Complete Genome Sequence of *Acidaminococcus intestini* RYC-MR95, a Gram-Negative Bacterium from the Phylum *Firmicutes*

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***Acidaminococcus intestini* belongs to the family Acidaminococcaceae, order Selenomonadales, class Negativicutes, phylum Firmicutes. Negativicutes show the double-membrane system of Gram-negative bacteria, although their chromosomal backbone is closely related to that of Gram-positive bacteria of the phylum Firmicutes. The complete genome of a clinical *A. intestini* strain is here presented.**

In 2007, *Acidaminococcus intestini* was defined as a new species belonging to the family *Acidaminococcaceae* (9). Its taxonomic location is controversial, with various taxonomical reassignments occurring. Initially, *Acidaminococcus* was included as a member of the family *Neisseriaceae* according to its phenotypic characteristics (12). In 1984, anaerobic Gram-negative cocci such as *Acidaminococcus* were transferred from *Neisseriaceae* to the *Veillonellaceae* family (13). Based on the 16S rRNA gene sequence, *Acidaminococcus* was reclassified as belonging to cluster IX in the class *Clostridia* in the phylum *Firmicutes* (5). Since then, this cluster has been continuously enriched with novel species (6). Recently, a new class has been proposed within the phylum *Firmicutes*, named *Negativicutes* and containing all genera with a Gram-negative cell wall, including the family *Acidaminococcaceae* (10). It has been suggested that the class *Negativicutes* could have resulted from a different evolutionary trajectory than that of traditional Gram-negative bacteria, giving more interest to assessing the complete genome of members of this class (8).

A. intestini is known to be a normal commensal of the human gut, representing ~1% of the fecal bacterial population (2). It has been occasionally related to infective processes but always associated with polymicrobial infections (3, 6, 11) and might act as a reservoir of antibiotic resistance mechanisms (7). The *A. intestini* RYC-MR95 strain was isolated from a perianal abscess of a diabetic patient. It was originally grown on brucella agar plates supplemented with hemin and vitamin K1 and incubated at 37°C in an anaerobic atmosphere. The identification was performed according to the detection of accumulated butyric acid using gas-liquid chromatography and sequencing of the 16S rRNA gene.

The genome was sequenced using the 454 GS FLX system. The starting data set before assembly contained about 400,000

GS FLX single reads and a half 3-kb paired-end run which produced about 390,000 sequences, of which about 164,000 were made by paired-end couples. All reads were assembled *de novo* by MIRA software (4). Assembly was completed manually with the use of Gap4 software from the Staden package (14). Finally, repeated and dubious regions were confirmed by Sanger resequencing.

The chromosomal size was 2,488,745 bp; 2,167 open reading frames (ORFs) were annotated covering 86.7% of the genome length; 52 tRNAs covering all bacterial amino acids and three ribosomal operons were annotated. Small ribosomal proteins RP-S1 to RP-S19 and large ribosomal proteins RP-L1 to RP-L35 and RP-L7A were also found.

A bacteriophage resistance system, CRISPR (1), was also identified; it comprised 52 repeats as well as at least two CRISPR-associated proteins.

Nucleotide sequence accession number. The genome was deposited in GenBank under accession number CP003058.

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