Genome Sequences of the Guillain-Barré Syndrome Outbreak-Associated Campylobacter jejuni Strains ICDCCJ07002 and ICDCCJ07004

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The first world-known and largest outbreak of 36 cases of Guillain-Barré syndrome caused by a preceding Campylobacter jejuni infection was reported previously in China. During the outbreak, Campylobacter jejuni strain ICDCCJ07002 was isolated from a patient with persistent diarrhea for 21 days, and C. jejuni strain ICDCCJ07004 was from a healthy carrier without any clinical symptoms at the same time. Here, we report the draft genome sequence of strain ICDCCJ07002 (1,698,407 bp, with a G+C content of 30.45%) and the genome resequencing result of strain ICDCCJ07004 (1,701,584 bp, with a G+C content of 30.51%), and we compared these with the completed genome of C. jejuni strain ICDCCJ07001.

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