Complete Sequence of the First Chimera Genome Constructed by Cloning the Whole Genome of Synechocystis Strain PCC6803 into the Bacillus subtilis 168 Genome

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Genome synthesis of existing or designed genomes is made feasible by the first successful cloning of a cyanobacterium, Synechocystis PCC6803, in Gram-positive, endospore-forming Bacillus subtilis. Whole-genome sequence analysis of the isolate and parental B. subtilis strains provides clues for identifying single nucleotide polymorphisms (SNPs) in the 2 complete bacterial genomes in one cell.

A method to connect small DNA segments in Bacillus subtilis, originally termed megacloning, enabled the combination of a whole genome from Synechocystis PCC6803 with the B. subtilis genome (3). When the project started in 1997, the sequence of the whole bacterial genome to be used was the minimal requirement for such an approach. This prerequisite, combined with the fact that the strain is not harmful to humans, led us to choose the Synechocystis PCC6803 strain for the project. The chimeric genome strain BEST7613 (3) has raised a number of poorly argued issues (1). To the best of our knowledge, growth of Synechocystis in a suitable medium, a complete synthetic medium for photosynthesis with no carbon sources, has not been achieved yet; therefore, BEST7613 must always be cultivated in a B. subtilis growth medium. Given that the genomes from the Synechocystis genome are properly expressed, conversion of the cellular gene regulatory network from that of B. subtilis to that of the other partner is expected. A number of factors and components that were provided by a switch in gene expression from the other partner is expected. A number of factors and components that were provided by a switch in gene expression from the other partner is expected. A number of factors and components that were provided by a switch in gene expression from the other partner is expected.

The genome sequences for these strains have been deposited at DDBJ/EMBL/GenBank under accession numbers AP012495 (BEST7613) and AP012496 (BEST7003).

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REFERENCES