

1 **Genomic insights into the taxonomic status of the *Bacillus cereus* group**

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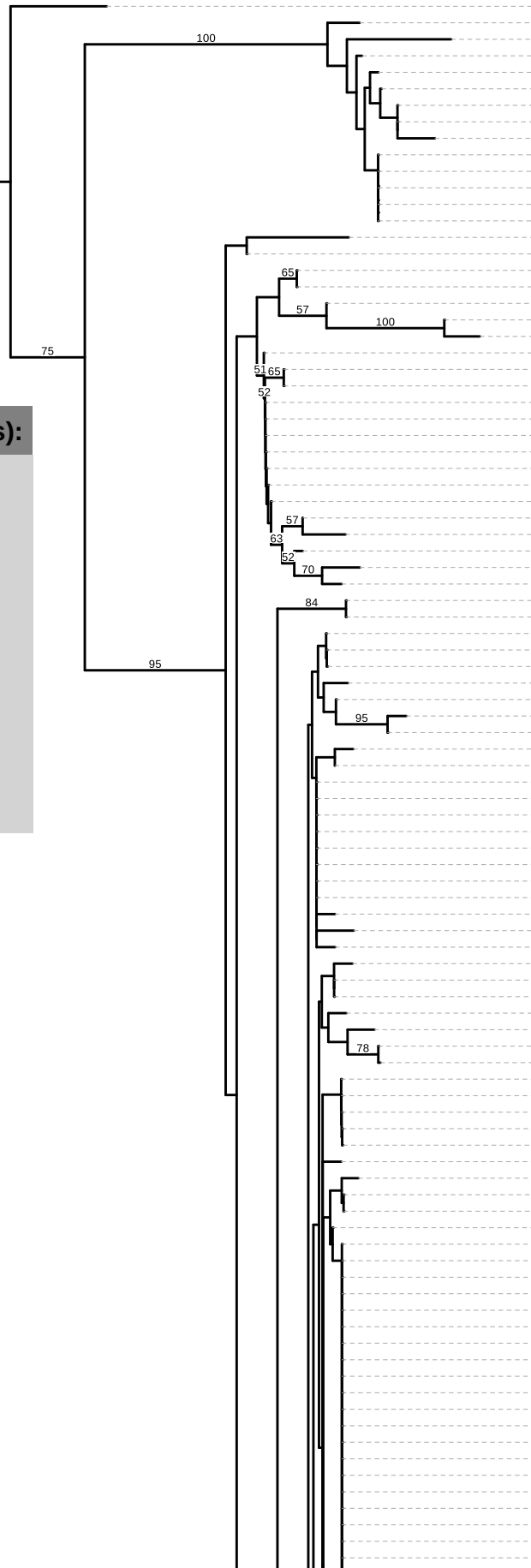
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Supplementary Data

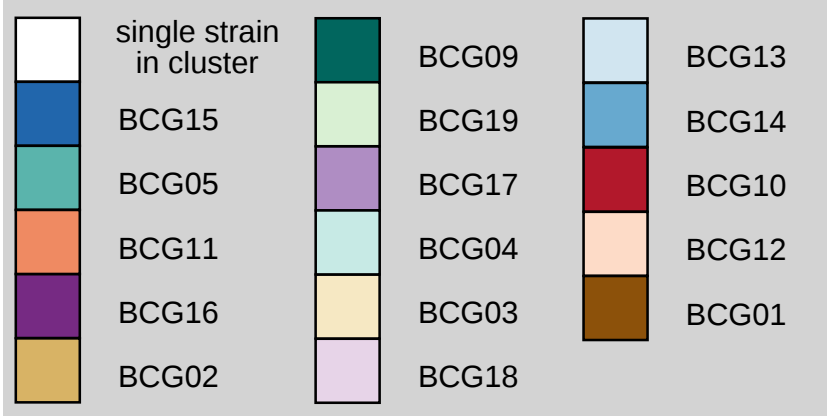
- Data S1 | Complete list of the 225 strains used in this study with detailed annotations
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Figure S1 | Whole-genome phylogeny of 224 bacteria of the *B. cereus* group inferred using the latest GBDP version and rooted with *Bacillus subtilis* ATCC 6051^T. Numbers above branches are greedy-with-trimming pseudo-bootstrap support values from 100 replicates if larger than 50%. Leaves are colored according to their affiliation to clusters. The three outer circles show whether or not the (i) *cry* locus, (ii) pXO1(-like) plasmid and/or the (iii) pXO2(-like) plasmid is found. Type strains are printed with “T”. The strains with a complete genome sequence are marked by an asterisk (*). The tree was inferred using FastME and visualized using iTOL. The leaf labels are strain names according to the NCBI database. Please note that the species names “*B. gaemokensis*”, “*B. manliponensis*” and “*B. bingmayongensis*” are effectively but not yet validly published.

*B. subtilis**
 BCG07-01-01*
 BCG08-01-08*
 BCG08-01-01*
 BCG08-01-05*
 BCG08-01-06*
 BCG08-01-13*
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Clusters (see color of leaves; numbers are cluster IDs):



— 0.001

64

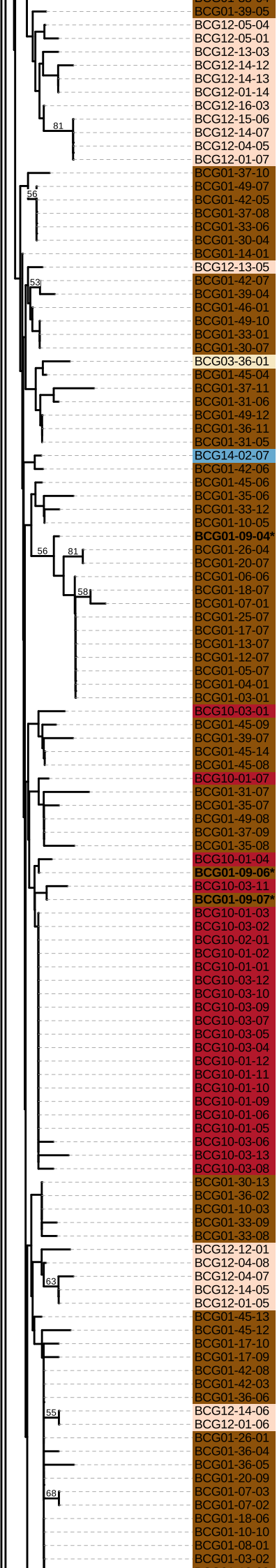
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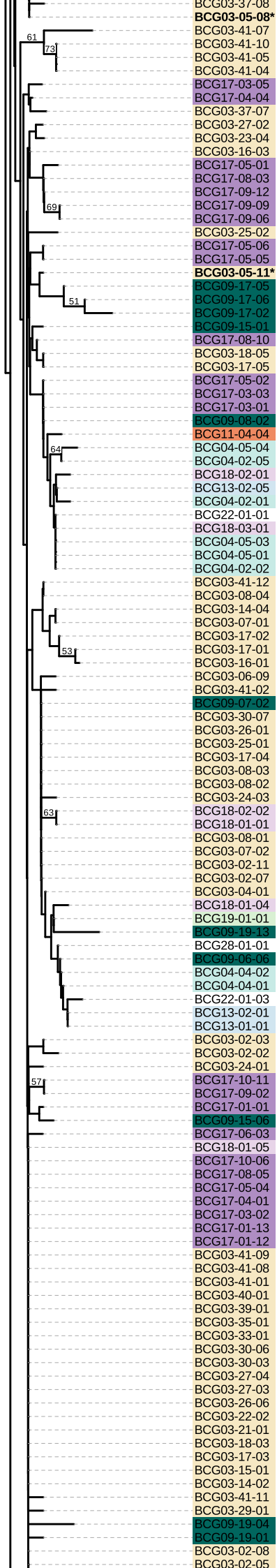
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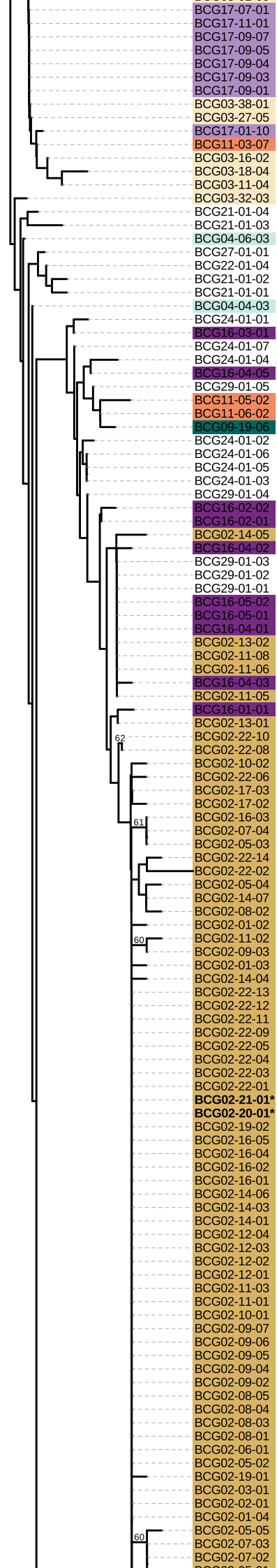


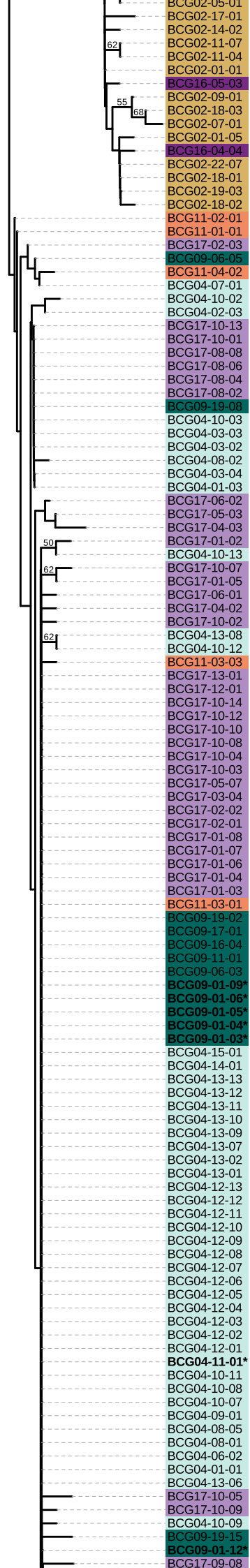
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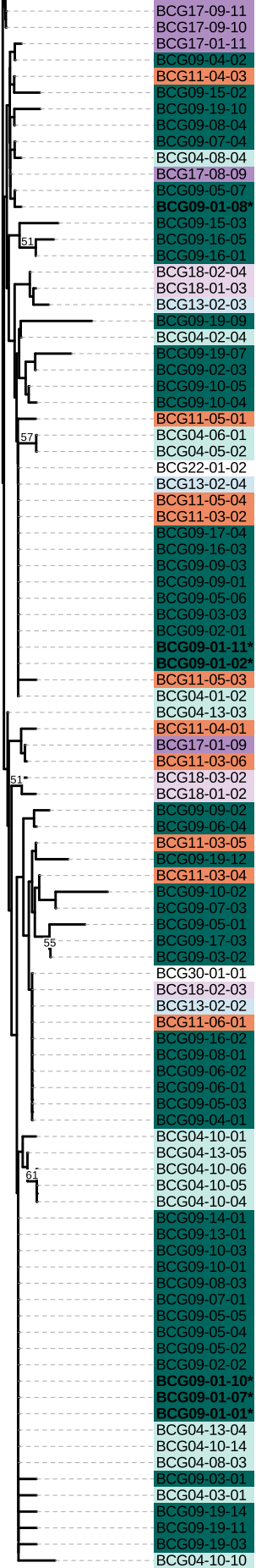
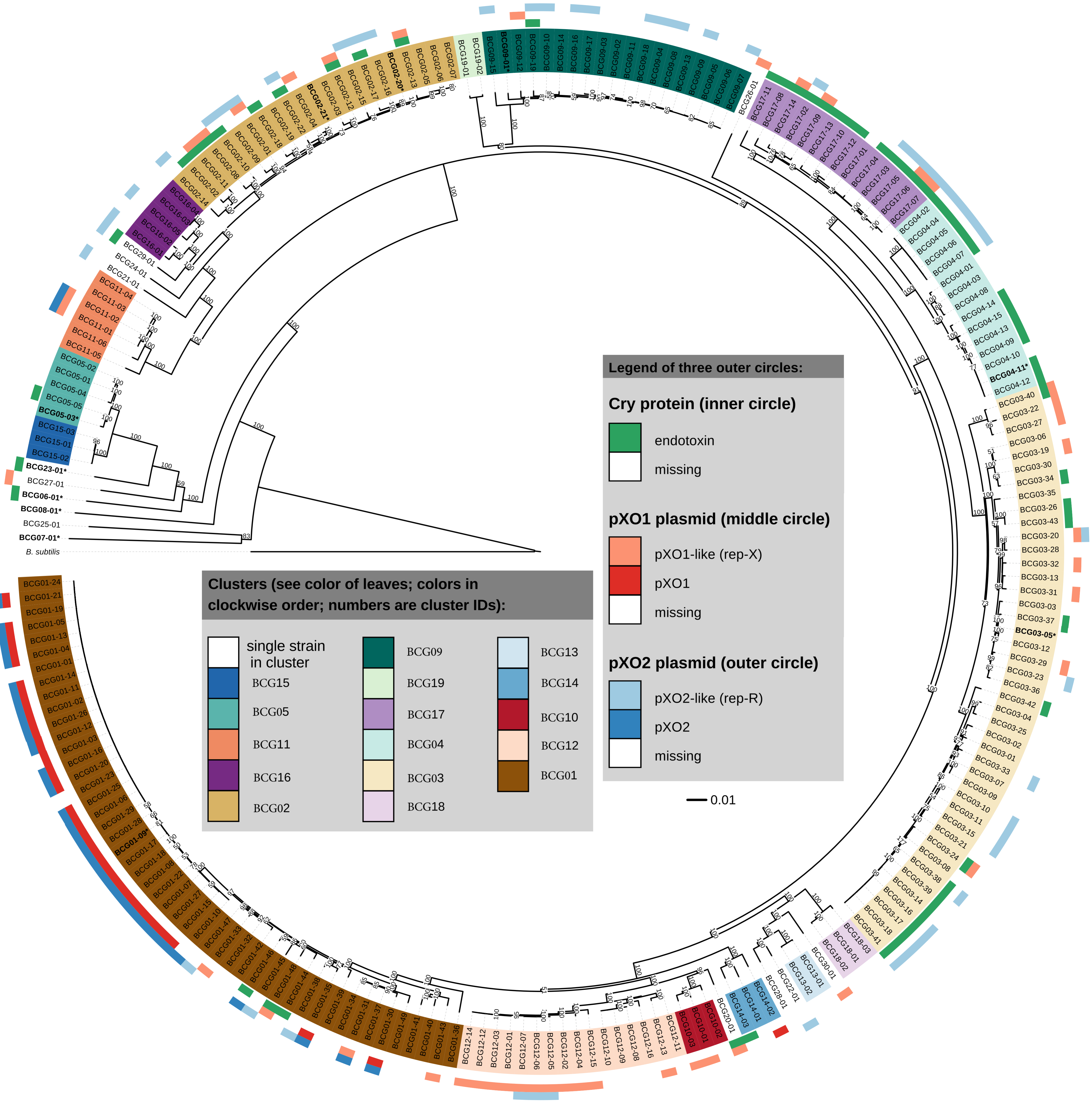


Figure S2 | Phylogenetic tree inferred from 1007 copies of the 16S rRNA gene of 202 bacteria of the *B. cereus* group. A total of 1007 copies of the 16S rRNA gene were complete from site 352 to site 1051 in the complete 16S rRNA gene, and used to construct the tree. *B. subtilis* ATCC 6051^T (BSU6051_0082022) was used as the outgroup. The 16S rRNA genes extracted from type strains are marked by the asterisk symbol (*) and printed in bold font. See the main text for more descriptions.



Legend of three outer circles:

Cry protein (inner circle)

- endotoxin
- missing

pXO1 plasmid (middle circle)

- pXO1-like (rep-X)
- pXO1
- missing

pXO2 plasmid (outer circle)

- pXO2-like (rep-R)
- pXO2
- missing

— 0.01

Clusters (see color of leaves; colors in clockwise order; numbers are cluster IDs):

- | | | |
|---|---|--|
| single strain in cluster | BCG09 | BCG13 |
| BCG15 | BCG19 | BCG14 |
| BCG05 | BCG17 | BCG10 |
| BCG11 | BCG04 | BCG12 |
| BCG16 | BCG03 | BCG01 |
| BCG02 | BCG18 | |

Figure S3 | nMLSA-based phylogenetic tree of 224 bacteria of the *B. cereus* group using 20 housekeeping genes. Numbers on branches are bootstrap support values from 1,000 replicates given in percent. Branches are scaled in terms of the expected number of substitutions per site. Leaves are colored according to their affiliation to clusters (compare Figure 1). The three outer circles show whether or not the (i) *cry* locus, (ii) pXO1(-like) plasmid and/or the (iii) pXO2(-like) plasmid are found. Type strains are printed in bold font and marked by an asterisk (*). *Bacillus subtilis* ATCC 6051^T (CP003329) was used as the outgroup.



Legend of three outer circles:

Cry protein (inner circle)

- endotoxin
- missing

pXO1 plasmid (middle circle)

- pXO1-like (rep-X)
- pXO1
- missing

pXO2 plasmid (outer circle)

- pXO2-like (rep-R)
- pXO2
- missing

— 0.01

Clusters (see color of leaves; colors in clockwise order; numbers are cluster IDs):

 single strain in cluster	 BCG09	 BCG13
 BCG15	 BCG19	 BCG14
 BCG05	 BCG17	 BCG10
 BCG11	 BCG04	 BCG12
 BCG16	 BCG03	 BCG01
 BCG02	 BCG18	

Figure S4 | Phylogenetic trees inferred from the *ccpA* gene of 224 bacteria of the *B. cereus* group. Numbers on branches are bootstrap support values from 1,000 replicates given in percent. Branches are scaled in terms of the expected number of substitutions per site. Leaves are colored according to their affiliation to clusters (compare Figure 1). The three outer circles show whether or not the (i) *cry* locus, (ii) pXO1(-like) plasmid and/or the (iii) pXO2(-like) plasmid are found. Type strains are printed in bold font and marked by an asterisk (*). *Bacillus subtilis* ATCC 6051^T (CP003329) was used as the outgroup.