

Effects of the Continuous Cropping and Soilborne Diseases of *Panax ginseng* C. A. Meyer on Rhizosphere Soil Physicochemical Properties, Enzyme Activities, and Microbial Communities

Table S1. Diversity and richness indexes of bacterial communities

| Sample name | Shannon index | Simpson index | Ace index | Chao1 index | Coverage index |
|-------------|---------------|---------------|-----------------|-----------------|----------------|
| CK | 5.52±0.08b | 0.015±0.00ab | 1821.59±45.02b | 1823.41±50.86b | 0.989±0.00b |
| CH | 5.00±0.28c | 0.028±0.01a | 1314.14±66.68c | 1327.93±52.75c | 0.992±0.00a |
| CD | 6.21±0.55a | 0.007±0.01b | 2467.66±502.63a | 2479.71±502.20a | 0.986±0.00c |

Note: CH and CD represent biennial ginseng seedlings transplanted and then continuously cropped for four years, healthy ginseng rhizosphere soil of woodland with biennial ginseng seedlings transplanted and then continuously cropped for four years, and severe soilborne disease ginseng rhizosphere soil of woodland, whereas CK represents the soil sample from woodland without ginseng planting. Values are means ± standard deviation. The same letters within a column indicate no significant differences between the means ($p > 0.05$). Different letters within a column indicate significant differences ($p < 0.05$).

Table S2. Diversity and richness indexes of fungal communities

| Sample name | Shannon index | Simpson index | Ace index | Chao1 index | Coverage index |
|-------------|---------------|---------------|---------------|---------------|----------------|
| CK | 4.13±0.28a | 0.085±0.04ab | 952.06±33.60a | 943.61±36.70a | 0.996±0.00c |
| CH | 2.87±0.55b | 0.142±0.07a | 429.11±37.51b | 438.59±51.69b | 0.998±0.00a |
| CD | 4.36±0.04a | 0.039±0.00b | 901.88±19.76a | 900.10±24.09a | 0.997±0.00b |

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Table S3. The relative abundance of bacterial communities at the phylum level

| | CK | CH | CD |
|-------------------|-------------|--------------|-------------|
| Proteobacteria | 33.97±1.23a | 23.03±1.60b | 22.34±1.94b |
| Actinobacteriota | 17.57±2.45b | 20.97±2.70ab | 24.39±0.69a |
| Chloroflexi | 6.62±1.67b | 22.99±5.20a | 16.51±1.58a |
| Acidobacteriota | 25.32±0.43a | 3.97±0.45c | 13.64±2.32b |
| Firmicutes | 1.65±0.36b | 21.15±8.47a | 9.27±0.65b |
| Verrucomicrobiota | 4.38±0.72a | 0.16±0.02c | 1.75±0.96b |
| Gemmatimonadota | 1.03±0.29b | 1.32±0.49b | 3.18±0.15a |
| Bacteroidota | 1.27±0.18b | 1.47±0.13ab | 1.61±0.14a |
| Myxococcota | 1.64±0.42a | 0.24±0.15b | 1.86±0.18a |
| Patescibacteria | 0.52±0.40b | 2.51±0.18a | 0.58±0.10b |
| Planctomycetota | 2.43±0.42a | 0.47±0.13b | 0.49±0.15b |

| | | | |
|-------------------|------------|------------|------------|
| Methylomirabilota | 0.99±0.17a | 0.01±0.01b | 1.43±0.49a |
| WPS-2 | 0.75±0.13b | 1.32±0.33a | 0.20±0.10c |

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Table S4. The relative abundance of fungal communities at the phylum level

| | CK | CH | CD |
|----------------------|--------------|--------------|-------------|
| Ascomycota | 34.19±10.01c | 80.11±10.61a | 60.83±0.92b |
| Basidiomycota | 53.89±11.97a | 13.01±9.25b | 13.46±0.24b |
| Mortierellomycota | 8.34±1.61b | 5.48±0.74c | 21.70±0.76a |
| Unclassified-k-Fungi | 1.81±0.57a | 0.69±0.47b | 2.07±0.23a |
| Rozellomycota | 1.37±0.45a | 0.02±0.03c | 0.79±0.09b |

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Table S5. The relative abundance of bacterial communities at the genus level

| | CK | CH | CD |
|------------------------|------------|-------------|-------------|
| Bacillus | 0.66±0.32b | 14.21±7.05a | 4.74±0.71b |
| Acidothermus | 5.36±1.18a | 4.15±0.95ab | 2.36±0.50b |
| Rhodanobacter | 0.36±0.10b | 8.43±3.32a | 0.12±0.06b |
| Bradyrhizobium | 5.18±0.18a | 0.64±0.17c | 1.03±0.20b |
| Arthrobacter | 0.05±0.01b | 2.99±0.85a | 2.92±0.19a |
| Candidatus_Udaeobacter | 3.41±0.49a | 0.11±0.02c | 1.47±0.80b |
| HSB_OF53-F07 | 0.70±0.17a | 2.42±2.02a | 1.72±0.58a |
| Chujaibacter | 0.00±0.00b | 4.80±1.67a | 0.02±0.00b |
| Bryobacter | 2.61±0.17a | 1.34±0.27b | 0.46±0.07c |
| Mycobacterium | 2.53±0.34a | 0.80±0.24b | 1.05±0.14b |
| Paenibacillus | 0.54±0.08b | 2.50±1.23a | 1.18±0.07ab |
| Candidatus_Solibacter | 2.47±0.29a | 0.09±0.02c | 0.62±0.16b |
| Gaiella | 0.26±0.11b | 0.26±0.20b | 2.17±0.07a |
| Sphingomonas | 0.19±0.07c | 0.50±0.16b | 1.36±0.08a |
| Roseiarcus | 1.35±0.14a | 0.09±0.05b | 0.20±0.09b |

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within a column indicate no significant differences between the means ($p > 0.05$). Different letters within a column indicate significant differences ($p < 0.05$). Table shows groups with relative abundance greater than 1% (removing unclassified, unidentified and no rank).

Table S6. The relative abundance of bacterial communities at the genus level

| | CK | CH | CD |
|--------------------|-------------|-------------|-------------|
| Mortierella | 8.04±1.56b | 4.96±0.69c | 21.48±0.71a |
| Trichocladium | 0.01±0.01b | 27.14±9.38a | 4.46±0.15b |
| Russula | 26.96±9.06a | 0.00±0.00b | 0.01±0.02b |
| Fusarium | 0.71±1.20b | 11.06±2.04a | 9.54±1.24a |
| Neocosmospora | 0.00±0.00b | 19.11±6.22a | 1.24±0.07b |
| Saitozyma | 1.74±0.50a | 5.06±3.07a | 2.85±0.72a |
| Trichoderma | 2.33±0.93a | 2.62±0.84a | 1.15±0.04a |
| Penicillium | 0.45±0.14c | 1.58±0.58b | 3.97±0.39a |
| Tomentella | 4.82±0.27a | 0.00±0.00b | 0.29±0.06b |
| Oidiodendron | 3.14±0.03a | 1.59±0.83b | 0.09±0.03c |
| Solicoccozyma | 1.42±0.29a | 1.03±0.78a | 1.75±0.20a |
| Schizothecium | 0.00±0.00c | 0.24±0.11b | 3.80±0.06a |
| Chaetomium | 0.02±0.01b | 3.06±1.07a | 0.74±0.27b |
| Microglossum | 3.24±0.90a | 0.00±0.00b | 0.00±0.00b |
| Paracylindrocarpon | 0.00±0.00b | 0.35±0.26b | 2.74±0.27a |
| Cladorrhinum | 0.00±0.00b | 0.01±0.02b | 3.00±0.13a |
| Sebacina | 2.74±1.90a | 0.00±0.00b | 0.01±0.01b |
| Lactarius | 2.47±1.44a | 0.00±0.00b | 0.02±0.01b |
| Hypomyces | 1.04±0.70a | 0.53±0.12a | 0.81±0.20a |
| Gibellulopsis | 0.00±0.00b | 0.01±0.01b | 2.35±0.68a |
| Cladophialophora | 1.82±0.16a | 0.38±0.21b | 0.07±0.01b |
| Pleotrichocladium | 0.27±0.09b | 0.32±0.34b | 1.37±0.07a |
| Neonectria | 0.60±0.11b | 0.14±0.13c | 1.21±0.17a |
| Phialophora | 0.00±0.00b | 1.72±1.21a | 0.01±0.00b |
| Laccaria | 1.32±0.60a | 0.00±0.00b | 0.04±0.02b |
| Paraphaeosphaeria | 0.10±0.16b | 0.16±0.10b | 1.07±0.17a |
| Aspergillus | 0.04±0.01b | 1.07±0.60a | 0.08±0.03b |
| Helvellosebacina | 0.00±0.00b | 0.00±0.00b | 1.10±0.32a |
| Truncatella | 0.00±0.00b | 0.02±0.01b | 1.07±0.07a |
| Clavulinopsis | 1.07±0.81a | 0.00±0.00b | 0.01±0.00b |
| Hygrocybe | 1.01±0.39a | 0.00±0.00b | 0.00±0.00b |

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