**Changes in soil properties and microbial communities are associated with continuous cropping obstacles of American ginseng (Panax quinquefolius L.)**

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**Figure S1** Structural formula of nine standard phenolic acids



**Figure S2** Chromatogram of nine standard phenolic acids at 280 nm. 1: *p*-coumaric acid; 2: protocatechuic acid; 3: *p*-hydroxybenzoic acid; 4: vanillic acid; 5: caffeic acid; 6: syringic acid; 7: ferulic acid; 8: salicylic acid; 9: cinnamic acid

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**Figure S3** The flow chart of the sequencing experimental procedure

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**Figure S4** The Venn diagram of OUT. RS: 10-year post-ginseng rotation soil; CS: soil in which no ginseng was grown before ginseng planting. Each ellipse represents one Group samples, the overlapping area between ellipses indicates the shared OTUs among samples groups, and the number of each block indicates the number of shared (or unique) OTUs of the samples groups contained in the block

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**Figure S5** Species accumulation curves measuring the observed species in bacterial communities. The abscissa represents the sample size, the ordinate represents the number of detected objects, and the blue shadow reflects the confidence interval of the curve. The results reflect the increasing rate of new species observed during the process of population sampling. Using the species accumulation curve to judge whether the sample size is large enough, the sharp rise of the curve indicates that the sample size is insufficient and needs to be expanded; otherwise, it indicates that the sample size is enough to reflect the richness of the community****

**Figure S6** Comparison of four alpha diversity indices (Simpson, Shannon, ACE and Chao1) between 10-year post-ginseng rotation soil (RS) and soil in which no ginseng was grown (CS) before ginseng planting. Mean (n = 4) data shown; error bars represent SE.



**Figure S7** The correlation coefficient of Spearman rank among the top 50 dominant genera was calculated by Spearman correlation network analysis, for which Rho > 0.6 and P value< 0.01 related dominant genera to construct an associated network node represents each dominant genus, identified by different colors, the connection between nodes indicates that there is a correlation between the two genera, the red line indicates a positive correlation, and the green line indicates a negative correlation. The more connections through a node, the more association the genus has with other members of the flora

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**Table S1** Standard curve equations of the nine phenolic compounds

|  |  |  |  |
| --- | --- | --- | --- |
| **Standard substances** | **Standard curve equations** | **Regression degree** | **Linear ranges** |
| *p*-Coumaric acid | Y = 31530x-28246 | 0.9999 | 0.001–0.1 |
| Protocatechuic acid | Y = 27889x-25769 | 0.9999 | 0.001–0.1 |
| *p*-Hydroxybenzoic acid | Y = 29916x-27528 | 0.9999 | 0.001–0.1 |
| Vanillic acid | Y = 35119x-31949 | 0.9999 | 0.001–0.1 |
| Caffeic acid | Y = 72852x-65440 | 0.9999 | 0.001–0.1 |
| Syringic acid | Y = 57725x-52334 | 0.9999 | 0.001–0.1 |
| Ferulic acid | Y = 52004x-46029 | 0.9999 | 0.001–0.1 |
| Salicylic acid | Y = 10682x-10920 | 0.9999 | 0.001–0.1 |
| Cinnamic acid | Y = 170030x-146718 | 0.9999 | 0.001–0.1 |

**Table S2** Comparisons of relative abundance of major lineages in the bacterial communities of 10-year post-ginseng rotation soil (RS) and soil in which no ginseng was grown (CS) before ginseng planting

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Taxonomy | % relative abundance (mean ± SE) in: | | |  |
|  | RS% | CS% | P |  |
| Proteobacteria | 33.23±1.74 | 30.13±2.01 | 0.289 |  |
| Alphaproteobacteria | 18.53 ±1.02 | 19.98± 1.45 | 0.472 |  |
| **Sphingomonadales** | **1.68±0.00** | **2.98±0.00** | **0.002** |  |
| **Sphingomonadaceae** | **1.48±0.00** | **2.88±0.00** | **0.004** |  |
| **Novosphingobium** | **0.20±0.00** | **0.03±0.00** | **0.035** |  |
| **Sphingomonas** | **1.10±0.00** | **2.83±0.00** | **0.000** |  |
| Rhizobiales | 10.75±0.01 | 10.03±0.01 | 0.666 |  |
| Bradyrhizobiaceae | 2.03±0.00 | 2.65±0.00 | 0.069 |  |
| Methylobacteriaceae | 0.28±0.00 | 0.08±0.00 | 0.097 |  |
| **uncultured** | **0.13±0.00** | **0.00±0.00** | **0.015** |  |
| **Nitrobacter** | **0.75±0.00** | **1.13±0.00** | **0.038** |  |
| Rhodospirillales | 5.08±0.01 | 6.00± 0.00 | 0.377 |  |
| Caulobacterales | 0.95±0.00 | 0.80±0.00 | 0.432 |  |
| **Gammaproteobacteria** | **9.08 ± 1.54** | **4.20±0.31** | **0.048** |  |
| **Xanthomonadales** | **7.83±0.02** | **2.73±0.00** | **0.040** |  |
| **Xanthomonadaceae** | **6.93±0.01** | **1.33±0.00** | **0.027** |  |
| **Mizugakiibacter** | **2.28±0.00** | **0.63±0.00** | **0.048** |  |
| **Rhodanobacter** | **3.45±1.00** | **0.38±0.06** | **0.050** |  |
| Xanthomonadales\_Incertae\_Sedis | 0.50±0.00 | 0.83±0.00 | 0.059 |  |
| Legionellales | 0.75±0.00 | 0.68±0.00 | 0.391 |  |
| Enterobacteriales | 0.13±0.00 | 0.50±0.00 | 0.459 |  |
| Pseudomonadales | 0.20±0.00 | 0.13±0.00 | 0.638 |  |
| **Pseudomonas** | **0.15±0.00** | **0.03±0.00** | **0.029** |  |
| HTA4 | 0.08±0.00 | 0.10±0.00 | 0.638 |  |
| Betaproteobacteria | 4.15±0.25 | 4.15±1.26 | 1.000 |  |
| BurkhReriales | 1.68±0.01 | 1.78±0.01 | 0.948 |  |
| Comamonadaceae | 0.35±0.00 | 0.53±0.00 | 0.694 |  |
| **unidentified** | **0.13±0.00** | **0.03±0.00** | **0.030** |  |
| SC-I-84 | 1.78±0.00 | 1.60±0.00 | 0.759 |  |
| Nitrosomonadales | 0.63±0.00 | 0.70±0.00 | 0.841 |  |
| Rhodocyclales | 0.03±0.00 | 0.00±0.00 | 0.391 |  |
| Deltaproteobacteria | 1.48±0.35 | 1.78±0.25 | 0.542 |  |
| Myxococcales | 0.93±0.00 | 1.40±0.00 | 0.237 |  |
| Desulfurellales | 0.43±0.00 | 0.18±0.00 | 0.206 |  |
| Oligoflexales | 0.05±0.00 | 0.08±0.00 | 0.391 |  |
| Bdellovibrionales | 0.08 0.00 | 0.10±0.00 | 0.391 |  |
| Actinobacteria | 18.33±0.72 | 21.08±1.15 | 0.098 |  |
| **Actinobacteria** | **9.38±1.11** | **12.60±0.66** | **0.049** |  |
| **Frankiales** | **3.80±0.00** | **7.38±0.01** | **0.023** |  |
| **Frankiaceae** | **0.78±0.00** | **1.18±0.00** | **0.040** |  |
| **Jatrophihabitans** | **0.75±0.00** | **1.15±0.00** | **0.048** |  |
| **Acidothermaceae** | **2.40±0.00** | **5.40±0.01** | **0.030** |  |
| **Acidothermus** | **2.40±0.00** | **5.40±0.01** | **0.030** |  |
| Pseudonocardiales | 1.43±0.00 | 1.10±0.00 | 0.528 |  |
| Micrococcales | 1.63±0.00 | 0.85±0.00 | 0.283 |  |
| **Micrococcaceae** | **0.50±0.00** | **0.08±0.00** | **0.007** |  |
| **Arthrobacter** | **0.43 ±0.00** | **0.03±0.00** | **0.001** |  |
| Streptomycetales | 0.70 ±0.00 | 0.93±0.00 | 0.523 |  |
| Micromonosporales | 0.60± 0.00 | 0.70±0.00 | 0.876 |  |
| Catenulisporales | 0.33±0.00 | 0.95±0.00 | 0.061 |  |
| **Actinospicaceae** | **0.05±0.00** | **0.63±0.00** | **0.006** |  |
| **Actinospica** | **0.05±0.00** | **0.63±0.00** | **0.049** |  |
| Corynebacteriales | 0.40±0.00 | 0.35±0.00 | 0.769 |  |
| Thermoleophilia | 6.85±0.64 | 6.78±0.68 | 0.906 |  |
| Gaiellales | 5.35±0.01 | 5.23±0.00 | 0.833 |  |
| uncultured | 5.20±0.01 | 5.15±0.00 | 0.934 |  |
| Solirubrobacterales | 1.50±0.00 | 1.55±0.00 | 0.752 |  |
| JG30-KF-CM45 | 0.45±0.00 | 0.50±0.00 | 0.752 |  |
| Acidimicrobiia | 1.98±0.09 | 1.63±0.13 | 0.155 |  |
| Acidimicrobiales | 1.998±0.00 | 1.63±0.00 | 0.155 |  |
| Acidobacteria | 16.60±1.01 | 15.80±0.72 | 0.544 |  |
| **Acidobacteria** | **7.28±0.68** | **9.45±0.53** | **0.046** |  |
| **Acidobacteriales** | **7.28±0.01** | **9.45±0.01** | **0.046** |  |
| **Acidobacteriaceae\_(Subgroup\_1)** | **7.28±0.00** | **9.45±0.00** | **0.046** |  |
| Solibacteres | 3.13±0.48 | 3.13±0.32 | 1.000 |  |
| Solibacterales | 3.13±0.00 | 3.13±0.00 | 1.000 |  |
| Subgroup\_2 | 3.63±0.76 | 1.80±0.01 | 0.081 |  |
| Subgroup\_6 | 0.90±0.32 | 1.2±0.14 | 0.881 |  |
| **Subgroup\_13** | **0.700.11** | **0.25 ± 0.00** | **0.021** |  |
| **uncultured\_bacterium** | **0.45±0.00** | **0.18±0.00** | **0.017** |  |
| **uncultured\_bacterium** | **0.45±0.00** | **0.18±0.00** | **0.035** |  |
| Holophagae | 0.40 ± 0.10 | 0.13 ± 0.00 | 0.151 |  |
| Subgroup\_7 | 0.18±0.00 | 0.10±0.00 | 0.650 |  |
| **Holophagales** | **0.23±0.00** | **0.03±0.00** | **0.016** |  |
| **Holophagaceae** | **0.23±0.00** | **0.03±0.00** | **0.048** |  |
| **Holophaga** | **0.20±0.00** | **0.03±0.00** | **0.048** |  |
| Blastocatellia | 0.48±0.28 | 0.08±0.00 | 0.289 |  |
| Blastocatellales | 0.48±0.00 | 0.08±0.00 | 0.289 |  |
| Chloroflexi | 12.13±0.02 | 14.78±0.02 | 0.333 |  |
| Ktedonobacteria | 7.08±2.04 | 9.53±0.02 | 0.417 |  |
| Ktedonobacterales | 4.78±0.02 | 6.38±0.01 | 0.488 |  |
| Ktedonobacteraceae | 0.18±0.00 | 0.50±0.00 | 0.041 |  |
| **Thermosporotrichaceae** | **0.15±0.00** | **0.65±0.00** | **0.038** |  |
| Thermosporothrix | 0.08±0.00 | 0.35±0.00 | 0.074 |  |
| JG30-KF-AS9 | 1.23±0.00 | 1.58±0.00 | 0.271 |  |
| KD4-96 | 1.53±0.38 | 1.40±0.01 | 0.851 |  |
| JG37-AG-4 | 1.00±0.30 | 1.43±0.00 | 0.547 |  |
| TK10 | 0.78±0.12 | 0.60±0.00 | 0.412 |  |
| **unidentified** | **0.08±0.00** | **0.28±0.00** | **0.016** |  |
| **unidentified** | **0.08±0.00** | **0.28±0.00** | **0.016** |  |
| JG30-KF-CM66 | 0.60±0.10 | 0.70±0.00 | 0.658 |  |
| Firmicutes | 6.63±0.01 | 5.85±0.02 | 0.443 |  |
| Bacilli | 3.73±0.37 | 2.98±0.00 | 0.179 |  |
| Bacillales | 3.70±0.00 | 2.95±0.00 | 0.206 |  |
| Clostridia | 2.78±0.32 | 2.85±0.01 | 0.927 |  |
| Clostridiales | 1.25±0.00 | 0.35±0.00 | 0.012 |  |
| **Peptostreptococcaceae** | **0.35±0.00** | **0.00±0.00** | **0.027** |  |
| **Peptoclostridium** | **0.20±0.00** | **0.00±0.00** | **0.016** |  |
| **Clostridiaceae\_1** | **0.75±0.00** | **0.18±0.00** | **0.011** |  |
| **Clostridium\_sensu\_stricto\_1** | **0.45±0.00** | **0.03±0.00** | **0.023** |  |
| Halanaerobiales | 1.45±0.00 | 2.40±0.01 | 0.301 |  |
| Thermoanaerobacterales | 0.05±0.00 | 0.10±0.00 | 0.182 |  |
| Erysipelotrichia | 0.13±0.05 | 0.03±0.00 | 0.252 |  |
| Erysipelotrichales | 0.13±0.00 | 0.03±0.00 | 0.252 |  |
| Gemmatimonadetes | 4.45±0.02 | 4.30±0.01 | 0.929 |  |
| Gemmatimonaetes | 4.45±0.84 | 4.30±0.73 | 0.897 |  |
| Gemmatimonadales | 4.45±0.02 | 4.30±0.01 | 0.897 |  |
| Gemmatimonadaceae | 4.45±0.02 | 4.30±0.01 | 0.897 |  |
| Bacteroidetes | 2.05±0.00 | 1.60±0.00 | 0.288 |  |
| Sphingobacteriia | 1.93±0.11 | 1.43±0.00 | 0.247 |  |
| Sphingobacteriales | 1.93±0.00 | 1.43±0.00 | 0.247 |  |
| **Chitinophagaceae** | **1.20±0.00** | **0.65±0.00** | **0.032** |  |
| **uncultured** | **0.98±0.00** | **0.53±0.00** | **0.049** |  |
| Cytophagia | 0.13±0.09 | 0.15±0.00 | 0.761 |  |
| Cytophagales | 0.13±0.00 | 0.15±0.00 | 0.761 |  |
| Flavobacteriia | 0.05±0.05 | 0.05±0.00 | 1.000 |  |
| Planctomycetes | 1.30±0.00 | 1.63±0.00 | 0.301 |  |
| Planctomycetacia | 1.23±0.23 | 1.55±0.00 | 0.437 |  |
| Saccharibacteria | 1.15±0.00 | 1.53±0.00 | 0.270 |  |
| uncultured\_bacterium | 1.00±0.15 | 1.18±0.00 | 0.574 |  |
| soil\_bacterium\_WF55 | 0.00±0.00 | 0.10±0.00 | 0.252 |  |
| Cyanobacteria | 1.50±0.01 | 0.53±0.00 | 0.432 |  |
| Cyanobacteria | 1.00±1.00 | 0.00±0.00 | 0.391 |  |
| Chloroplast | 0.35±0.10 | 0.30±0.00 | 0.718 |  |
| Verrucomicrobia | 0.65±0.00 | 0.63±0.00 | 0.932 |  |
| Spartobacteria | 0.43±0.18 | 0.25±0.00 | 0.188 |  |
| OPB35\_soil\_group | 0.15±0.03 | 0.30±0.00 | 0.339 |  |
| Opitutae | 0.03±0.03 | 0.08±0.00 | 0.495 |  |
| Nitrospirae | 0.58±0.00 | 0.65 ± 0.00 | 0.215 |  |
| Nitrospira | 0.58±0.10 | 0.65 0.00 | 0.215 |  |
| Nitrospirales | 0.56±0.00 | 0.65±0.00 | 0.215 |  |
| Nitrospiraceae | 0.48±0.00 | 0.65±0.00 | 0.076 |  |
| Armatimonadetes | 0.23±0.00 | 0.48±0.00 | 0.127 |  |
| Chthonomonadetes | 0.13±0.03 | 0.23±0.00 | 0.308 |  |
| Armatimonadia | 0.03±0.03 | 0.10±0.00 | 0.319 |  |
| **Chlamydiae** | **0.28±0.00** | **0.10±0.00** | **0.035** |  |
| **Chlamydiae** | **0.28±0.00** | **0.10±0.00** | **0.035** |  |
| **Chlamydiales** | **0.28±0.00** | **0.10±0.00** | **0.035** |  |
| **Simkaniaceae** | **0.15±0.00** | **0.03±0.00** | **0.015** |  |
| **uncultured** | **0.15±0.00** | **0.03±0.00** | **0.017** |  |
| Chlorobi | 0.05±0.00 | 0.13±0.00 | 0.215 |  |
| Chlorobia | 0.05±0.00 | 0.13±0.00 | 0.215 |  |