Complete Genome Sequence of Bacillus subtilis subsp. subtilis Strain ∆6

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Bacillus subtilis ∆6 is a genome-reduced strain that was cured from six prophages and AT-rich islands. This strain is of great interest for biotechnological applications. Here, we announce the full-genome sequence of this strain. Interestingly, the conjuga-
tive element ICEBs1 has most likely undergone self-excision in B. subtilis ∆6.

Bacillus subtilis ∆6 is a derivative of the laboratory wild-type strain B. subtilis 168, which was cured from six prophages and AT-rich islands. For this purpose, the prophages SPβ and PBSX, the prophage-like elements prophage 1, prophage 3, and skin, as well as the polyketide synthase operon pks were deleted. Inter-
stingly, this genome reduction by 7.7% did not have a major impact on physiology, metabolic flux patterns, or genetic competence (1).

B. subtilis ∆6 is a promising starting point for further genome reduction. Moreover, it can serve as a chassis strain in the context of biotechnological applications, that is, highly efficient protein secretion and vitamin production (2–4). Indeed, B. subtilis ∆6 has recently been used to obtain a total genome reduction of 13.6% (5). For a better understanding with respect to future projects, we have sequenced the genome of B. subtilis ∆6. The chromosomal DNA was isolated from a stationary phase culture using a commer-
cially available kit (peqGOLD Bacterial DNA Kit, VWR International GmbH). We obtained 6.63 million reads from an Illu-
mina 75-bp single-read run and mapped them to the B. subtilis 168 genome (GenBank accession number NC_000964) (6) using the Geneious Read Mapper (Geneious version 9.0.5 software, Biom-
atters, Ltd.) (7). The alignment showed a 118-fold average cover-
age and a 99.5% pairwise identity to the reference genome of B. subtilis 168. The insertion and the correct sequence of the chlor-
amphenoil resistance gene at the pks operon locus were verified

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