

Supplementary Materials

Table S1: Bacterial and fungal concentrations (CFU g⁻¹) in soil before treatment and at 15 and 33 days after treatment (DAT), and effects of soil disinfestation treatments (SD): non-treated soil (NT), *Trichoderma*-based biological control (*T. spp.*), and biofumigation (BF).

	Bacterial Concentration CFU g ⁻¹	Fungal Concentration CFU g ⁻¹
Before Treatment	4.8 × 10 ⁶ ± 2.6 × 10 ⁵	4.8 × 10 ⁶ ± 2.6 × 10 ⁵
Days After Treatment (DAT)		
15	1.9 × 10 ⁶ ± 4.2 × 10 ⁴	1.9 × 10 ⁶ ± 4.2 × 10 ⁴
33	3.1 × 10 ⁶ ± 8.1 × 10 ⁵	3.1 × 10 ⁶ ± 8.1 × 10 ⁵
Treatment (SD)		
NT	1.5 × 10 ⁶ ± 1.4 × 10 ^{5b}	1.5 × 10 ⁶ ± 1.4 × 10 ^{5b}
<i>T. spp.</i>	1.3 × 10 ⁶ ± 2.3 × 10 ^{5c}	1.3 × 10 ⁶ ± 2.3 × 10 ^{5c}
BF	4.8 × 10 ⁶ ± 9.2 × 10 ^{5a}	4.8 × 10 ⁶ ± 9.2 × 10 ^{5a}
Significance		
DAT	ns	*
SD	***	***

ns,*,*** denote non-significant or significant effects at $p \leq 0.05$ and 0.001. All data expressed as mean ± SE, n = 18 for DAT, n = 12 for T. Different letters within each column indicate significant differences according to Tukey's HSD test ($p = 0.05$). Independent t-tests were performed to compare microbial loads between 15 and 33 DAT for each microbial group.

Table S2. Predominant soilborne fungal genera in soil samples collected before and after the application of soil disinfestation treatments.

Stage	Treatment	Most Abundant Fungal Genera And Species	Notes
Before treatment	-	<i>Fusarium spp.</i> , <i>Aspergillus Sesamicola</i> , <i>Pennicillium spp</i> , <i>Phytium spp.</i>	High baseline fungal diversity; <i>Fusarium</i> dominant and indicative of pathogen presence prior to disinfestation.
15 days after treatment	NT	<i>Fusarium spp.</i> , <i>Aspergillus Sesamicola</i> , <i>Pennicillium spp</i> , <i>Phytium spp.</i>	<i>Fusarium</i> persists only in the untreated soil; overall fungal load strongly reduced relative to pre-treatment.
	<i>T. spp.</i>	<i>Aspergillus Sesamicola</i> , <i>Pennicillium spp.</i> , <i>Phytium spp.</i>	<i>Fusarium</i> fully suppressed following <i>Trichoderma</i> application; strong antifungal effect evident.
	BF	<i>Aspergillus Sesamicola</i> , <i>Pennicillium spp.</i> , <i>Phytium spp.</i>	Biofumigation eliminates <i>Fusarium</i> ; fungal community shifts toward saprophytic taxa.
33 days after treatment	NT	<i>Aspergillus Sesamicola</i> , <i>Pennicillium spp.</i> , <i>Phytium spp.</i>	<i>Fusarium</i> no longer detected; partial fungal resurgence dominated by saprophytes.
	<i>T. spp.</i>	<i>Aspergillus Sesamicola</i> , <i>Pennicillium spp.</i> , <i>Phytium spp.</i>	Fungal load remains strongly suppressed; <i>Trichoderma</i> maintains long-lasting antagonistic activity.
	BF	<i>Aspergillus Sesamicola</i> , <i>Pennicillium spp.</i> , <i>Phytium spp.</i>	Fungal community stabilizes at intermediate levels; continued absence of <i>Fusarium</i> .

Soil-borne fungi at three sampling stages (before treatment, 15 days after treatment, and 33 days after treatment) under non-treated soil (NT), *Trichoderma*-based biological control (*T. spp.*), and biofumigation (BF). The most abundant fungal taxa were identified at the genus or species level based on macroscopic and microscopic morphology.