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Reuß, Daniel R; Thürmer, Andrea; Daniel, Rolf; Quax, Wim J; Stülke, Jörg

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# Complete Genome Sequence of *Bacillus subtilis* subsp. *subtilis* Strain $\Delta 6$

Daniel R. Reuß,<sup>a</sup> Andrea Thürmer,<sup>b</sup> Rolf Daniel,<sup>b</sup> Wim J. Quax,<sup>c</sup> Jörg Stülke<sup>a</sup>

Department of General Microbiology, Georg-August-University Göttingen, Göttingen, Germany<sup>a</sup>; Department of Genomics and Applied Microbiology and Göttingen Genomics Laboratory, Georg-August-University Göttingen, Göttingen, Germany<sup>b</sup>; Groningen Research Institute of Pharmacy, University of Groningen, Groningen, The Netherlands<sup>c</sup>

***Bacillus subtilis*  $\Delta 6$  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 conjugative element ICEBs1 has most likely undergone self-excision in *B. subtilis*  $\Delta 6$ .**

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Address correspondence to Jörg Stülke, [jstuelk@gwdg.de](mailto:jstuelk@gwdg.de).

*Bacillus subtilis*  $\Delta 6$  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 SP $\beta$  and PBSX, the prophage-like elements prophage 1, prophage 3, and *skin*, as well as the polyketide synthesis operon *pks* were deleted. Interestingly, this genome reduction by 7.7% did not have a major impact on physiology, metabolic flux patterns, or genetic competence (1).

*B. subtilis*  $\Delta 6$  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*  $\Delta 6$  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*  $\Delta 6$ . The chromosomal DNA was isolated from a stationary phase culture using a commercially available kit (peqGOLD Bacterial DNA Kit, VWR International GmbH). We obtained 6.63 million reads from an Illumina 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, Biomatters, Ltd.) (7). The alignment showed a 118-fold average coverage and a 99.5% pairwise identity to the reference genome of *B. subtilis* 168. The insertion and the correct sequence of the chloramphenicol resistance gene at the *pks* operon locus were verified by a standard PCR. The final genome sequence of *B. subtilis*  $\Delta 6$  has a length of 3,876,919 bp.

We identified 28 variations (single-nucleotide polymorphism, deletion, insertion, and substitution) with a minimal coverage of 25 $\times$  and a minimum variant frequency of 0.8. Four of these mutations have an effect on the amino acids sequence of the encoded protein (*carA*, *yobM*, *ywbD*, and *walH*), whereas four mutations are silent (*yczC*, *yjnA*, *glcF*, and *amyX*). The remaining 20 variants are located in intergenic and RNA-encoding regions. All variations can be requested from the corresponding author. In addition, we could confirm the presence of all six deletions performed by Westers et al. (1). Interestingly, *B. subtilis*  $\Delta 6$  contains a seventh

large deletion of 20.5 kb (25 genes; genome position: 529,422 to 549,925 bp). This deletion corresponds to the mobile genetic element ICEBs1 (8), which likely has undergone self-excision, as it has been reported for other *B. subtilis* strains (9). Taken together, *B. subtilis*  $\Delta 6$  is lacking 376 genes at seven different locations covering 8.03% of the reference genome of *B. subtilis* 168. These deletions increased the GC content from 43.5% to 43.9%.

**Nucleotide sequence accession number.** The genome sequence of *B. subtilis* subsp. *subtilis* strain  $\Delta 6$  is deposited in GenBank under the accession number CP015975.

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