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The growth rate and abundance of strains EGB and FOC in the soil from the 0800, 1420, and 1800 m depths were determined as described above. The total abundances of strain EGB and FOC were calculated by qPCR. To determine the growth rate of strain EGB and FOC, the soil DNA samples were extracted from the soils collected from the 010cm, 1030cm, and 1800cm depths. The soils from the 010 and 1030cm depths were selected because (i) the highest temperatures and (ii) the highest soil moisture occurred in these depths. The PCR was performed using the primer sets FANO1 and RANO1 for FOC and

FAMO3 and FANO3 for strain EGB, which had been previously shown to amplify the 16S rRNA gene of FOC and the myxobacterial 16S rRNA gene, respectively [42, 72]. Activities of all strains were assessed by using a culture medium with Bacillus amyloliquefaciens IOC4782 (B. amyloliquefaciens IOC4782, B. amyloliquefaciens IOC4782S and B. amyloliquefaciens IOC4782F) as the positive control and without inoculation (negative control). The water extract of the soil treated with strain EGB (EGBW) was used for the assay of strain EGB. The bacterial numbers of EGBW, EGBWF and EGBWFOCW were determined using DAPI staining in situ at 15 and 27 dai. The staining solution (0.1mgml-1 DAPI in sterile water) was poured into the tubes; the wells were covered with micropore tape and incubated in the dark for 10min at room temperature. The numbers of bacteria stained in the treatments were calculated by counting the fluorescent cells under an epifluorescent microscope. Each experiment was repeated three times.

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Previous findings have shown that strain EGB significantly reduced the abundance of both FOC and soil bacteria, indicating that strain EGB was more effective in competing with soil bacteria than FOC [31]. Here, the reduced abundance of FOC in the EGBFOC treatment indicated a decreased soil microbiome diversity and abundance. An increased network modularity and number per node indicated that the soil microbiomes were more complicated under the EGBFOC treatment. The decreased abundance of EGB also led to an additional shift of ecological interactions. This finding revealed the importance of the soil microbiome structure on the biocontrol of plant soil-borne diseases. Similar to the findings of previous studies in which the soil microbiomes were changed by microbial activities [68, 69, 70], the abundance of FOC bacteria was decreased by strain EGB in this study. This finding was in agreement with previous studies reporting that the abundance of other BCAs (Pseudomonas spp., Bacillus spp., and Streptomyces spp.) was reduced by

strain EGB [31]. Our findings showed that an effective BCA can be used to reduce the abundance of other BCAs and influence the soil microbiome structure to a certain extent. Therefore, the effects of strain EGB on the soil microbiome could also be detected. By controlling the soil microbiome, a BCA with multiple mechanisms may have a greater impact on the soil microbial community structure and the biocontrol efficiency of the BCA. By adjusting the amount of water per pipe during the course of the experiment, the moisture content of the substrate can be regulated at the field capacity (FC). Therefore, we set an arbitrary criterion for judging microbial consortium stability in the field: pH measured in soils was 8.5 to be a sign of a good microbial consortium. If the pH of soil was low when the cucumber seedlings were grown in pots, we adjusted soil pH by adding lime, and then we changed the treatments. To prevent soil degradation, we added a balanced microbial consortium and protected organic acid and nitrogen. We added a piece of sterilized apple wood charcoal under the

soil surface in pots; for long-term use, we planted the row berry and selected wild berry in the experimental plot to prevent wood charcoal degradation. The trial area was covered with Chinese jute cloth to prevent rainwater and wind damage. The soil density for the three treatments were equal in each stage. 5ec8ef588b