

A New Biocontrol Agent *Bacillus velezensis* SF334 Against Rubber Tree Fungal Leaf Anthracnose and Its Genome Analysis of Versatile Plant Probiotic Traits

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Table S1. The plant growth promotion-associated genes in *B. velezensis* SF334

| Gene ID | KO | Gene | Function | Class |
|---------------|--------|-------------------|--------------------------------------|---|
| SF334GL002344 | K01695 | <i>trpA</i> | tryptophan synthase alpha chain | Phenylalanine, tyrosine and tryptophan biosynthesis |
| SF334GL003147 | K14155 | <i>patB, malY</i> | cysteine-S-conjugate beta-lyase | Biosynthesis of secondary metabolites |
| SF334GL002056 | K00128 | <i>aldh</i> | aldehyde dehydrogenase (NAD+) | Tryptophan metabolism |
| SF334GL002972 | K00128 | <i>aldh</i> | aldehyde dehydrogenase (NAD+) | Tryptophan metabolism |
| SF334GL004032 | K00128 | <i>aldh</i> | aldehyde dehydrogenase (NAD+) | Tryptophan metabolism |
| SF334GL002345 | K01696 | <i>trpB</i> | tryptophan synthase beta chain | Phenylalanine, tyrosine and tryptophan biosynthesis |
| SF334GL002347 | K01609 | <i>trpC</i> | indole-3-glycerol phosphate synthase | Phenylalanine, tyrosine and tryptophan biosynthesis |

Table S2. General features of genomes of *B. velezensis* SF334, *B. velezensis* FZB42, *B. velezensis* SQR9, *B. amyloliquefaciens* DSM7, and *B. subtilis* 168

| General features | <i>B. velezensis</i> SF334 | <i>B. velezensis</i> FZB42 | <i>B. velezensis</i> SQR9 | <i>B. amyloliquefaciens</i> DSM7 | <i>B. subtilis</i> 168 |
|--------------------------------|--------------------------------------|--------------------------------------|-------------------------------------|--|----------------------------------|
| Genome size (bp) | 4,078,641 | 3,918,596 | 4,117,023 | 3,980,199 | 4,227,167 |
| GC content | 46.5% | 46.48% | 46.10% | 46.08% | 43.49% |
| Coding density (%) | 89.33 | 89.026 | 89.68 | 88.54 | 88.33 |
| Protein coding sequences (CDS) | 4,142 | 3,888 | 4,111 | 4,220 | 4,388 |
| tRNA | 86 | 89 | 72 | 94 | 86 |
| 5s rRNA | 9 | 10 | 7 | 10 | 10 |
| 16s rRNA | 9 | 9 | 7 | 10 | 10 |
| 23s rRNA | 9 | 10 | 7 | 10 | 10 |
| Repeat region | 30 | 31 | 20 | 43 | 38 |

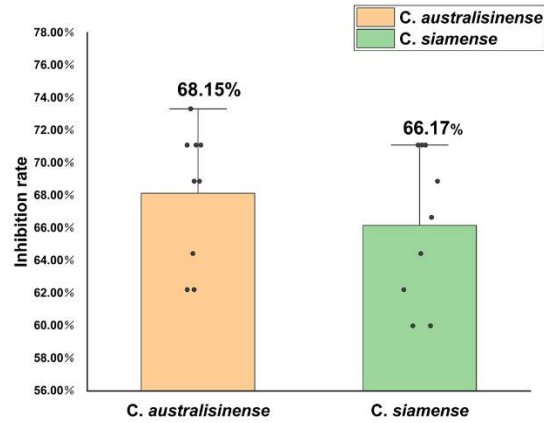


Figure S1. Antagonistic effect of strain SF334 against *C. siamense* and *C. australisnense*, which are major pathogens causing leaf anthracnose of rubber trees in the Hainan province of China. The average inhibition rates of SF334 against *C. siamense* and *C. australisnense* were calculated.

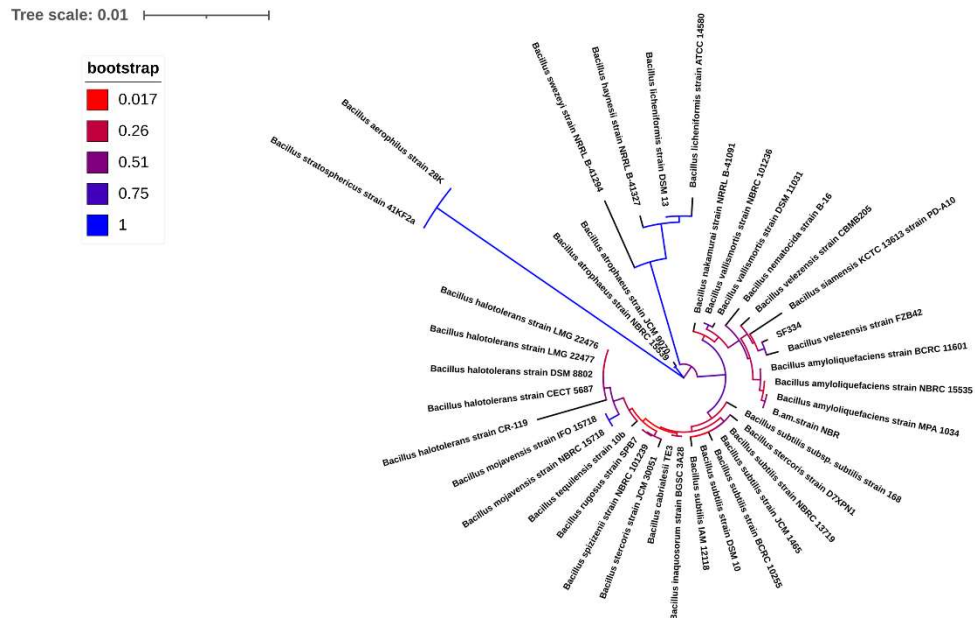


Figure S2. The phylogenetic tree of strain SF334 based on 16S *rDNA* sequences constructed through the TYGS platform. The sequence of 16S *rRNA* of 39 strains with the lowest E-value in the National Center for Biotechnology Information (NCBI) database were selected as the reference sequences. The results were finally imported into MEGA 11 soft to construct a phylogenetic tree by the NJ (1200 bootstrap) method.

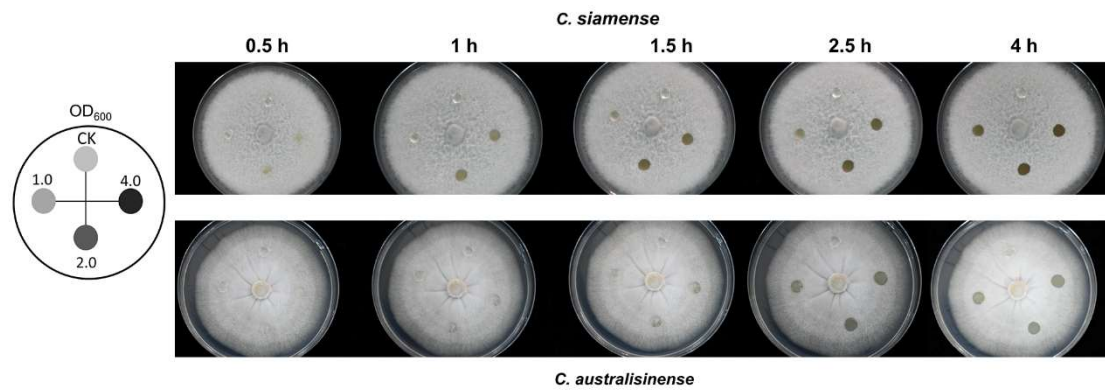


Figure S3. Observation of the hyphal lysis of *C. siamense* and *C. australisinese* when interacting with the CSs of *B. velezensis* SF334 on PDA plates. The mycelium of *C. siamense* and *C. australisinese* were inoculated with the indicated bacterial concentration for 0.5 h, 1 h, 1.5 h, 2.5 h and 4 h.

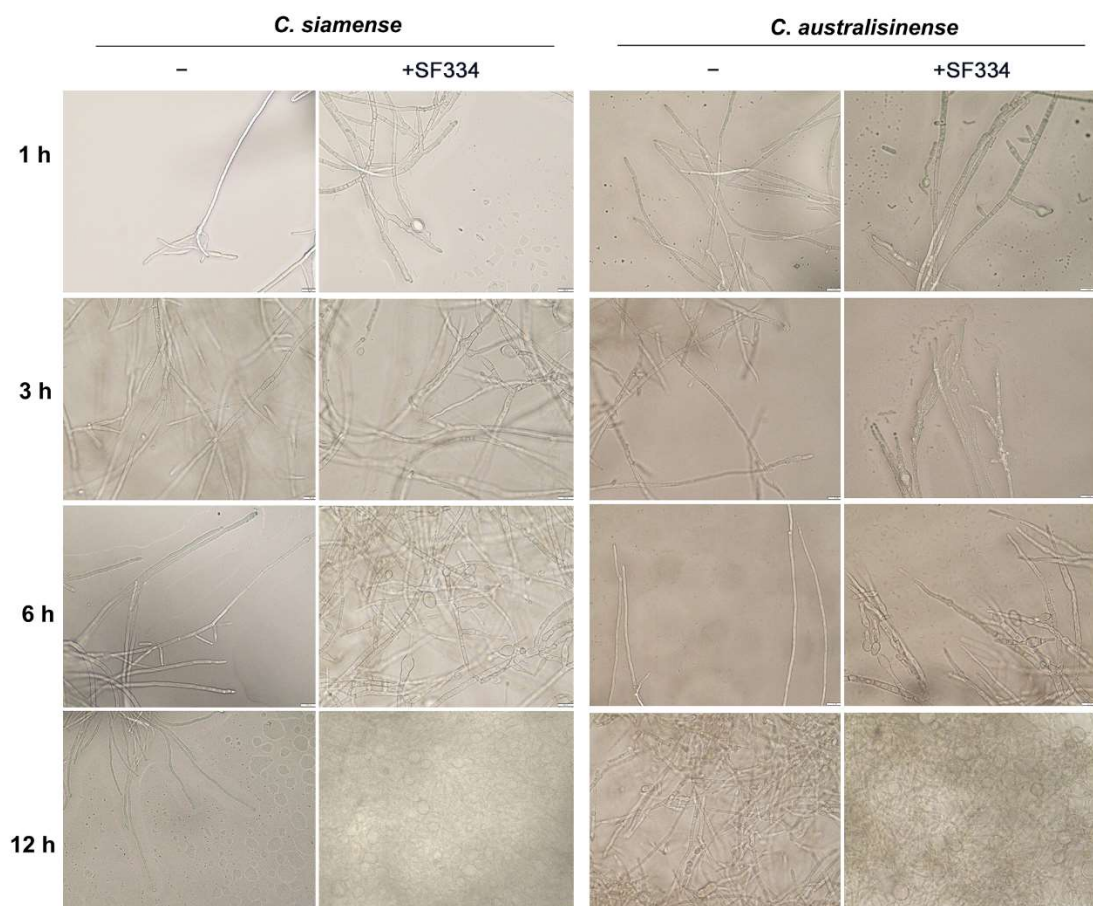


Figure S4. Observation of mycelium morphology of *C. siamense* and *C. australisinese* when interacting with the CSs of *B. velezensis* SF334 for 1 h, 3 h, 6 h, and 12 h in PDB medium using an optical microscope. Scale bar, 10 μ m.

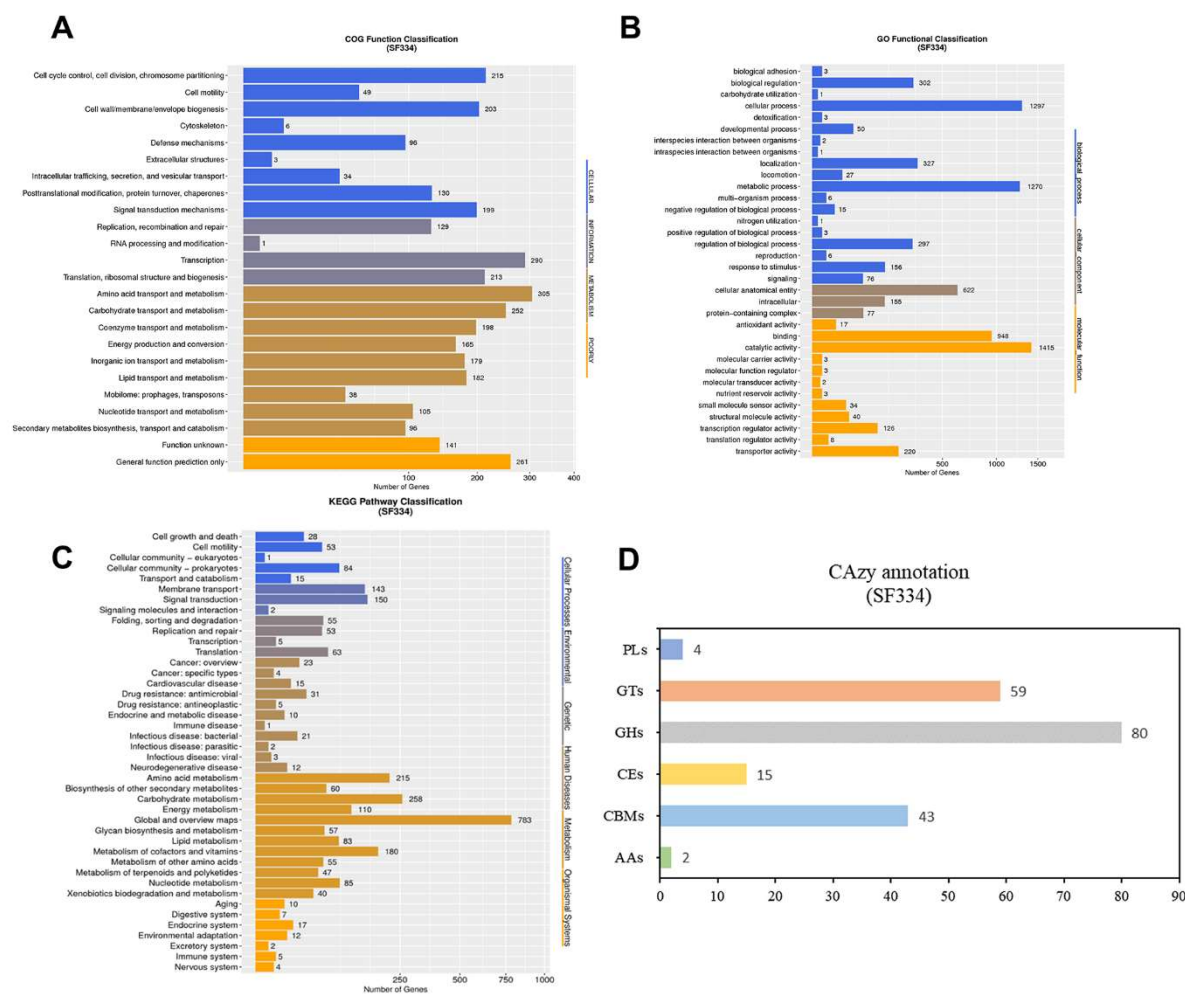


Figure S5. Genomic analysis of *B. velezensis* SF334. The COG analysis (A), GO analysis (B), KEGG pathway analysis (C) and CAZy annotation (D) of *B. velezensis* SF334

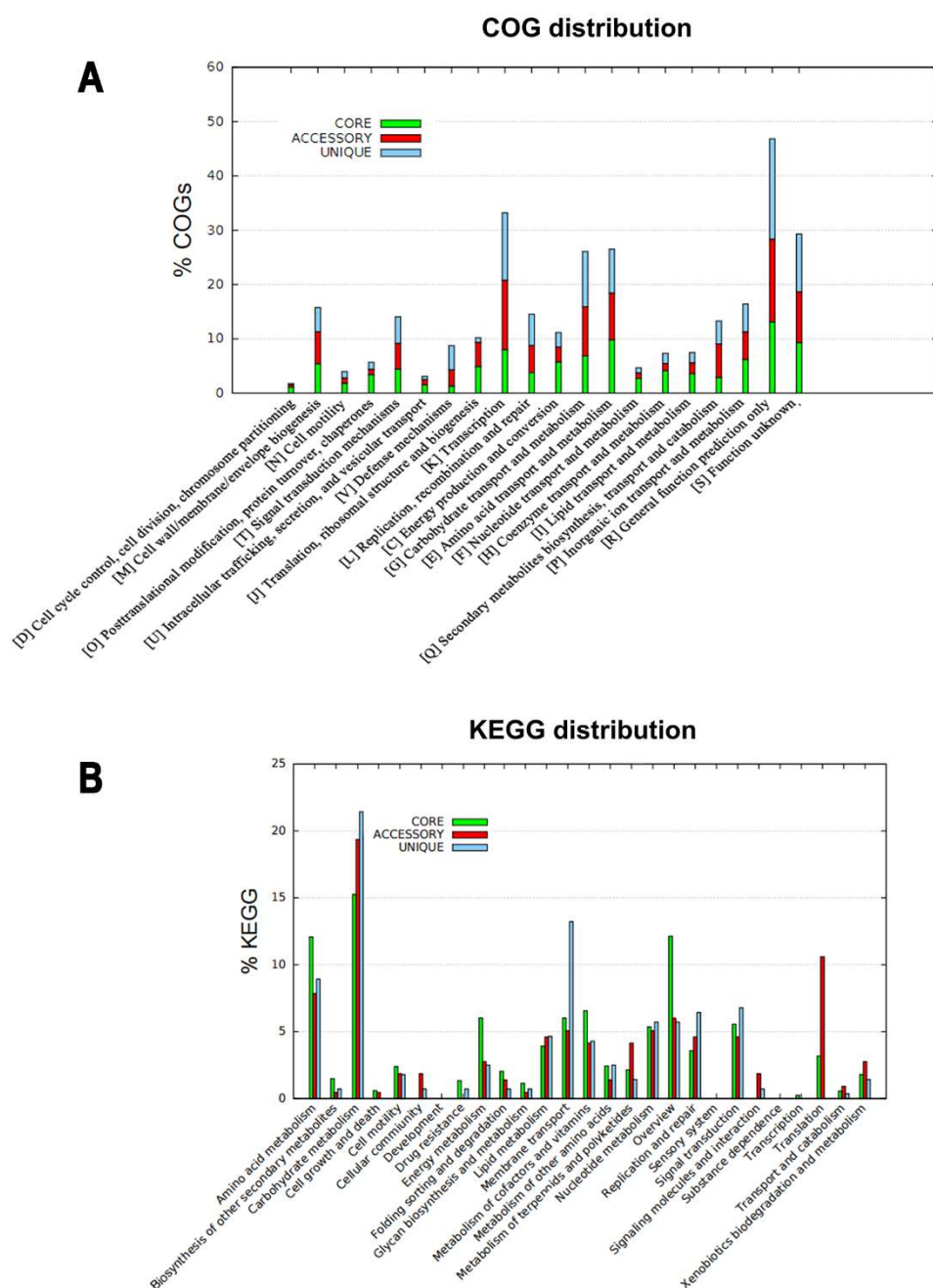


Figure S6. Comparative genomic analysis of *B. velezensis* SF334 with four other related *Bacillus* species. The COG analysis (A) and KEGG pathway analysis (B) of *B. velezensis* SF334 with *B. velezensis* FZB42, *B. velezensis* SQR9, *B. amyloliquefaciens* DSM7, and *B. subtilis* 168. Green, red and blue boxes indicate core genes, accessory and unique genes between five strains.