Request for an Opinion

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Proposal of a neotype strain (A1-86) for *Eubacterium rectale*. Request for an Opinion

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Eubacterium rectale is one of the most abundant bacterial species recovered from human faeces. *E. rectale* (Hauduroy *et al.* 1937) appears in the 'List of Bacterial Names with Standing in Nomenclature', but it is noted that the originally proposed type strain, VPI 0989^T, has been lost and its possible replacement by another strain (VPI 0990) from the same faecal sample has never been formally proposed. It is therefore proposed that strain A1-86 (=DSM 17629=NCIMB 14373), isolated from human adult faeces, be formally recognized as the neotype strain of *Eubacterium rectale*.

Eubacterium rectale is reported to be one of the most abundant bacterial species in human faeces both from anaerobic cultivation (Finegold *et al.*, 1983; Moore & Holdeman Moore, 1986) and culture-independent analysis of 16S rRNA sequences (Hold *et al.*, 2002; Eckburg *et al.*, 2005; Aminov *et al.*, 2006). The genus *Eubacterium* includes many species of obligately anaerobic bacteria, with *Eubacterium limosum* designated as the type species. Species of the genus *Eubacterium* produce mixtures of organic acids as fermentation products from carbohydrates, including butyric, acetic, lactic or formic acids, but not propionic and succinic acids, as major products (Krumholz & Bryant, 1986; Andreessen, 1992). Most also produce hydrogen gas.

Phylogenetic analysis based on 16S rRNA sequences confirms that *E. rectale* belongs to clostridial cluster XIVa as defined by Collins *et al.* (1994) within the phylum *Firmicutes* (Barcenilla *et al.*, 2000; Aminov *et al.*, 2006). *E. rectale* (Hauduroy *et al.*, 1937) appears in the 'List of Bacterial Names with Standing in Nomenclature' (<http://www.bacterio.cict.fr/>), but it is noted that the originally proposed type strain (VPI 0989^T) has been lost, and its possible replacement by another strain (VPI 0990) from the same faecal sample has not been formally proposed. The species description is from Prévot *et al.* (1967) and Moore & Holdeman (1974).

The purpose of this note is to formally propose a neotype strain for *E. rectale* based on recent isolation work. Bacterial strains that have 16S rRNA sequences closely related to *E. rectale* VPI 0990 (=ATCC 33656=CIP 105953) were newly isolated in our laboratory from stool samples provided by four healthy human volunteers (Barcenilla *et al.*, 2000; Louis *et al.*, 2004; Aminov *et al.*, 2006). These strains were loosely related to four recently

defined species of the genus *Roseburia* of human gut origin (Duncan *et al.*, 2002, 2006), but formed a distinct, tight cluster within the phylogenetic tree (Aminov *et al.*, 2006). The phenotypic properties of four of these strains, each of which was recovered from a different individual, are reported here together with those of *E. rectale* strain CIP 105953 (=VPI 0990) which was obtained from the Institut Pasteur, France. All five strains fitted the phenotypic description of *E. rectale* (Moore & Holdeman Moore, 1986) (see Supplementary Table S1 in IJSEM Online). The only observed difference was that the five strains failed to grow on arabinose, whereas fermentation of arabinose was reported for the type strain originally proposed by Moore & Holdeman Moore (1986). We are therefore proposing that one of these strains, A1-86 (=DSM 17629=NCIMB 14373, 16S rRNA gene sequence GenBank accession no. AJ270475) (Barcenilla *et al.*, 2000), should become the neotype strain for *E. rectale*. Strain A1-86 shared no more than 94% 16S rRNA gene sequence similarity with the type strains of *Roseburia intestinalis*, *Roseburia hominis*, *Roseburia faecis* and *Roseburia inulinivorans*.

E. rectale is one of the major species in the human colon that is responsible for butyrate formation. This is an important trait, as butyrate, which is one of the three major short chain fatty acids (SCFA) formed in the colon, is the preferred energy source for colonocytes and has a protective effect against colon disease (Archer *et al.*, 1998; Avivi-Green *et al.*, 2000; Pryde *et al.*, 2002).

Cells of *E. rectale* A1-86 are slightly curved slender rods of moderate (0.5 × 2.0–5.0 µm) length. Cells are Gram-positive, but decolourize readily to give a Gram-negative staining reaction. Cells from early to mid-exponential phase cultures are clearly motile when examined by phase-contrast microscopy. The DNA G + C content of *E. rectale* A1-86 is 41.2 mol%, which is similar to the values for the type strains of *R. intestinalis* (ranging from 41.1 to 42.6 mol%),

A supplementary table detailing substrate utilization by five strains of *Eubacterium rectale* is available with the online version of this paper.

Table 1. Changes in fermentation products (mM) for five strains of *Eubacterium rectale* following growth for 24 h on YCFA medium containing 0.5 % glucose

Strain	Formate	Acetate	Butyrate	Lactate	Hydrogen
A1-86	7.0	−6.41	13.7	10.3	3.5
M104/1	5.1	−0.06	9.2	9.0	5.3
L2-21	5.7	−0.05	9.2	8.8	3.5
TI-815	6.0	−4.90	11.0	9.1	4.3
VPI 0990	4.1	−3.68	10.3	9.1	3.6

R. inulinivorans (41.4 mol%), *R. faecis* (42.0 mol%) and *R. hominis* (47.4 mol%) (Duncan *et al.*, 2006).

Strain A1-86, along with four other strains of *E. rectale* (M104/1, L2-21, TI-815 and VPI 0990), is able to utilize glucose, cellobiose, melezitose, fructose, sucrose, raffinose, melibiose, soluble starch and chicory inulin as energy sources for growth in anaerobic YCFA medium, but is unable to utilize glycerol (see Supplementary Table S1 in IJSEM Online). Fermentation of sugars or carbohydrates by *E. rectale* A1-86 can be accompanied by net utilization of acetate and butyrate is formed along with lactate and formate as major products (Table 1). Abundant H₂ is also produced. No changes need be suggested to the species description for *E. rectale* as a result of the proposal of strain A1-86 as the neotype. *E. rectale* strains were originally assigned to five different groups based on phenotypic characteristics (Moore & Holdeman Moore, 1986). It should be noted however that some strains that share many of the phenotypic characteristics of this species are now classified into four novel species of the genus *Roseburia* of human gut origin, with the benefit of 16S rRNA gene sequencing (Duncan *et al.*, 2002, 2006). Cells of *E. rectale* A1-86 resemble strains belonging to the *E. rectale*-I group in being Gram-positive, slightly curved slender rods that ferment melibiose, melezitose, raffinose, sucrose and xylose. Fermentation results in the production of large quantities of H₂ (Barcenilla *et al.*, 2000) (Table 1). The neotype strain A1-86 is motile, although motility has previously been reported to be variable for this species. The definition of the four novel species of the genus *Roseburia* from the human gut (Duncan *et al.*, 2002, 2006) means that fewer strains will now be classified as *E. rectale* based on their phenotypic characteristics and 16S rRNA gene sequences, creating a tighter species than was originally proposed. Nevertheless, *E. rectale* A1-86-related sequences accounted for 1.5 % of all bacterial 16S rRNA gene sequences obtained from human faecal samples by direct PCR amplification (Aminov *et al.*, 2006) confirming that *E. rectale* should still be regarded as one of the most abundant bacterial species in the human colon.

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