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\textsuperscript{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; Andreesen, 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\textsuperscript{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 x 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%),...
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

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

*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 chichory 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 to 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, 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 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.

Acknowledgements

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References


Krumholz, L. R. & Bryant, M. P. (1986). *Eubacterium oxidoreducens* sp. nov. requiring H2 or formate to degrade gallate, pyrogallol, phloroglucinol and quercetin. *Arch Microbiol* 144, 8–14.


