# Supplementary information

## Cyclic lipopeptides fengycins from marine bacterium *Bacillus subtilis* kill plant pathogenic fungus *Magnaporthe grisea* by inducing reactive oxygen species production and chromatin condensation

Linlin Zhang[a,b,c,d], Chaomin Sun[a,b,d*]

CAS Key Laboratory of Experimental Marine Biology, Institute of Oceanology, Chinese Academy of Sciences, Qingdao, 266071, China[a]; Laboratory for Marine Biology and Biotechnology, Qingdao National Laboratory for Marine Science and Technology, Qingdao, 266071, China[b]; University of Chinese Academy of Sciences, Beijing, 100049, China[c]. Center for Ocean Mega-Science, Chinese Academy of Sciences, Qingdao, 266071, China[d].

*Corresponding author

Chaomin Sun Tel.: +86 532 82898857; fax: +86 532 82898648.

E-mail address: sunchaomin@qdio.ac.cn

**TABLE S1** General genome features of *B. subtilis* BS155

| Features | Value |
|---|---|
| Genome size (bp) | 4,325,794 |
| G+C content (%) | 43.49 |
| Chromosome | 1 |
| Total number of genes | 6,222 |
| rRNAs | 30 |
| tRNAs | 86 |
| Genomic island | 10 |
| NRPS and PKS | 11 |

**TABLE S2** Oligonucleotides used in this study

| Oligonucleotides | Sequence (5'-3') |
|---|---|
| Actin-se | AGCGTGGTATCCTCACTTTGC |
| Actin-an | ATCTGCGTCATCTTCTCTCGG |
| Conden1-se | ACATCTGCCTCGAGCAATACG |
| Conden1-an | AGCCTTGGGCTTCAGGAACA |
| Conden2-se | TGTGCGTGTCGGCAGAATACT |
| Conden2-an | CATGTCACCAAGGGCGATAAC |

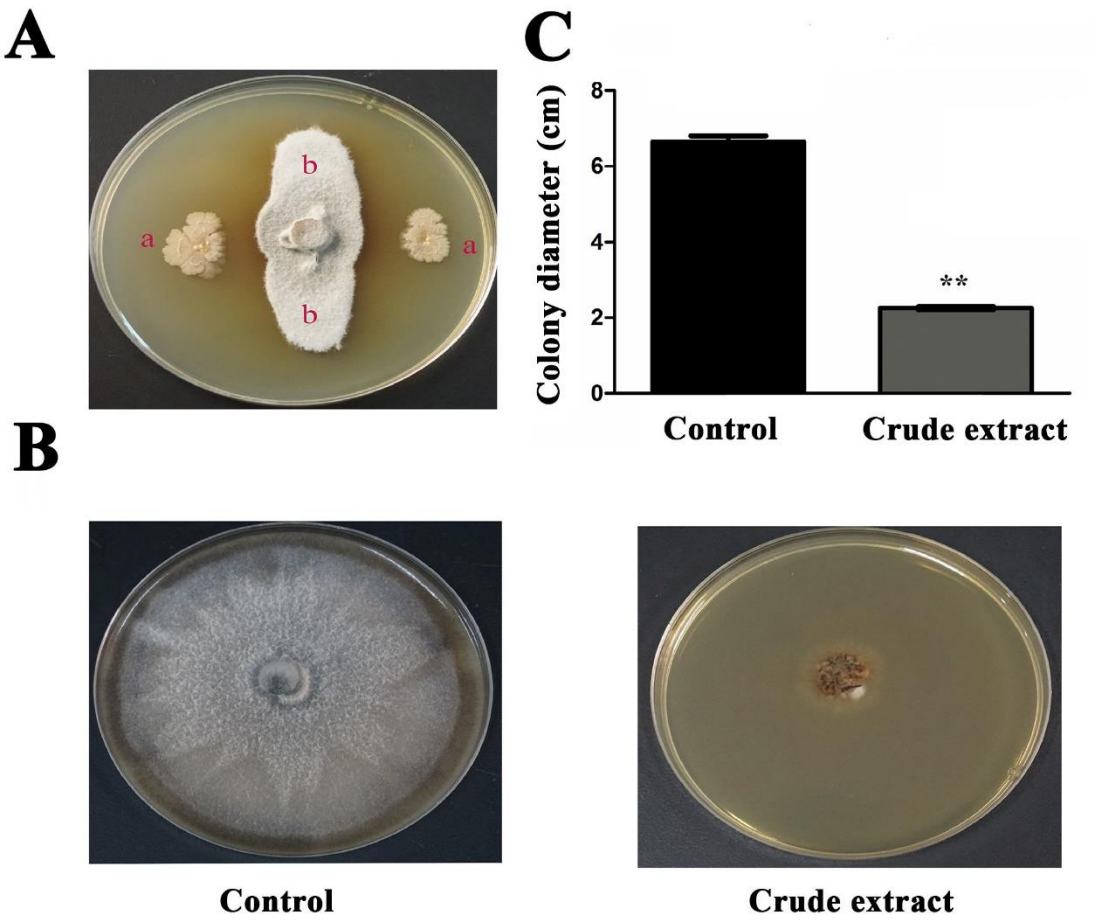



**FIG S1** Antifungal activity of marine strain *B. subtilis* BS155 and its crude extract against *Magnaporthe grisea*. (A) Antagonistic activity of marine bacterium *B. subtilis* BS155 against *M. grisea*. a, strain *B. subtilis* BS155; b, fungal pathogen *M. grisea*. (B) Representative pictures of antagonistic activity assay of crude extracts (40 μg/mL) from *B. subtilis* BS155 against *M. grisea.* (C) Quantitative assays of antagonistic activity of crude extracts (40 μg/mL) from *B. subtilis* BS155 against *M. grisea*. **, $P < 0.01$.

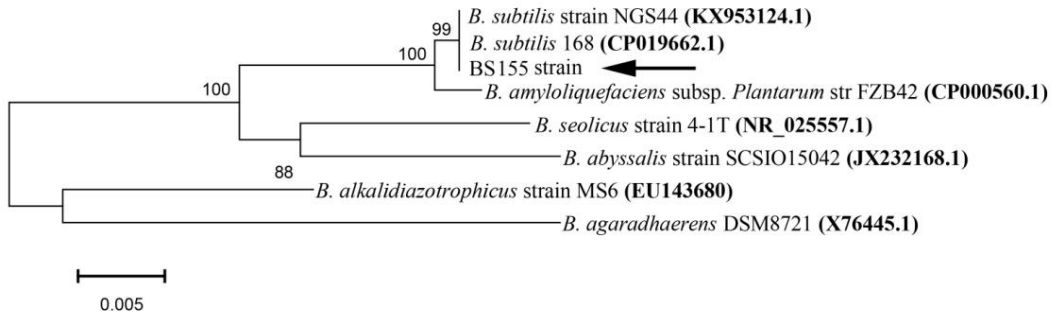



**FIG S2** The consensus phylogenetic tree of marine bacterium BS155 with other related strains obtained from GenBank (accession numbers are indicated after the species name) constructed by the neighbor-joining method, respectively. Numbers above the branches are bootstrap values based on 1000 replicates.

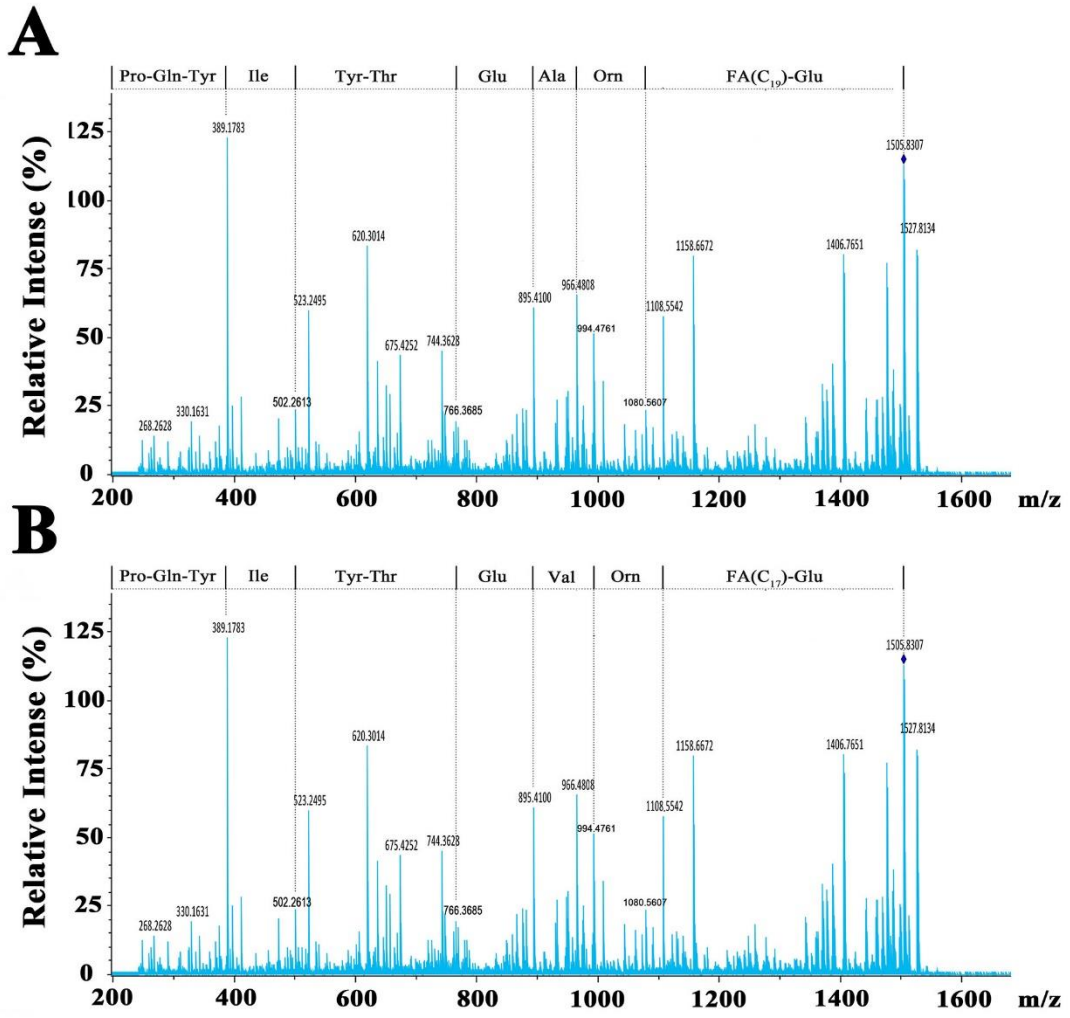
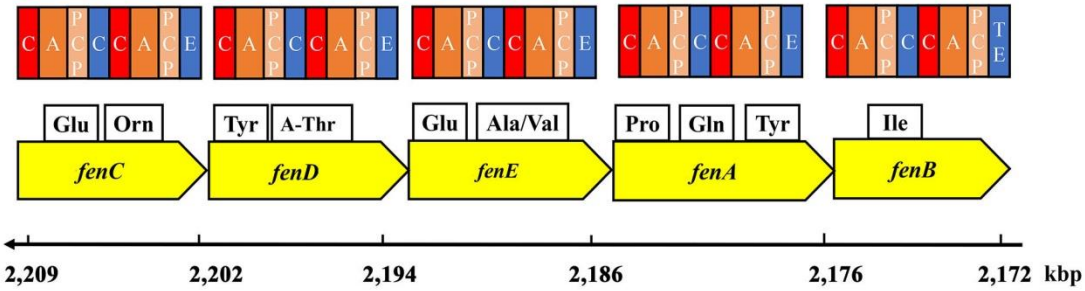



**FIG S3** Fragmentation MS/MS spectrum of active compound peaks isolated from *B. subtilis* BS155. (A) The MS/MS spectrum of $C_{19}$ fengycin A ion peaks from 200 Da to 1800 Da. (B) The MS/MS spectrum of $C_{17}$ fengycin B ion peaks from 500 Da to 1500 Da.




***fenA-E* gene cluster in *B. subtilis* BS155**

**FIG S4** The predicted *fenA-E* gene cluster which was responsible for fengycin BS155 biosynthesis in the genome of *B. subtilis* BS155.

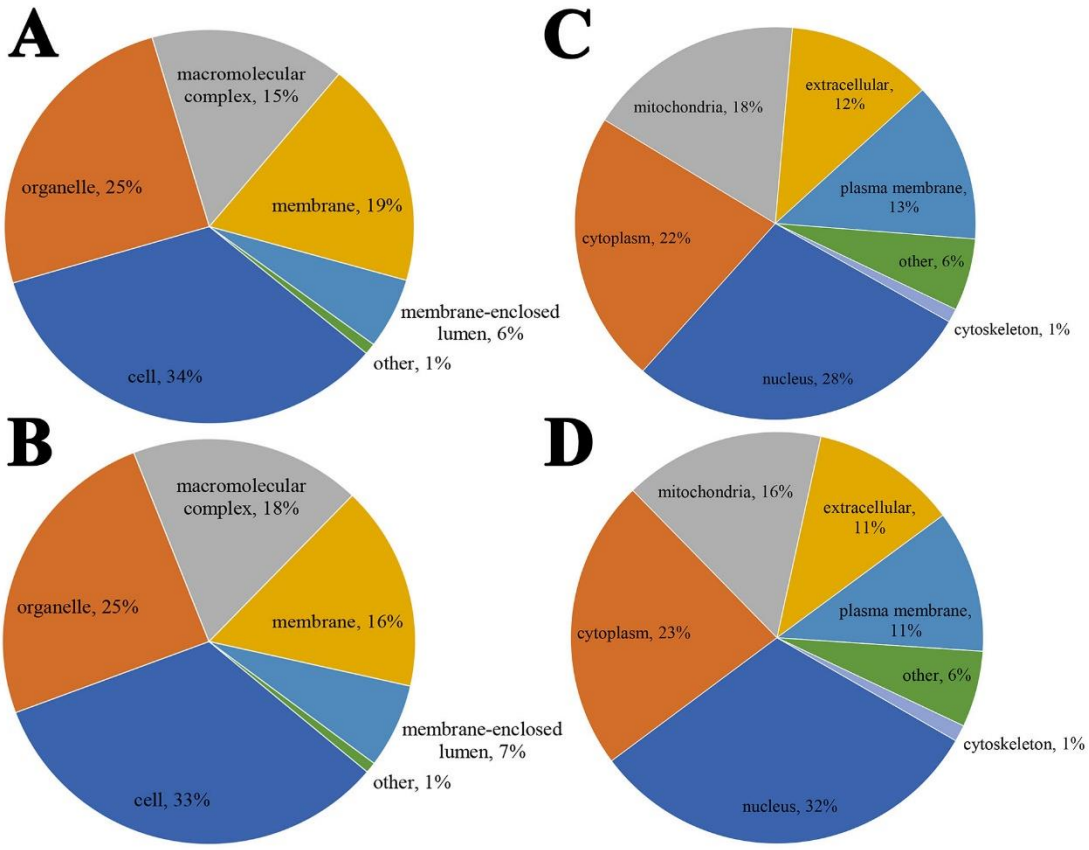



**FIG S5** Hyphal cellular component cluster analyses of differentially expressed proteins according to the gene ontology annotation after *M. grisea* hypha was treated with 20 μg/ml (A) and 50 μg/ml fengycin BS155 (B). Subcellular localization analyses of differentially expressed proteins after the hyphal cells were treated with 20 μg/ml (C) and 50 μg/ml fengycin BS155 (D).