Genus *Megamonas* should be placed in the lineage of *Firmicutes*, *Clostridia*, *Clostridiales*, ‘*Acidaminococcaceae*’, *Megamonas*

Masami Morotomi, Fumiko Nagai and Hiroshi Sakon

Yakult Central Institute for Microbiological Research, 1796 Yaho, Kunitachi, Tokyo 186-8650, Japan

*Megamonas hypermegale* is the sole species of the genus *Megamonas* included in the List of Prokaryotic Names with Standing in Nomenclature and in the databases of DDBJ, EBI/EMBL and NCBI/GenBank it is placed in the lineage of *Bacteroidetes*, *Bacteroidetes* (class); ‘*Bacteroidales*’; *Bacteroidaceae*; *Megamonas*. Phylogenetic analysis based on comparative 16S rRNA gene sequencing showed that this species clustered with species of the family ‘*Acidaminococcaceae*’ but not with those of the *Bacteroidaceae*. The genus *Megamonas* should be placed in the lineage of *Firmicutes*, *Clostridia*, *Clostridiales*, ‘*Acidaminococcaceae*’, *Megamonas*.

Strain DSM 1672<sup>T</sup> was isolated from chicken caecum and described as *Bacteroides hypermegae* (Harrison & Hansen, 1963), and subsequently transferred to the new genus *Megamonas* by Shah & Collins (1982). The name *Megamonas hypermegae* was validly published (Shah & Collins, 1983) and the original spelling of the specific epithet has been corrected as *Megamonas hypermegale* (Euzeby, 1998). *M. hypermegale* is the sole species of the genus *Megamonas* included in the List of Prokaryotic Names with Standing in Nomenclature and in the databases of DDBJ, EBI/EMBL and NCBI/GenBank it is given as a member of *Bacteroidetes*, *Bacteroidetes* (class); ‘*Bacteroidales*’; *Bacteroidaceae*; *Megamonas*. In 2001, the sequence of the 16S rRNA gene of *M. hypermegale* DSM 1672<sup>T</sup> was determined and deposited in the EMBL/GenBank/ DDBJ databases (J. Swiderski, unpublished; accession no. AJ420107).

The closest known relatives of *M. hypermegale* were determined by performing database searches. These sequences were retrieved from DDBJ and aligned and a phylogenetic tree was constructed according to the

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**Fig. 1.** Phylogenetic tree showing the positions of *M. hypermegale*, other species belonging to the order *Clostridiales* and type species of the order ‘*Bacteroidales*’ based on 16S rRNA gene sequence similarity data. The tree was rooted with *Escherichia coli* ATCC 11775<sup>T</sup> and constructed by using the neighbour-joining method, with bootstrap values expressed as percentages of 1000 replications. GenBank/EMBL/DDBJ accession numbers are shown in parentheses. Bar, 10% sequence divergence.
neighbour-joining method with the programs CLUSTAL_X and TreeView (Fig. 1). As indicated in Fig. 1, M. hypermegale clustered with species of the family ‘Acidaminococcaceae’. Similarity of the sequence of M. hypermegale DSM 1672\(^\text{T}\) with that of the closest type strain, Pectinatus haikarae VTT E-88329\(^\text{T}\) (= DSM 16980\(^\text{T}\)), was 93.4 %, whereas the similarity with the sequence of the type strain of the type species of Bacteroides, Bacteroides fragilis ATCC 25285\(^\text{T}\), was 70.2 %.

These data indicate that the genus Megamonas should be placed not in the lineage of Bacteroidetes, Bacteroidetes (class); 'Bacteroidales'; Bacteroidaceae; Megamonas, but in the lineage of Firmicutes; Clostridia; Clostridiales; ‘Acidaminococcaceae'; Megamonas.

References


