Draft Genome Sequence of the Nontoxigenic \textit{Clostridium difficile} Strain CD37

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Here we report the draft genome sequence of \textit{Clostridium difficile} strain CD37, the first nontoxigenic strain sequenced. Every sequenced strain of \textit{Clostridium difficile} has been shown to contain multiple different mobile genetic elements. The draft genome sequence of strain CD37 reveals the presence of two putative conjugative transposons.

\textit{Clostridium difficile} is an anaerobic, spore-forming, Gram-positive bacterium that is an opportunistic pathogen of humans and other mammals (2). The main virulence factors are the toxins A and B and the less-well-characterized binary toxin (18). Interestingly, nontoxigenic \textit{C. difficile} strains (which lack the genes for toxins A and B and the binary toxin) are relatively common, although little is known about their biology (18). \textit{C. difficile} has previously been shown to contain various mobile genetic elements, such as conjugative transposons (5, 6, 17, 19, 20), mobilizable transposons (11), prophages (12), and other elements, such as the IStron (4) and the \textit{C. difficile} skin (\textit{skin}CD) element (13).

Genome shotgun sequencing of strain CD37, ribotype 009 (5), was performed using an Illumina GAII-X. A total of 7,515,781 high nucleotide sequence similarity to CTn\textit{4} and CTn\textit{7} of strain 630 (\textit{96\% and \textit{98\%}, respectively). These mobile genetic elements, such as conjugative transposons (5, 6, 17, 19, 20), mobilizable transposons (11), prophages (12), and other elements, such as the IStron (4) and the \textit{C. difficile} skin (\textit{skin}CD) element (13).

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited in DDBJ/EMBL/GenBank under accession number AHJJ00000000. The version described in this paper is the first version, AHJJ01000000.

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