Taxonomic
Note

Correspondence

Masami Morotomi
masami-morotomi@yakult.co.jp

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^T was isolated from chicken caecum and described as *Bacteroides hypermegas* (Harrison & Hansen, 1963), and subsequently transferred to the new genus *Megamonas* by Shah & Collins (1982). The name *Megamonas hypermegas* was validly published (Shah & Collins, 1983) and the original spelling of the specific epithet has been corrected as *Megamonas hypermegale* (Euzéby, 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rRNA gene of *M. hypermegale* DSM 1672^T was determined and deposited in the EMBL/GenBank/DDBJ databases (J. Swiderski, unpublished; accession no.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

Fig. 1. Phylogenetic tree showing the positions of *M. hypermegale* and 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^T 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^T with that of the closest type strain, *Pectinatus haikarae* VTT E-88329^T (=DSM 16980^T), was 93.4 %, whereas the similarity with the sequence of the type strain of the type species of *Bacteroides*, *Bacteroides fragilis* ATCC 25285^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

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