# *Paenibacillus polymyxa* NSY50 suppresses *Fusarium* wilt in cucumbers by regulating the rhizospheric microbial community

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## Supplementary Table 1

The criterions of choosing the raw 16S rRNA genes and ITS sequence pyrosequencing data.

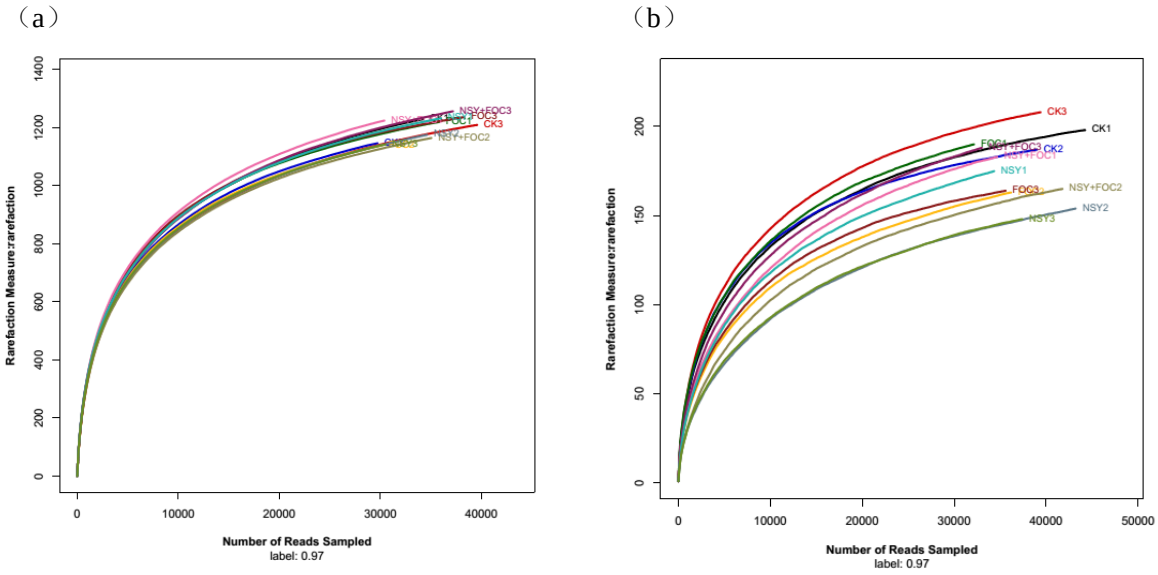
| | criterions |
|---|---|
| **(1)** | The 250 bp reads were truncated at any site receiving an average quality score <20 over a 10 bp sliding window, discarding the truncated reads that were shorter than 50bp; |
| **(2)** | exact barcode matching, 2 nucleotide mismatch in primer matching, reads containing ambiguous characters were removed; |
| **(3)** | only sequences that overlap longer than 10 bp were assembled according to their overlap sequence. Reads which could not be assembled were discarded. |

## Supplementary Table 2

The number of Penicillum spp. in different samples at the species level.

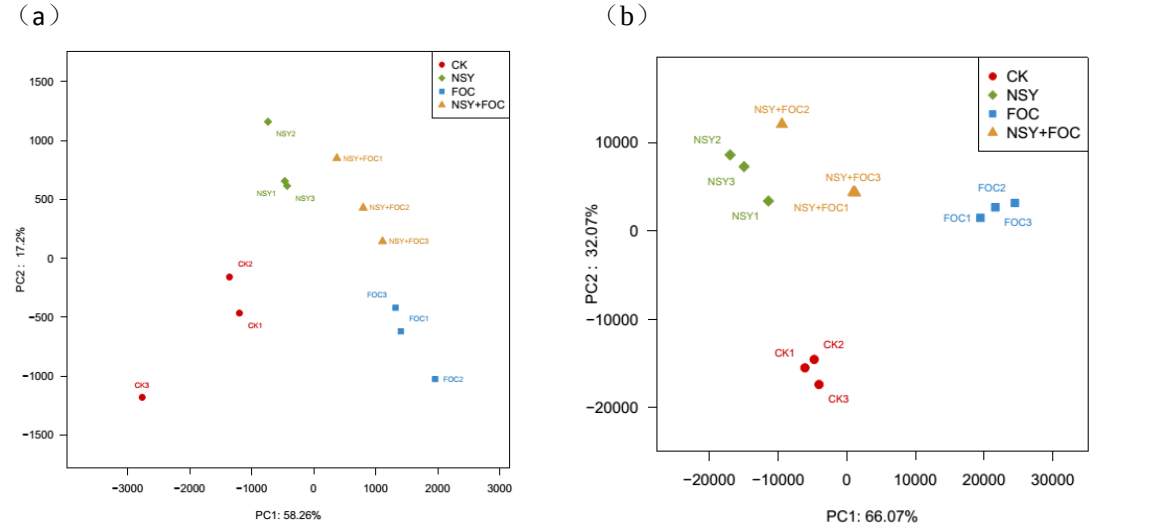
| OTU ID | CK1 | CK2 | CK3 | FOC1 | FOC2 | FOC3 | NSY1 | NSY2 | NSY3 | NSY+FOC1 | NSY+FOC2 | NSY+FOC3 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Penicillium brasilianum | 6 | 8 | 0 | 0 | 0 | 0 | 2 | 2 | 0 | 7 | 0 | 6 |
| Penicillium citrinum | 14 | 5 | 0 | 1 | 0 | 1 | 2 | 0 | 0 | 0 | 0 | 1 |
| Penicillium coffeae | 9 | 8 | 11 | 10 | 4 | 11 | 2 | 1 | 1 | 1 | 6 | 1 |
| Penicillium mallochii | 0 | 0 | 0 | 1 | 1 | 0 | 0 | 2 | 1 | 0 | 0 | 0 |
| Penicillium olsonii | 114 | 112 | 132 | 7 | 4 | 0 | 5 | 3 | 2 | 3 | 8 | 6 |
| Penicillium oxalicum | 15 | 3 | 7 | 2 | 2 | 2 | 10 | 1 | 0 | 2 | 3 | 1 |
| Penicillium sumatrense | 0 | 2 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 2 | 0 | 0 |
| Penicillium toxicarium | 1 | 0 | 0 | 3 | 0 | 3 | 0 | 2 | 0 | 0 | 0 | 0 |
| Penicillium tularense | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 26 | 0 | 0 | 0 |
| Penicillium_Unclassified | 12972 | 11012 | 8678 | 296 | 220 | 225 | 7595 | 5905 | 4505 | 4151 | 3096 | 3487 |

**Supplementary Figure 1.**



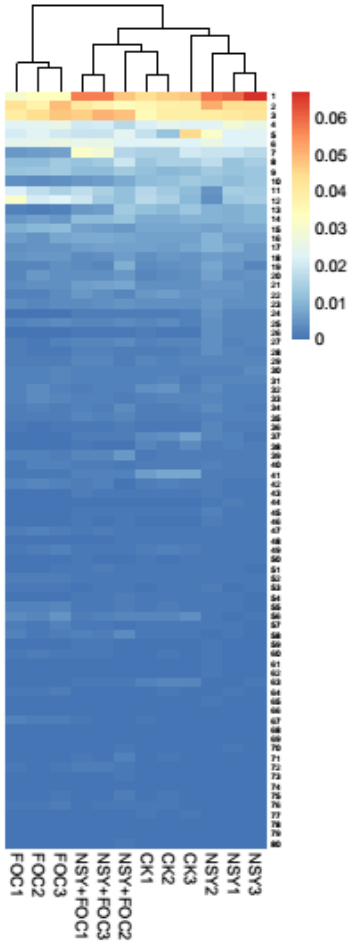

**Supplementary Figure 1.** Rarefaction analysis at 3% dissimilarity levels for soil samples collected from the four treatments (CK, untreated plants (control); NSY50, plants challenged with NSY50 ($2.5\times10^8$ CFU/mL); FOC, plants challenged with FOC ($1\times10^8$ CFU/mL); NSY50 + FOC: plants challenged with NSY50 for 3 days, and then with FOC). (a) bacterial; (b)fungi. The *vertical axis* shows the average number of OUTs that would be expected to be found after sampling the number of sequences shown on the *hoorizontal axis*.

**Supplementary Figure 2.**



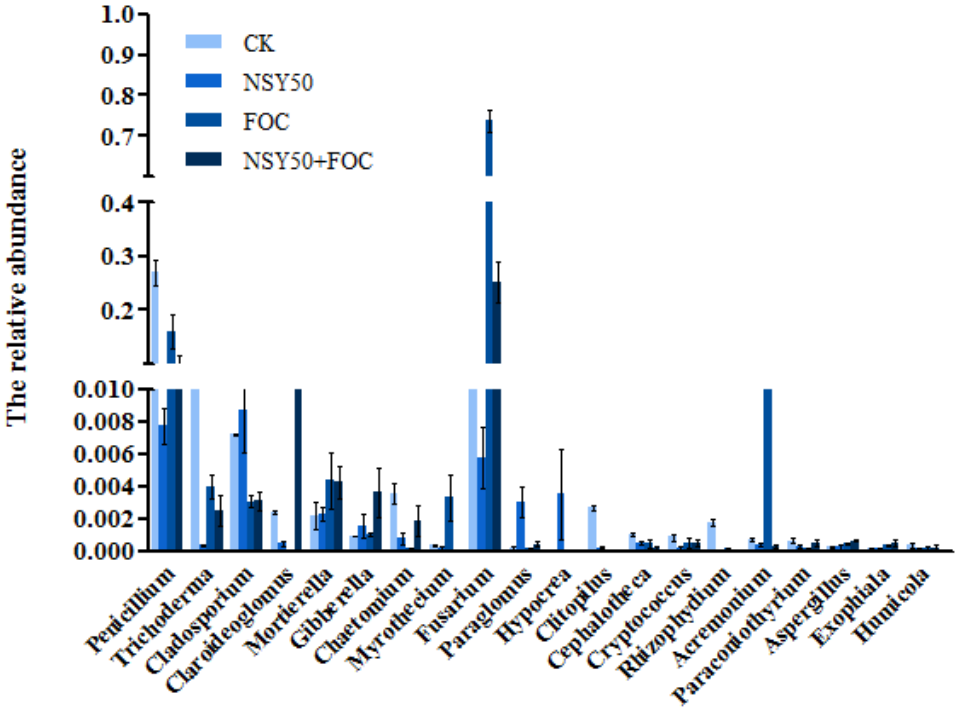

**Supplementary Figure 2.** Principal Component Analysis for soil samples collected from the four treatments (CK, untreated plants (control); NSY50, plants challenged with NSY50 ($2.5\times10^8$ CFU/mL); FOC, plants challenged with FOC ($1\times10^8$ CFU/mL); NSY50 + FOC: plants challenged with NSY50 for 3 days, and then with FOC). (a) bacteria; (b) fungi.

**Supplementary Figure 3.**




**Supplementary Figure 3.** Heatmap of the top 80 classified bacterial genera for soil samples collected from the four treatments (CK, untreated plants (control); NSY50, plants challenged with NSY50 ($2.5 \times 10^8$ CFU/mL); FOC, plants challenged with FOC ($1 \times 10^8$ CFU/mL); NSY50 + FOC: plants challenged with NSY50 for 3 days, and then with FOC). The color gradient from blue to red indicates increasing the relative abundance.

**Supplementary Figure 4.**




**Supplementary Figure 4.** The relative abundance of the main fungal genera for the soil samples collected from the four treatment groups (CK, untreated plants (control); NSY50, plants challenged with NSY50 ($2.5\times10^8$ CFU/mL); FOC, plants challenged with FOC ($1\times10^8$ CFU/mL); NSY50 + FOC: plants challenged with NSY50 for 3 days, and then with FOC). Each histogram represents the mean ± SE of three independent biological experiments ($n$=3).