Genome Sequences of Two Nondomesticated *Bacillus subtilis* Strains Able To Form Thick Biofilms on Submerged Surfaces

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Genomes of two nondomesticated strains of *Bacillus subtilis* subspecies *subtilis*, NDmed and NDfood, have been sequenced. Both strains form very thick and spatially complex biofilms on submerged surfaces. Moreover, biofilms of the NDmed isolate were shown to be highly resistant to antimicrobials action.

*Bacillus subtilis* is a non-pathogenic Gram-positive bacterium largely used in biotechnological processes and academic research. Although this bacterium is mainly found in the soil, several strains have recently been isolated from other environments (1–6). *B. subtilis* is able to form structured biofilms in which cells are embedded in a self-produced matrix of polymers. For studying biofilm properties and the associated genetic regulation, most researchers have used the “less domesticated” strain NCIB3610 instead of the reference strain 168, which is defective for determinants involved in multicellular behavior (7). Here we present the genome sequences of two *B. subtilis* natural isolates. The first strain, NDmed, was isolated from an endoscope washer disinfectant in a hospital in England (8). The second strain, NDfood, was isolated from a dairy product in France (9). Both strains are able to form spatially organized biofilms with protruding structures on submerged surfaces as well as wrinkled macrocolonies and robust pellicles (9). In addition, submerged biofilms of NDmed exhibited high resistance to antimicrobials and the ability to protect pathogens (10).

Genome sequencing of *B. subtilis* NDmed and NDfood strains was performed using Illumina MiSeq technology. A total of 4,595,294 and 3,622,152 reads were obtained for NDmed and NDfood, respectively. The raw sequences generated were mapped to the reference strain 168 genome (11) and using the CLC NGS assembler, the reads were assembled into 10 contigs for NDmed (ranging from 4.9 kb to 1.2 Mb) and 12 contigs for NDfood (ranging from 1.4 kb to 1.1 Mb), with an average coverage of 271-fold and 214-fold, respectively. For both strains the total size of the assembly was around 4.06 Mb and the G+C content about 43.7%.

Comparison of NDmed and NDfood sequences to the genome shotgun projects have been deposited at DDBJ/EMBL/GenBank under the accession numbers JPVW00000000 for *B. subtilis* NDmed and JPVX00000000 for *B. subtilis* NDfood. The versions described in this paper are the first versions, JPVW01000000 and JPVX01000000.

**Nucleotide sequence accession numbers.** These two whole-genome shotgun projects have been deposited at DDBJ/EMBL/GenBank under the accession numbers JPVW00000000 for *B. subtilis* NDmed and JPVX00000000 for *B. subtilis* NDfood. The versions described in this paper are the first versions, JPVW01000000 and JPVX01000000.

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