylamidase were weak and variable. All strains were negative for the remaining 18 enzymes, resulting in a profile of \( 45^0/1 \) 6402 \( 2^0/2 \), although weak 6-phospho-\( \beta \)-galactosidase reactions were sometimes noted but scored negative.

From the data presented above, it is clear that the four strains studied constitute a homogeneous group that is sufficiently distant in its 16S rRNA gene sequence from *Prevotella* species with validly published names to warrant creation of a novel species, for which we propose the name *Prevotella micans* sp. nov.

Biochemical tests that differentiate *P. micans* from other species in the cluster are shown in Table 1. However, some pairs of species differ only by a single test, and 16S rRNA species in the cluster are shown in Table 1. However, some pairs of species differ only by a single test. Indole is produced, but not catalase. Nitrate is not reduced. No growth in 20 % bile. The Rapid ID32A profile is \( 45^0/1 \) 6402 \( 2^0/2 \) and is positive for \( \alpha \)-galactosidase, \( \beta \)-galactosidase, \( \alpha \)-glucosidase, N-acetyl-\( \beta \)-glucosaminidase, \( \alpha \)-fucosidase, alkaline phosphatase, leucyl glycine arylamidase and alanine arylamidase and weakly and variably positive for \( \beta \)-glucosidase and glutamyl glutamic acid arylamidase. The G+C content of the DNA of the type strain is 46 mol%.

The type strain is E7.56\(^T\) (=DSM 21469\(^T\) =CCUG 56105\(^T\)), isolated from the human oral cavity.

### Acknowledgements

This work was supported by a grant from the Guy’s and St Thomas’s Charity (ref. R050724).

### References


