

Figure S1. Bacterial genus-level cluster 9 of OTU abundance at just prior -5 dph and after harvest 10, 41, 73, 198 and 231 dph. Percentage abundance per total OTUs is given at each time point. Cluster centroid was created by the average within the K-means cluster.

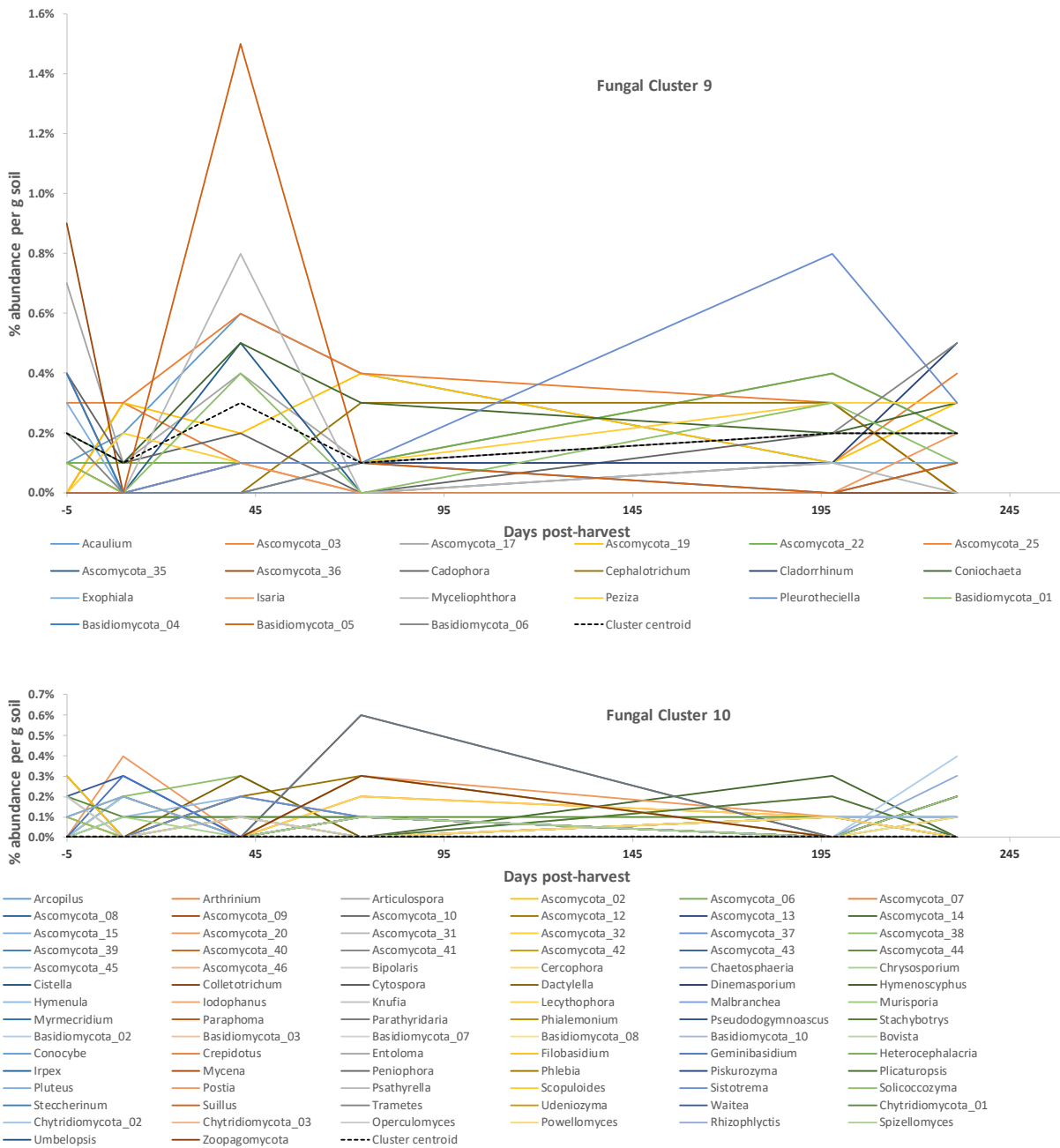


Figure S2. Fungal genus-level clusters 9 and 10 of OTU abundance over time at just prior -5 dph and after harvest 10, 41, 73, 198 and 231 dph. Percentage abundance per total OTUs is given at each time point. Cluster centroid was created by the average within the K-means cluster.

Table S1. Comparison of bacterial genus-level cluster 1 of OTU abundance over time. Average number of genus-level OTUs per g soil from five plots in a commercial American ginseng *Panax quinquefolius* garden at just prior -5 dph and after harvest 10, 41, 73, 198 and 231 dph. Genus names for OTUs identified based on 97% nt identity of the 440 - 476 bp V3-V4 region of the 16S rRNA using USEARCH with the SILVA 132 SSU NR99 database (<https://www.arb-silva.de/>).

| Percentage of abundance per OTUs per genera in cluster 1 ^a | | | | | | | |
|---|--------------------------|---------------------|---------|--------|--------|--------|--------|
| Phylum | Genus | -5 dph | 10 dph | 41 dph | 73 dph | 198dph | 231dph |
| Actinobacteria | <i>Arthrobacter</i> | 4.2% A ^b | 2.1% B | 0.6% C | 0% D | 0% D | 0% D |
| Actinobacteria | <i>Demequina</i> | 6.1% A | 1.2% B | 0.2% B | 0.6% B | 1.1% B | 0.1% B |
| Actinobacteria | <i>Pseudoclavibacter</i> | 6.1% A | 0% C | 0% C | 0.1% C | 1.5% B | 0% C |
| Proteobacteria | <i>Rhodoplanes</i> | 7.2% A | 1.4% CD | 3.0% B | 1.9% C | 0.9% D | 4.1%B |
| Cluster centroid | | 5.9%A | 1.2% B | 0.9%B | 0.6%B | 0.9%B | 1.1%B |

^aCluster was created by K-means clustering algorithm in R separating OTU abundance over dph into 10 clusters [35]. Cluster centroid was created by the average within the K-mean cluster.

^bLetter following percentages indicate significant difference over time based on general lineal model ANOVA followed by Fisher's Least Significant Difference LSD test $p < 0.05$.

Table S2. Comparison of bacterial genus-level cluster 2 of OTU abundance over time. Average number of genus-level OTUs per g soil from five plots in a commercial American ginseng *Panax quinquefolius* garden at just prior -5 dph and after harvest 10, 41, 73, 198 and 231 dph. Genus names for OTUs identified based on 97% nt identity of the 440 - 476 bp V3-V4 region of the 16S rRNA using USEARCH with the SILVA 132 SSU NR99 database (<https://www.arb-silva.de/>).

| Percentage of abundance per OTUs per genera in cluster 2 ^a | | | | | | | |
|---|-----------------------|-------------------|--------|--------|--------|--------|---------|
| Phylum | Genus | -5 dph | 10 dph | 41 dph | 73 dph | 198dph | 231 dph |
| Actinobacteria | <i>Lapillicoccus</i> | 0% C ^b | 3.7% A | 0% C | 0% C | 0.4% B | 0% C |
| Actinobacteria | <i>Micromonospora</i> | 0.5% B | 3.2% A | 0.3% C | 0.2% D | 0.5% B | 0.2%CD |
| Actinobacteria | <i>Streptomyces</i> | 1.6% A | 2.1% A | 0.5% C | 1.6% B | 0.4% D | 0.4% D |
| Firmicutes | <i>Terribacillus</i> | 0% B | 3.8% A | 0% B | 0% B | 0% B | 0% B |
| Proteobacteria | <i>Bauldia</i> | 0.6% C | 2.7% A | 0% D | 1.6% B | 0% D | 0.7% C |
| Proteobacteria | <i>Bosea</i> | 0.4%BC | 4.2% A | 0.3% C | 0% D | 0.7% B | 0% D |
| Proteobacteria | <i>Ensifer</i> | 0% C | 5.6% A | 0% C | 0% C | 1.1% B | 0% C |
| Proteobacteria | <i>Pseudolabrys</i> | 0% C | 5.6% A | 0% C | 2.0% B | 0% C | 1.5% B |
| Cluster centroid | | 0.4% B | 3.8% A | 0.1% B | 0.7% B | 0.4% B | 0.4% B |

^aCluster was created by K-means clustering algorithm in R separating OTs abundance over dph into 10 clusters [35]. Cluster centroid was created by the average within the K-mean cluster.

^bLetter following percentages indicate significant difference over time based on general lineal model ANOVA followed by Fisher's Least Significant Difference LSD test $p < 0.05$.

Table S3. Comparison of bacterial genus-level cluster 3 of OTU abundance over time. Average number of genus-level OTUs per g soil from five plots in a commercial American ginseng *Panax quinquefolius* garden at just prior -5 dph and after harvest 10, 41, 73, 198 and 231 dph. Genus names for OTUs identified based on 97% nt identity of the 440 - 476 bp V3-V4 region of the 16S rRNA using USEARCH with the SILVA 132 SSU NR99 database (<https://www.arb-silva.de/>).

| Percentage of abundance per OTUs per genera in cluster 3 ^a | | | | | | | |
|---|-----------------------|---------------------|--------|--------|--------|---------|---------|
| Phylum | Genus | -5 dph | 10 dph | 41 dph | 73 dph | 198 dph | 231 dph |
| Actinobacteria | <i>Aeromicrobium</i> | 0.2% B ^b | 0% B | 4.4% A | 0.7% B | 0.1% B | 0.1% B |
| Actinobacteria | <i>Blastococcus</i> | 0.2% C | 0.2% C | 6.2% A | 1.4% B | 0.3% C | 0.8% BC |
| Actinobacteria | <i>Phycoccus</i> | 0% B | 0% B | 6.2% A | 0% B | 0% B | 0% B |
| Proteobacteria | <i>Hyphomicrobium</i> | 2.4% C | 1.7% C | 4.4% A | 1.2% C | 2.9% B | 0% D |
| Proteobacteria | <i>Mesorhizobium</i> | 0% C | 0% C | 4.0% A | 2.5% B | 2.4% B | 0% C |
| Cluster centroid | | 0.6% B | 0.4% B | 5.1% A | 1.2% B | 1.1% B | 0.2% BC |

^aCluster was created by K-means clustering algorithm in R separating OTU abundance over dph into 10 clusters [35]. Cluster centroid was created by the average within the K-mean cluster.

^bLetter following percentages indicate significant difference over time based on general lineal model ANOVA followed by Fisher's Least Significant Difference LSD test $p < 0.05$.

Table S4. Comparison of bacterial genus-level cluster 4 of OTU abundance over time. Average number of genus-level OTUs per g soil from five plots in a commercial American ginseng *Panax quinquefolius* garden at just prior -5 dph and after harvest 10, 41, 73, 198 and 231 dph. Genus names for OTUs identified based on 97% nt identity of the 440 - 476 bp V3-V4 region of the 16S rRNA using USEARCH with the SILVA 132 SSU NR99 database (<https://www.arb-silva.de/>).

| Percentage of abundance per OTUs per genera in cluster 4 ^a | | | | | | | |
|---|--------------------------|---------------------|---------|--------|---------|---------|---------|
| Phylum | Genus | -5 dph | 10 dph | 41 dph | 73 dph | 198 dph | 231 dph |
| Actinobacteria | <i>Cellulomonas</i> | 0.3% C ^b | 0.1% C | 0.8% B | 0.2% C | 1.4% A | 0% D |
| Actinobacteria | <i>Ilumatobacter</i> | 0.5% CD | 0.6% CD | 2.2% A | 0.1% D | 1.2% B | 0.8% BC |
| Actinobacteria | <i>Nakumurella</i> | 0.1% C | 0.1% C | 1.1% A | 0.1% C | 0.6% B | 0.8% B |
| Actinobacteria | <i>Rhodococcus</i> | 0.7% B | 0% C | 1.5% A | 0.0% C | 0% C | 1.0% B |
| Actinobacteria | <i>Streptosporangium</i> | 0.3% C | 0% D | 1.6% A | 0% D | 0.4% B | 0.6% B |
| Firmicutes | <i>Clostridium</i> | 0% B | 0% B | 0.8% A | 0% B | 0% B | 0% B |
| Firmicutes | <i>Domibacillus</i> | 0% B | 0% B | 0.7% A | 0% B | 0% B | 0% B |
| Firmicutes | <i>Paenisporosarcina</i> | 0% C | 0% B | 1.1% A | 0.1% B | 0% C | 0% B |
| Firmicutes | <i>Viridibacillus</i> | 0% B | 0% B | 0.8% A | 0% B | 0% B | 0% B |
| Proteobacteria | <i>Amaricoccus</i> | 0% B | 0% B | 2.1% A | 0% B | 0% B | 0% B |
| Proteobacteria | <i>Phenyllobacterium</i> | 0.6% C | 0% D | 3.5% A | 1.2% BC | 1.3% B | 0.8% C |
| Cluster centroid | | 0.2% B | 0.1% B | 1.4% A | 0.2% B | 0.4% B | 0.4% B |

^aCluster was created by K-means clustering algorithm in R separating OTU abundance over dph into 10 clusters [35]. Cluster centroid was created by the average within the K-mean cluster.

^bLetter following percentages indicate significant difference over time based on general lineal model ANOVA followed by Fisher's Least Significant Difference LSD test $p < 0.05$.

Table S5. Comparison of bacterial cluster 5 of OTU abundance over time. Average number of genus-level OTUs per g soil from five plots in a commercial American ginseng *Panax quinquefolius* garden at just prior - 5 dph and after harvest 10, 41, 73, 198 and 231 dph. Genus names for OTUs identified based on 97% nt identity of the 440 - 476 bp V3-V4 region of the 16S rRNA using USEARCH with the SILVA 132 SSU NR99 database (<https://www.arb-silva.de/>).

| Percentage of abundance per OTUs per genera in cluster 5 ^a | | | | | | | |
|---|---------------------------|--------------------|--------|--------|--------|---------|---------|
| Phylum | Genus | -5 dph | 10 dph | 41 dph | 73 dph | 198 dph | 231 dph |
| Actinobacteria | <i>Actinomadura</i> | 0.3%B ^b | 0% C | 0% C | 1.0%A | 0% C | 0% C |
| Actinobacteria | <i>Catellatospora</i> | 0% D | 0% D | 0.9% B | 1.6%A | 0% D | 0.8% C |
| Actinobacteria | <i>Knoellia</i> | 0% B | 0% B | 0% B | 2.4%A | 0% B | 0% B |
| Actinobacteria | <i>Lysinimonas</i> | 0% D | 0.5%B | 0% D | 1.0%A | 0.7% A | 0.2% C |
| Actinobacteria | <i>Nocardioidea</i> | 0.6% B | 0.8%B | 1.7% A | 2.0%A | 1.3% A | 1.5% A |
| Proteobacteria | <i>Altererythrobacter</i> | 0% C | 0% C | 1.6%AB | 2.4%A | 0.7%BC | 0.8%BC |
| Proteobacteria | <i>Arsenicitalea</i> | 0% B | 0% B | 0% B | 1.0%A | 0% B | 0% B |
| Proteobacteria | <i>Brevundimonas</i> | 0% B | 0% B | 0.9% A | 1.0%A | 0% B | 0.4% B |
| Cluster centroid | | 0.1% C | 0.2% C | 0.6% B | 1.5%A | 0.3% B | 0.5% B |

^aCluster was created by K-means clustering algorithm in R separating OTU abundance over dph into 10 clusters [35]. Cluster centroid was created by the average within the K-mean cluster.

^bLetter following percentages indicate significant difference over time based on general lineal model ANOVA followed by Fisher's Least Significant Difference LSD test $p < 0.05$.

Table S6. Comparison of bacterial cluster 6 of OTU abundance over time. Average number of genus-level OTUs per g soil from five plots in a commercial American ginseng *Panax quinquefolius* garden at just prior -5 dph and after harvest 10, 41, 73, 198 and 231 dph. Genus names for OTUs identified based on 97% nt identity of the 440 - 476 bp V3-V4 region of the 16S rRNA using USEARCH with the SILVA 132 SSU NR99 database (<https://www.arb-silva.de/>).

| Percentage of abundance per OTUs per genera in cluster 6 ^a | | | | | | | |
|---|------------------------------|---------------------|---------|--------|---------|--------|--------|
| Phylum | Genus | -5 dph | 10 dph | 41dph | 73 dph | 198dph | 231dph |
| Acidobacteria | <i>Candidatus Solibacter</i> | 0.4% B ^b | 0.9% A | 0.1% C | 0.5% B | 0.5% B | 0.5% B |
| Acidobacteria | <i>Stenotrophobacter</i> | 0% C | 1.4% A | 0% D | 0.1% C | 0.7% B | 0.9% B |
| Actinobacteria | <i>Acrocarpospora</i> | 0% B | 1.6% A | 0% B | 0% B | 0% B | 0% B |
| Actinobacteria | <i>Iamia</i> | 0.4% C | 0.6% A | 0.6% A | 0.4% C | 0.4% C | 0.6% A |
| Actinobacteria | <i>Microbispora</i> | 0.9% A | 0% C | 0% C | 0.4% B | 0.4% B | 0.4% B |
| Firmicutes | <i>Bacillus</i> | 1.0% A | 1.4% A | 0.5% B | 0.5% B | 1.2% A | 1.2% A |
| Firmicutes | <i>Fictibacillus</i> | 0.4% B | 0.1% C | 0% C | 1.0% A | 0.8% A | 0% C |
| Proteobacteria | <i>Caulobacter</i> | 2.0% A | 0% B | 0% B | 0% B | 0% B | 0% B |
| Proteobacteria | <i>Dongia</i> | 0.5% AB | 0% C | 0% C | 0% C | 0.7% A | 0.4% B |
| Proteobacteria | <i>Labrys</i> | 1.1% A | 0% C | 0% C | 0% C | 0.7% B | 0.9% B |
| Proteobacteria | <i>Pedomicrobium</i> | 0.3% BC | 0.9% AB | 1.1% A | 0.1% C | 0.9% A | 0% D |
| Proteobacteria | <i>Sphingobium</i> | 0% C | 0.7% AB | 1.0% A | 0.5% AB | 0.8% A | 0% C |
| Proteobacteria | <i>Sphingorhabdus</i> | 2.2% A | 0% B | 0% B | 0% B | 0% B | 0% B |
| Cluster centroid | | 0.7% A | 0.6% A | 0.2% B | 0.3% B | 0.5% A | 0.4% B |

^aCluster was created by K-means clustering algorithm in R separating OTU abundance over dph into 10 clusters [35]. Cluster centroid was created by the average within the K-mean cluster.

^bLetter following percentages indicate significant difference over time based on general lineal model ANOVA followed by Fisher's Least Significant Difference LSD test $p < 0.05$.

Table S7. Comparison of bacterial cluster 7 of OTU abundance over time. Average number of genus-level OTUs per g soil from five plots in a commercial American ginseng *Panax quinquefolius* garden at just prior - 5 dph and after harvest 10, 41, 73, 198 and 231 dph. Genus names for OTUs identified based on 97% nt identity of the 440 - 476 bp V3-V4 region of the 16S rRNA using USEARCH with the SILVA 132 SSU NR99 database (<https://www.arb-silva.de/>).

| Percentage of abundance per OTUs per genera in cluster 7 ^a | | | | | | | |
|---|-----------------------|---------------------|---------|--------|---------|---------|---------|
| Phylum | Genus | -5 dph | 10 dph | 41dph | 73 dph | 198 dph | 231 dph |
| Actinobacteria | <i>Terrabacter</i> | 0.5% C ^b | 1.1% B | 1.2% A | 1.3% AB | 1.4% A | 1.8% A |
| Proteobacteria | <i>Bradyrhizobium</i> | 2.4% A | 0% D | 0% D | 0.2% D | 0.7% C | 1.9% B |
| Proteobacteria | <i>Devosia</i> | 2.6% B | 1.3% C | 0.5% C | 0% D | 0% D | 5.3% A |
| Proteobacteria | <i>Methylosula</i> | 0% C | 0% C | 0% C | 0% C | 3.2% A | 2.3% B |
| Proteobacteria | <i>Sphingomonas</i> | 4.2% B | 1.1% A | 0% D | 0.6% BC | 3.3% C | 3.8% C |
| Cluster centroid | | 1.9% A | 0.7% AB | 0.4% B | 0.4% B | 1.7% A | 3.0% A |

^aCluster was created by K-means clustering algorithm in R separating OTU abundance over dph into 10 clusters [35]. Cluster centroid was created by the average within the K-mean cluster.

^bLetter following percentages indicate significant difference over time based on general lineal model ANOVA followed by Fisher's Least Significant Difference LSD test $p < 0.05$.

Table S8. Comparison of bacterial cluster 8 of OTU abundance over time. Average number of genus-level OTUs per g soil from five plots in a commercial American ginseng *Panax quinquefolius* garden at just prior -5 dph and after harvest 10, 41, 73, 198 and 231 dph. Genus names for OTUs identified based on 97% nt identity of the 440 - 476 bp V3-V4 region of the 16S rRNA using USEARCH with the SILVA 132 SSU NR99 database (<https://www.arb-silva.de/>).

| Percentage of abundance per OTUs per genera in cluster 8 ^a | | | | | | | |
|---|--------------------------------|------------------|--------|--------|--------|---------|--------|
| Phylum | Genus | -5 dph | 10 dph | 41 dph | 73 dph | 198 dph | 231dph |
| Acidobacteria | <i>Paludibaculum</i> | 0%D ^b | 0.4%B | 0% D | 0.6%A | 0.1% C | 0.8% A |
| Actinobacteria | <i>Marmoricola</i> | 0% D | 0.2% C | 0.2%C | 0.5% B | 0.3% C | 0.8% A |
| Actinobacteria | <i>Pseudarthrobacter</i> | 0% D | 1.7% A | 0.2%C | 0% D | 1.0%AB | 1.1% B |
| Proteobacteria | <i>Allo-Neo-Para-Rhizobium</i> | 0% D | 0% D | 0.3%C | 0.1% D | 0.6% B | 1.9% A |
| Proteobacteria | <i>Aminobacter</i> | 0% B | 0% B | 0% B | 0% B | 0% B | 1.9% A |
| Proteobacteria | <i>Microvirga</i> | 0% C | 0% C | 0.3%B | 0% C | 1.0% A | 1.8% A |
| Proteobacteria | <i>Novosphingobium</i> | 0% C | 1.1% A | 0% C | 0% C | 0.3% B | 0.8% A |
| Proteobacteria | <i>Rhodopseudomonas</i> | 0% B | 0% B | 0% B | 0% B | 0% B | 0.8% A |
| Proteobacteria | <i>Sphingaurantiacus</i> | 0% B | 0% B | 0.8%A | 0% B | 0% B | 1.9% A |
| Cluster centroid | | 0% C | 0.4% B | 0.2%B | 0.1% B | 0.4% B | 1.3% A |

^aCluster was created by K-means clustering algorithm in R separating OTU abundance over dph into 10 clusters [35]. Cluster centroid was created by the average within the K-mean cluster.

^bLetter following percentages indicate significant difference over time based on general lineal model ANOVA followed by Fisher's Least Significant Difference LSD test $p < 0.05$.

Table S9. Comparison of bacterial cluster 9 of OTU abundance for described bacteria at genus level over time. Average number of genus-level OTUs per g soil from five plots in a commercial American ginseng *Panax quinquefolius* garden at just prior -5 dph and after harvest 10, 41, 73, 198 and 231 dph. Genus names for OTUs identified based on 97% nt identity of the 440 - 476 bp V3-V4 region of the 16S rRNA using USEARCH with the SILVA 132 SSU NR99 database (<https://www.arb-silva.de/>).

| Percentage of abundance per OTUs per genera in cluster 9 ^a | | | | | | | |
|---|------------------------------|-------------------------------|---------|---------|---------|--------|---------|
| Phylum | Genus | -5 dph | 10 dph | 41 dph | 73 dph | 198dph | 231 dph |
| Acidobacteria | <i>Bryobacter</i> | 0.1% ^{C^b} | 0.3%B | 0.3%B | 0.1%C | 0.1%C | 0.5%A |
| Acidobacteria | <i>Candidatus Koribacter</i> | 0.04%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Acidobacteria | <i>Luteitalea</i> | 0.02%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Acidobacteria | <i>Vicinamibacter</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Actinobacteria | <i>Acidotherrmus</i> | 0.03%A | 0% B | 0.01% B | 0% B | 0% B | 0.01% B |
| Actinobacteria | <i>Actinoallomurus</i> | 0.01%B | 0.01%B | 0% C | 0.02%A | 0% C | 0% C |
| Actinobacteria | <i>Agromyces</i> | 0.01%C | 0.03%BC | 0.08% A | 0.02%C | 0.02%C | 0.04% B |
| Actinobacteria | <i>Amycolatopsis</i> | 0.04%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Actinobacteria | <i>Angustibacter</i> | 0.48%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Actinobacteria | <i>Conexibacter</i> | 0.03%D | 0.1% B | 0.03% D | 0.06%C | 0.11%A | 0.01% E |
| Actinobacteria | <i>Dactylosporangium</i> | 0.02%C | 0.1% A | 0.01% D | 0.07%B | 0% D | 0% D |
| Actinobacteria | <i>Frigoribacterium</i> | 0.55%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Actinobacteria | <i>Gaiella</i> | 0.03%D | 0.07% B | 0.06% C | 0.05%C | 0.09%A | 0.02% D |
| Actinobacteria | <i>Geodermatophilus</i> | 0% B | 0% B | 0% B | .05% A | 0% B | 0.02% B |
| Actinobacteria | <i>Hamadaea</i> | 0.02%A | 0% A | 0% A | .02% A | 0% A | 0% A |
| Actinobacteria | <i>Leifsonia</i> | 0.59%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Actinobacteria | <i>Leucobacter</i> | 0.35%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Actinobacteria | <i>Luedemannella</i> | 0.02%B | 0.03% B | 0.11% A | 0.03%B | 0.02%B | 0% B |
| Actinobacteria | <i>Mycobacterium</i> | 0.06%C | 0.17% B | 0.17% B | 0.24% A | 0.08%C | 0.03% D |
| Actinobacteria | <i>Nocardia</i> | 0% B | 0% B | 0% B | 0% B | 0.12%A | 0% B |
| Actinobacteria | <i>Nonomuraea</i> | 0% B | 0% B | 0% B | 0% B | 0.07%A | 0% B |
| Actinobacteria | <i>Oerskovia</i> | 0.09%A | 0% A | 0% A | 0% A | 0% A | 0.12% A |
| Actinobacteria | <i>Paenarthrobacter</i> | 0.75%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Actinobacteria | <i>Promicromonospora</i> | 0.72%A | 0% A | 0% A | 0% A | 0% A | 0% A |

| | | | | | | | |
|----------------|----------------------------------|--------|---------|---------|---------|---------|----------|
| Actinobacteria | <i>Pseudonocardia</i> | 0.01%D | 0.01% D | 0.04% B | 0.07% A | 0.02%C | 0.01% CD |
| Actinobacteria | <i>Rhizocola</i> | 0.02%A | 0.01% B | 0.02% A | 0% B | 0% B | 0% B |
| Actinobacteria | <i>Rubrobacter</i> | 0.02%A | 0.01%A | 0.01%AB | 0% C | 0.01%C | 0.01% BC |
| Actinobacteria | <i>Saccharopolyspora</i> | 0.01%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Actinobacteria | <i>Salana</i> | 0.16%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Actinobacteria | <i>Sanguibacter</i> | 0.04%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Actinobacteria | <i>Solirubrobacter</i> | 0.07%D | 0.04% E | 0.09% C | 0.18%A | 0.11%B | 0.1% BC |
| Actinobacteria | <i>Sporichthya</i> | 0.09%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Actinobacteria | <i>Thermocatellispora</i> | 0.26%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Actinobacteria | <i>Williamsia</i> | 0.01%B | 0% B | 0.05% A | 0% B | 0% B | 0% B |
| Bacteroidetes | <i>Adhaeribacter</i> | 0.01%C | 0.01% B | 0.03% A | 0.01%B | 0.01% B | 0% C |
| Bacteroidetes | <i>Chryseobacterium</i> | 0% B | 0% B | 0.01% A | 0% B | 0% B | 0% B |
| Bacteroidetes | <i>Chryseolinea</i> | 0.02%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Bacteroidetes | <i>Cytophaga</i> | 0.02%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Bacteroidetes | <i>Dyadobacter</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Bacteroidetes | <i>Ferruginibacter</i> | 0% C | 0% C | 0.01% C | 0.02%B | 0.03%A | 0.01% C |
| Bacteroidetes | <i>Flaviumibacter</i> | 0% C | 0% C | 0.02% B | 0.03%A | 0% C | 0.02% B |
| Bacteroidetes | <i>Flavisolibacter</i> | 0% C | 0.02% A | 0% C | 0% C | 0.01%B | 0.01% B |
| Bacteroidetes | <i>Flavitalea</i> | 0.02%B | 0.03% A | 0.01% D | 0.01%C | 0% D | 0% D |
| Bacteroidetes | <i>Flavobacterium</i> | 0% D | 0.02% C | 0.03%BC | 0.03%C | 0.05%B | 0.09% A |
| Bacteroidetes | <i>Hymenobacter</i> | 0% B | 0% B | 0.01% A | 0.01% A | 0% B | 0% B |
| Bacteroidetes | <i>Ohtaekwangia</i> | 0.11%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Bacteroidetes | <i>Parafilimonas</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Bacteroidetes | <i>Parasegetibacter</i> | 0% B | 0% B | 0.01% B | 0% B | 0.03%A | 0% B |
| Bacteroidetes | <i>Pedobacter</i> | 0% C | 0% C | 0.03% A | 0.02%B | 0.03%A | 0.01% C |
| Bacteroidetes | <i>Pontibacter</i> | 0% A | 0.01% A | 0% A | 0% A | 0% A | 0.01% A |
| Bacteroidetes | <i>Sphingobacterium</i> | 0.03%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Bacteroidetes | <i>Terrimonas</i> | 0.01%C | 0.02% A | 0% C | 0% C | 0.01% C | 0.02% B |
| Chlamydiae | <i>Candidatus Protochlamydia</i> | 0% B | 0.01% A | 0% B | 0% B | 0% B | 0.01% B |
| Chloroflexi | <i>Nitrolancea</i> | 0.02%A | 0% B | 0.03% A | 0% B | 0.02%A | 0.02% AB |
| Firmicutes | <i>Ammoniphilus</i> | 0% C | 0.01% B | 0.02%AB | 0% C | 0.02%A | 0% C |
| Firmicutes | <i>Brevibacillus</i> | 0.02%C | 0.02% B | 0.03% A | 0.02%C | 0.01%C | 0.01% D |

| | | | | | | | |
|------------------|------------------------------|--------|---------|---------|---------|---------|----------|
| Firmicutes | <i>Cohnella</i> | 0.01%B | 0% C | 0% C | 0.02% A | 0% C | 0.01% AB |
| Firmicutes | <i>Desulfosporosinus</i> | 0% B | 0% B | 0% AB | 0% A | 0% B | 0% B |
| Firmicutes | <i>Effusibacillus</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Firmicutes | <i>Lysinibacillus</i> | 0% C | 0.16% A | 0.02% C | 0% C | 0.1% B | 0% C |
| Firmicutes | <i>Oceanobacillus</i> | 0.08%A | 0% B | 0% B | 0.01%B | 0% B | 0% B |
| Firmicutes | <i>Oxalophagus</i> | 0% A | 0.01% A | 0% A | 0% A | 0% A | 0.01% A |
| Firmicutes | <i>Paenibacillus</i> | 0.11%B | 0.12% A | 0.12% A | 0.1% B | 0.09%B | 0.06% C |
| Firmicutes | <i>Pseudogracilibacillus</i> | 0.38%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Firmicutes | <i>Psychrobacillus</i> | 0.13%A | 0% B | 0% B | 0% B | 0.02%B | 0% B |
| Firmicutes | <i>Romboutsia</i> | 0.03%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Firmicutes | <i>Rummeliibacillus</i> | 0.19%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Firmicutes | <i>Shimazuella</i> | 0.14%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Firmicutes | <i>Sporosarcina</i> | 0.06%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Firmicutes | <i>Thermoactinomyces</i> | 0% B | 0% B | 0% B | 0% A | 0% B | 0% B |
| Firmicutes | <i>Tumebacillus</i> | 0.01%D | 0.03% A | 0.01% C | 0.01%C | 0.01%C | 0.01%CD |
| Gemmatimonadetes | <i>Gemmatimonas</i> | 0.16%C | 0.32% A | 0% E | 0.07% D | 0.11%D | 0.25% B |
| Gemmatimonadetes | <i>Gemmatirosa</i> | 0.02%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Nitrospirae | <i>Nitrospira</i> | 0.04%B | 0.04% B | 0.01% D | 0.02%C | 0.03%B | 0.06% A |
| Planctomycetes | <i>Aquisphaera</i> | 0.03%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Planctomycetes | <i>Blastopirellula</i> | 0.04%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Planctomycetes | <i>Candidatus Nostocoida</i> | 0.01%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Planctomycetes | <i>Fimbrioglobus</i> | 0% B | 0.01% B | 0.02% A | 0.01%B | 0% B | 0% B |
| Planctomycetes | <i>Gemmata</i> | 0.02%C | 0.05% A | 0.01% C | 0% C | 0.03% B | 0.06% A |
| Planctomycetes | <i>Pirellula</i> | 0.03%A | 0.02% B | 0.02% B | .01% C | 0.03%A | 0.03% A |
| Planctomycetes | <i>Planctomicrobium</i> | 0% B | 0% B | 0% B | 0% B | 0.02% A | 0% B |
| Planctomycetes | <i>Planctopirus</i> | 0% A | 0% A | 0% A | 0% A | 0.02% A | 0% A |
| Planctomycetes | <i>Singulisphaera</i> | 0.02%A | 0% C | 0.02% A | 0.02% A | 0.01%C | 0.01% C |
| Proteobacteria | <i>Acidibacter</i> | 0.03%B | 0.05% A | 0.02%BC | 0.01%E | 0.02%D | 0.01% DE |
| Proteobacteria | <i>Acinetobacter</i> | 0.01%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Aetherobacter</i> | 0.01%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Aquabacterium</i> | 0.04%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Aquicella</i> | 0.01%A | 0% A | 0% A | 0% A | 0% A | 0% A |

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|----------------|---------------------------------|--------|---------|---------|---------|---------|----------|
| Proteobacteria | <i>Arenimonas</i> | 0.01%C | 0.03% B | 0.04% B | 0.03%B | 0.05%A | 0.01% C |
| Proteobacteria | <i>Bacteriovorax</i> | 0% B | 0% B | 0% B | 0% B | 0% B | 0% A |
| Proteobacteria | <i>Bdellovibrio</i> | 0.05%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Caenimonas</i> | 0% B | 0% B | 0.2% B | 0% B | 0% B | 0.04% A |
| Proteobacteria | <i>Candidatus Alysiosphaera</i> | 0.03%B | 0% C | 0% C | 0% C | 0.8% A | 0% C |
| Proteobacteria | <i>Cellvibrio</i> | 0.05%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Coxiella</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Cupriavidus</i> | 0% B | 0% B | 0% B | 0.01% A | 0.01% A | 0% B |
| Proteobacteria | <i>Dokdonella</i> | 0.01%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Geminicoccus</i> | 0% B | 0% B | 0% B | 0.02% | 0% B | 0% B |
| Proteobacteria | <i>Haliangium</i> | 0.02%A | 0.01% C | 0% D | 0.01% D | 0% D | 0.01% B |
| Proteobacteria | <i>Herbaspirillum</i> | 0.04%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Hirschia</i> | 0% A | 0% A | 0.02% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Legionella</i> | 0.05%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Luteimonas</i> | 0.03%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Lysobacter</i> | 0.15%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Massilia</i> | 0% B | 0.01%B | 0.03%A | 0.03% A | 0.03% A | 0.02% A |
| Proteobacteria | <i>Methylibium</i> | 0.05%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Methylobacterium</i> | 0% A | 0% A | 0.08% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Methylothermobacter</i> | 0.05%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Minicystis</i> | 0.05%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Nannocystis</i> | 0% C | 0% B | 0% C | .01% A | 0% C | 0% C |
| Proteobacteria | <i>Nitrobacter</i> | 0% A | 0% A | 0% A | .02% A | 0% A | 0% A |
| Proteobacteria | <i>Nitrosospora</i> | 0% B | 0% B | 0.01% B | 0.12% | 0% B | 0.01% B |
| Proteobacteria | <i>Nordella</i> | 0.19%B | 0.48%A | 0% D | 0% D | 0.03%D | 0.17% BC |
| Proteobacteria | <i>Noviherbaspirillum</i> | 0.03%B | 0.04% A | 0% C | 0% C | 0% C | 0.04% A |
| Proteobacteria | <i>Pajaroellobacter</i> | 0.01%C | 0% C | 0.02% A | 0.02%B | 0.02%B | 0.02% B |
| Proteobacteria | <i>Peredibacter</i> | 0% B | 0% B | 0.01% A | 0% B | 0% B | 0% B |
| Proteobacteria | <i>Phaselicystis</i> | 0.07%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Polycyclovorans</i> | 0.01%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Porphyrobacter</i> | 0.12%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Pseudenhymyxa</i> | 0.01%A | 0% A | 0% A | 0% A | 0% A | 0% A |

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|------------------|-------------------------------|--------|---------|---------|--------|--------|----------|
| Proteobacteria | <i>Pseudomonas</i> | 0% C | 0.02% B | 0.02% B | 0.01%C | 0.04%A | 0.03% B |
| Proteobacteria | <i>Pseudoxanthomonas</i> | 0% B | 0% B | 0.01% A | 0% B | 0% B | 0% B |
| Proteobacteria | <i>Rahnella</i> | 0.01%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Ramlibacter</i> | 0.03%C | 0.09% A | 0.04% B | 0.04%B | 0.02%D | 0.02% CD |
| Proteobacteria | <i>Reyranella</i> | 0.1%A | 0% D | 0% D | 0.06%C | 0.12%A | 0.07% BC |
| Proteobacteria | <i>Roseomonas</i> | 0% B | 0.09% A | 0% B | 0% B | 0% B | 0% B |
| Proteobacteria | <i>Skermanella</i> | 0% B | 0% B | 0% B | 0% B | 0.02%B | 0.21% A |
| Proteobacteria | <i>Sorangium</i> | 0.07%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Stenotrophomonas</i> | 0.04%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Steroidobacter</i> | 0.03%A | 0.02% B | 0.01% D | 0.01% | 0.01%C | 0.01%CD |
| Proteobacteria | <i>Tabrizicola</i> | 0.24%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Proteobacteria | <i>Thermomonas</i> | 0% C | 0% C | 0% C | 0.01%B | 0.02%A | 0.01% AB |
| Proteobacteria | <i>Variovorax</i> | 0% C | 0.01% B | 0.01% C | 0.01%C | 0.04%A | 0.01% C |
| Proteobacteria | <i>Vulgatibacter</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Verrucomicrobia | <i>Candidatus Udaeobacter</i> | 0.02%B | 0.02% B | 0.01% C | 0.05A | 0.03%B | 0.02% BC |
| Verrucomicrobia | <i>Chthoniobacter</i> | 0.02%A | 0.01% C | 0.01% B | 0.01%C | 0.01%D | 0.01% BC |
| Verrucomicrobia | <i>Luteolibacter</i> | 0% B | 0.01% B | 0.03% A | 0.01%B | 0.02%A | 0.02% A |
| Verrucomicrobia | <i>Opitutus</i> | 0% A | 0% A | 0% A | 0% A | 0.07%A | 0.01% A |
| Verrucomicrobia | <i>Pedosphaera</i> | 0.02%A | 0% B | 0% B | 0% B | 0% B | 0% B |
| Verrucomicrobia | <i>Prostheco bacter</i> | 0.02%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Verrucomicrobia | <i>Roseimicrobium</i> | 0% C | 0% C | 0% C | 0% C | 0.01%B | 0.01% A |
| Verrucomicrobia | <i>Verrucomicrobium</i> | 0.01%A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Cluster centroid | | 0.06%A | 0.02%B | 0.01%B | 0.01%B | 0.01%B | 0.02% B |

^aCluster was created by K-means clustering algorithm in R separating OTU abundance over dph into 10 clusters [35]. Cluster centroid was created by the average within the K-mean cluster.

^bLetter following percentages indicate significant difference over time based on general lineal model ANOVA followed by Fisher's Least Significant Difference LSD test $p < 0.05$.

Table S10. Comparison of bacterial cluster 9 of OTU abundance for unidentified bacteria at genus level over time. Average number of genus-level OTUs per g soil from five plots in a commercial American ginseng *Panax quinquefolius* garden at just prior -5 dph and after harvest 10, 41, 73, 198 and 231 dph. Genus names for OTUs identified based on 97% nt identity of the 440 - 476 bp V3-V4 region of the 16S rRNA using USEARCH with the SILVA 132 SSU NR99 database (<https://www.arb-silva.de/>).

| Percentage of abundance per OTUs per undescribed genera in cluster 9-1 ^a | | | | | | | |
|---|-------|----------------------|----------|----------|----------|----------|----------|
| Phylum | Genus | -5 dph | 10 dph | 41 dph | 73 dph | 198 dph | 231 dph |
| Abditibacteriota | 1 | 0.08% A ^b | 0% A | 0% A | 0% A | 0% A | 0% A |
| Acidobacteria | 1 | 0.1% AB | 0.05% BC | 0% C | 0.01% C | 0.01% C | 0.14% A |
| Acidobacteria | 2 | 0.01% A | 0.01% A | 0.01% B | 0% C | 0.01% A | 0.01% A |
| Acidobacteria | 3 | 0% B | 0.02% A | 0% C | 0% BC | 0.01% A | 0% BC |
| Acidobacteria | 4 | 0.01% C | 0.08% B | 0% C | 0.29% A | 0.09% B | 0% C |
| Acidobacteria | 5 | 0.02% C | 0.01% C | 0.01% C | 0% D | 0.03% A | 0.02% B |
| Acidobacteria | 6 | 0% D | 0.01% B | 0% C | 0.01% A | 0% CD | 0% C |
| Acidobacteria | 7 | 0.01% A | 0% D | 0% C | 0% C | 0.01% B | 0% C |
| Acidobacteria | 8 | 0% B | 0.02% B | 0.01% B | 0% B | 0.2% A | 0.01% B |
| Acidobacteria | 9 | 0.07% A | 0.01% D | 0.01% D | 0.06% B | 0.06% B | 0.02% C |
| Acidobacteria | 10 | 0.04% B | 0% C | 0.05% A | 0% C | 0.01% C | 0% C |
| Acidobacteria | 11 | 0.01% B | 0% B | 0% B | 0% B | 0.02% B | 0.05% A |
| Acidobacteria | 12 | 0% C | 0.02% B | 0% C | 0.03% A | 0.01% C | 0.01% C |
| Acidobacteria | 13 | 0% C | 0% B | 0.01% A | 0% C | 0% B | 0% B |
| Acidobacteria | 14 | 0% CD | 0.02% A | 0.01% B | 0% C | 0% DE | 0% E |
| Acidobacteria | 15 | 0.02% A | 0.01% BC | 0.01% B | 0.01% B | 0.01% C | 0% D |
| Acidobacteria | 16 | 0.02% B | 0% D | 0% D | 0.01% C | 0% D | 0.03% A |
| Acidobacteria | 17 | 0.05% B | 0.01% C | 0% C | 0.01% C | 0.04% B | 0.1% A |
| Acidobacteria | 18 | 0.02% A | 0.01% A | 0% C | 0.02% A | 0.01% B | 0% BC |
| Acidobacteria | 19 | 0.01% B | 0.03% A | 0.01% B | 0.01% B | 0.03% A | 0.01% B |
| Acidobacteria | 20 | 0.01% D | 0.03% A | 0.01% CD | 0.01% C | 0.02% B | 0.03% AB |
| Actinobacteria | 1 | 0.02% AB | 0.04% A | 0.01% B | 0.01% B | 0.03% AB | 0.01% B |
| Actinobacteria | 2 | 0.02% B | 0.01% BC | 0.01% BC | 0.02% BC | 0% C | 0.29% A |
| Actinobacteria | 3 | 0.32% A | 0.07% C | 0.09% C | 0.01% D | 0.02% D | 0.17% B |
| Actinobacteria | 4 | 0.06% B | 0.25% A | 0.01% C | 0.01% C | 0% C | 0.01% C |
| Actinobacteria | 5 | 0.01% D | 0.03% D | 0.3% A | 0.06% CD | 0.16% B | 0.13% BC |
| Actinobacteria | 6 | 0.03% BC | 0% C | 0% C | 0.01% C | 0.07% B | 0.4% A |
| Actinobacteria | 7 | 0.05% B | 0.07% A | 0.04% B | 0% C | 0.08% A | 0.08% A |
| Actinobacteria | 8 | 0% C | 0.01% BC | 0% C | 0.02% BC | 0.02% B | 0.21% A |
| Actinobacteria | 9 | 0% D | 0.02% BC | 0% D | 0.12% A | 0.03% B | 0.01% CD |
| Actinobacteria | 10 | 0% D | 0.16% C | 0% D | 0.26% AB | 0.21% BC | 0.28% A |
| Actinobacteria | 11 | 0.1% B | 0.01% C | 0% C | 0.03% C | 0.16% A | 0% C |

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|------------------------|----|---------|----------|----------|----------|----------|----------|
| Actinobacteria | 12 | 0% C | 0% C | 0% C | 0.08% A | 0.01% C | 0.06% B |
| Armatimonadetes | 1 | 0% B | 0% B | 0% B | 0.01% B | 0.03% A | 0% B |
| Bacterial rice cluster | 1 | 0% B | 0% B | 0% B | 0% A | 0% B | 0% A |
| Bacteroidetes | 1 | 0.04% A | 0.01% C | 0% D | 0.01% CD | 0.02% B | 0% CD |
| Bacteroidetes | 2 | 0.01% B | 0.02% A | 0% C | 0% C | 0% C | 0% C |
| Bacteroidetes | 3 | 0% B | 0.01% A | 0% B | 0.01% A | 0% B | 0% B |
| Bacteroidetes | 4 | 0% C | 0% C | 0.01% B | 0% C | 0.01% A | 0% C |
| Bacteroidetes | 5 | 0% BC | 0% C | 0% B | 0% BC | 0% B | 0.01% A |
| Bacteroidetes | 6 | 0% B | 0% B | 0% B | 0% B | 0% B | 0% A |
| Bacteroidetes | 7 | 0% B | 0% B | 0.02% A | 0% B | 0.02% A | 0% B |
| Bacteroidetes | 8 | 0% B | 0% B | 0% B | 0% B | 0% A | 0% B |
| Bacteroidetes | 9 | 0% C | 0% C | 0% C | 0.03% B | 0.08% A | 0.01% C |
| Bacteroidetes | 10 | 0% B | 0% B | 0% B | 0.01% B | 0% B | 0.05% A |
| Bacteroidetes | 11 | 0% B | 0% B | 0% B | 0% B | 0.01% B | 0.02% A |
| Bacteroidetes | 12 | 0% B | 0% B | 0% B | 0% B | 0% B | 0.01% A |
| Bacteroidetes | 13 | 0% B | 0% B | 0% B | 0% B | 0.01% A | 0% B |
| Bacteroidetes | 14 | 0% B | 0% B | 0% B | 0% B | 0% B | 0.02% A |
| Bacteroidetes | 15 | 0% B | 0% B | 0% B | 0% B | 0% B | 0.01% A |
| Chlamydiae | 1 | 0% B | 0% B | 0% B | 0% A | 0% B | 0% B |
| Chloroflexi | 1 | 0% B | 0.18% AB | 0.65% A | 0.55% A | 0.14% AB | 0% B |
| Chloroflexi | 2 | 0% B | 0.74% A | 0% B | 0% B | 0.21% B | 0% B |
| Chloroflexi | 3 | 0.11% B | 0% C | 0.01% C | 0.01% C | 1.52% A | 0% C |
| Chloroflexi | 4 | 0.87% A | 0% C | 0.15% B | 0.07% BC | 0.01% C | 0.07% BC |
| Chloroflexi | 5 | 0% C | 0.27% A | 0% C | 0.01% C | 0.05% B | 0% C |
| Chloroflexi | 6 | 0% C | 0.01% C | 0.27% A | 0.1% B | 0.04% BC | 0% C |
| Chloroflexi | 7 | 0% C | 0.03% BC | 0% C | 0% BC | 0.03% B | 0.11% A |
| Chloroflexi | 8 | 0% E | 0.86% A | 0.31% B | 0.14% D | 0.02% E | 0.22% C |
| Chloroflexi | 9 | 0% D | 0.15% C | 0.2% C | 0.85% A | 0% D | 0.65% B |
| Chloroflexi | 10 | 0% C | 0.03% BC | 0% C | 0.08% A | 0.04% B | 0% C |
| Chloroflexi | 11 | 0% C | 0.09% C | 0.45% B | 1.29% A | 0% C | 0% C |
| Chloroflexi | 12 | 0.04% A | 0% B | 0% B | 0.05% A | 0.01% B | 0% B |
| Chloroflexi | 13 | 0% C | 0% C | 0.21% B | 0.01% C | 0.72% A | 0% C |
| Chloroflexi | 14 | 0.03% B | 0.01% B | 0% B | 0% B | 0.09% A | 0.11% A |
| Chloroflexi | 15 | 0% D | 0% D | 0% D | 0.12% C | 0.25% A | 0.19% B |
| Chloroflexi | 16 | 0.03% B | 0.05% A | 0.01% CD | 0.04% AB | 0.02% C | 0% D |
| Chloroflexi | 17 | 0.02% C | 0.06% B | 0% C | 0% C | 0.11% A | 0% C |
| Chloroflexi | 18 | 0.15% A | 0% B | 0% B | 0% B | 0% B | 0% B |
| Chloroflexi | 19 | 0% B | 0.15% A | 0% B | 0% B | 0% B | 0% B |
| Chloroflexi | 20 | 0% B | 0% B | 0.22% A | 0% B | 0% B | 0% B |

| | | | | | | | |
|------------------|----|----------|---------|----------|----------|---------|----------|
| Chloroflexi | 21 | 0% B | 0.04% A | 0% B | 0% B | 0% B | 0% B |
| Chloroflexi | 22 | 0.04% A | 0.04% A | 0% A | 0% A | 0% A | 0% A |
| Chloroflexi | 23 | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Chloroflexi | 24 | 0% B | 0.06% A | 0% B | 0% B | 0% B | 0% B |
| Chloroflexi | 25 | 0% A | 0.01% A | 0% A | 0% A | 0% A | 0% A |
| Chloroflexi | 26 | 1.56% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Cyanobacteria | 1 | 0% B | 0% B | 0.1% A | 0% B | 0% B | 0% B |
| Cyanobacteria | 2 | 0% B | 0.07% A | 0% B | 0% B | 0.02% B | 0.05% AB |
| Cyanobacteria | 3 | 0.11% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Dependentiae | 1 | 0.03% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Firmicutes | 1 | 0.01% C | 0.01% A | 0% C | 0% C | 0.01% B | 0% C |
| Firmicutes | 2 | 0.02% A | 0.02% A | 0% B | 0% B | 0% B | 0% B |
| Firmicutes | 3 | 0.02% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Gemmatimonadetes | 1 | 0.12% B | 0.03% C | 0.24% A | 0.03% C | 0.02% C | 0% C |
| Gemmatimonadetes | 2 | 0.22% A | 0.01% B | 0.03% B | 0.19% A | 0.05% B | 0.04% B |
| Gemmatimonadetes | 3 | 0.03% B | 0.07% A | 0% C | 0.02% BC | 0.03% B | 0.06% A |
| Gemmatimonadetes | 4 | 0% D | 0% D | 0% D | 0.09% A | 0.02% C | 0.06% B |
| Gemmatimonadetes | 5 | 0% C | 0% C | 0.02% BC | 0% BC | 0.11% A | 0.03% B |
| Gemmatimonadetes | 6 | 0% B | 0% B | 0% B | 0.09% A | 0% B | 0% B |
| Gemmatimonadetes | 7 | 0.04% B | 0.04% B | 0.02% C | 0.15% A | 0% CD | 0% D |
| Gemmatimonadetes | 8 | 0.01% B | 0% CD | 0% D | 0.02% A | 0% C | 0% C |
| Gemmatimonadetes | 9 | 0% A | 0% B | 0% B | 0% B | 0% A | 0% B |
| Gemmatimonadetes | 10 | 0% AB | 0% B | 0% A | 0% A | 0% AB | 0% B |
| Gemmatimonadetes | 11 | 0% A | 0% B | 0% A | 0% B | 0% AB | 0% B |
| Gemmatimonadetes | 12 | 0% A | 0% B | 0% B | 0% B | 0% B | 0% B |
| Gemmatimonadetes | 13 | 0.01% A | 0% A | 0% A | 0% A | 0.01% A | 0% A |
| Gemmatimonadetes | 14 | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Gemmatimonadetes | 15 | 0.01% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Gemmatimonadetes | 16 | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Hydrogenedentes | 1 | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Latescibacteria | 1 | 0% B | 0% B | 0% B | 0% B | 0% A | 0% B |
| Latescibacteria | 2 | 0.01% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Patescibacteria | 1 | 0.12% A | 0.02% B | 0% B | 0.02% B | 0.03% B | 0.01% B |
| Patescibacteria | 2 | 0% C | 0% C | 0% C | 0.03% A | 0.01% B | 0.03% A |
| Patescibacteria | 3 | 0.01% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Planctomycetes | 1 | 0.28% A | 0.04% B | 0.01% B | 0.03% B | 0% B | 0.28% A |
| Planctomycetes | 2 | 0% C | 0.02% B | 0.01% BC | 0% C | 0.05% A | 0% C |
| Planctomycetes | 3 | 0.01% BC | 0.01% B | 0.02% A | 0% D | 0.01% C | 0% D |
| Planctomycetes | 4 | 0.02% B | 0% D | 0% D | 0.03% A | 0.01% C | 0.01% C |

| | | | | | | | |
|----------------|----|----------|---------|----------|----------|---------|----------|
| Planctomycetes | 5 | 0.02% B | 0.01% B | 0.18% A | 0% B | 0% B | 0% B |
| Planctomycetes | 6 | 0.01% B | 0% E | 0% C | 0% D | 0.02% A | 0% D |
| Planctomycetes | 7 | 0% C | 0.01% A | 0% BC | 0.01% A | 0% B | 0% BC |
| Planctomycetes | 8 | 0% C | 0.01% A | 0.01% B | 0% C | 0% C | 0% C |
| Planctomycetes | 9 | 0.02% B | 0.02% B | 0% C | 0.01% B | 0% C | 0.27% A |
| Planctomycetes | 10 | 0.01% B | 0.01% B | 0% C | 0% C | 0% BC | 0.04% A |
| Planctomycetes | 11 | 0.01% B | 0.01% B | 0.04% B | 0.01% B | 0.1% A | 0.01% B |
| Planctomycetes | 12 | 0% D | 0% D | 0% CD | 0.01% A | 0% C | 0.01% B |
| Planctomycetes | 13 | 0% B | 0% C | 0% BC | 0% BC | 0% C | 0.01% A |
| Planctomycetes | 14 | 0.01% C | 0.02% A | 0% D | 0% D | 0.01% B | 0.02% A |
| Planctomycetes | 15 | 0.01% C | 0% D | 0.02% B | 0% D | 0.03% A | 0.02% BC |
| Proteobacteria | 1 | 0% B | 0% B | 0.02% B | 0.01% B | 1.64% A | 0.01% B |
| Proteobacteria | 2 | 0.19% B | 0% C | 0% C | 0% C | 0.43% A | 0% C |
| Proteobacteria | 3 | 0.01% C | 0% C | 0.03% C | 0.22% B | 0.01% C | 1.01% A |
| Proteobacteria | 4 | 0% C | 0.01% C | 0.01% C | 0.45% A | 0.36% B | 0.01% C |
| Proteobacteria | 5 | 0% BC | 0% C | 0% BC | 0% C | 0.05% B | 0.56% A |
| Proteobacteria | 6 | 0.36% A | 0.01% B | 0.01% B | 0.02% B | 0.01% B | 0.06% B |
| Proteobacteria | 7 | 0.01% B | 0.02% B | 0.07% B | 0% B | 0.66% A | 0.04% B |
| Proteobacteria | 8 | 0.02% CD | 0.09% B | 0% D | 0% D | 0.04% C | 0.29% A |
| Proteobacteria | 9 | 0% B | 0.8% A | 0% B | 0.01% B | 0% B | 0% B |
| Proteobacteria | 10 | 0% B | 0.02% B | 0% B | 0% B | 0.43% A | 0% B |
| Proteobacteria | 11 | 0% C | 0% C | 0.79% A | 0% C | 0.02% C | 0.08% B |
| Proteobacteria | 12 | 0% B | 0% B | 0% C | 0% A | 0% B | 0% C |
| Proteobacteria | 13 | 0.03% BC | 0.05% B | 0.01% C | 0.05% B | 0.01% C | 0.11% A |
| Proteobacteria | 14 | 0% C | 0% C | 0.11% A | 0% C | 0.04% B | 0.01% C |
| Proteobacteria | 15 | 0.02% B | 0% B | 0% B | 0% B | 0.68% A | 0% B |
| Proteobacteria | 16 | 0% B | 0.62% A | 0.09% B | 0% B | 0.03% B | 0% B |
| Proteobacteria | 17 | 2.3% A | 0% B | 0.01% B | 0% B | 0% B | 0.02% B |
| Proteobacteria | 18 | 0% B | 0.04% B | 0.16% A | 0.01% B | 0% B | 0% B |
| Proteobacteria | 19 | 0% B | 0.03% A | 0% B | 0% B | 0.02% A | 0% B |
| Proteobacteria | 20 | 0% C | 0.09% A | 0.01% B | 0% C | 0% C | 0% C |
| Proteobacteria | 21 | 0.01% C | 0% C | 0.18% A | 0.01% C | 0.13% B | 0% C |
| Proteobacteria | 22 | 0% C | 0.01% B | 0.15% A | 0% BC | 0% BC | 0.01% BC |
| Proteobacteria | 23 | 0.05% B | 0% D | 0.01% CD | 0.03% BC | 0.18% A | 0% D |
| Proteobacteria | 24 | 0% C | 0% C | 1.09% A | 0.23% B | 0.01% C | 0% C |
| Proteobacteria | 25 | 0% B | 0% B | 0.8% A | 0.02% B | 0% B | 0.01% B |
| Proteobacteria | 26 | 0% DE | 0% C | 0% E | 0% CD | 0.01% B | 0.01% A |
| Proteobacteria | 27 | 0% B | 0% B | 0.1% A | 0.1% A | 0.02% B | 0% B |
| Proteobacteria | 28 | 0.01% B | 0% B | 0% B | 0.06% A | 0% B | 0.04% A |

| | | | | | | | |
|------------------|----|----------|---------|----------|---------|---------|---------|
| Proteobacteria | 29 | 0% C | 0% C | 0% C | 0.01% B | 0.01% B | 0.02% A |
| Proteobacteria | 30 | 0% B | 0% B | 0.03% B | 0.01% B | 0.15% A | 0.02% B |
| Proteobacteria | 31 | 0.05% A | 0% B | 0% B | 0% B | 0.01% B | 0.01% B |
| Rokubacteria | 1 | 0.01% BC | 0.02% A | 0% CD | 0% D | 0.01% B | 0.01% B |
| Rokubacteria | 2 | 0% C | 0% C | 0% C | 0.01% A | 0.01% B | 0% BC |
| Rokubacteria | 3 | 0% B | 0% B | 0% B | 0% A | 0% B | 0% B |
| Rokubacteria | 4 | 0.06% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Verrucomicrobia | 1 | 0% C | 0% B | 0% C | 0% C | 0.01% A | 0% B |
| Verrucomicrobia | 2 | 0.01% AB | 0% B | 0.01% AB | 0% B | 0.02% A | 0% AB |
| Verrucomicrobia | 3 | 0.01% B | 0% B | 0.02% A | 0% B | 0.01% B | 0% B |
| Verrucomicrobia | 4 | 0.09% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Zixibacteria | 1 | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Cluster centroid | | 0.06% A | 0.04% A | 0.05% A | 0.04% A | 0.07% A | 0.04% A |

^aCluster was created by K-means clustering algorithm in R separating OTU abundance over dph into 10 clusters [35]. Cluster centroid was created by the average within the K-mean cluster.

^bLetter following percentages indicate significant difference over time based on general lineal model ANOVA followed by Fisher's Least Significant Difference LSD test $p < 0.05$.

Table S11. Comparison of fungal cluster 1 of OTU abundance over time. Average number of genus-level OTUs per g soil from five plots in a commercial American ginseng *Panax quinquefolius* garden at just prior -5 dph and after harvest 10, 41, 73, 198 and 231 dph. Genus names for OTUs identified based on 97% nt identity of the 220 - 280 bp ITS2 region of the 18S rRNA using QIIME 2 with the UNITE v8.0 database (release 2019.10, <https://QIIME2.org/>).

| Percentage of abundance per OTUs per genera in cluster 1 ^a | | | | | | | |
|---|-------------------|---------------------|--------|---------|----------|---------|---------|
| Phylum | Genus | -5 dph | 10 dph | 41 dph | 73 dph | 198 dph | 231 dph |
| Ascomycota | <i>Plenodomus</i> | 1.4% B ^b | 1.3% B | 8.0% AB | 10.3% AB | 29.7% A | 3.5% AB |

^aCluster was created by K-means clustering algorithm in R separating OTU abundance over dph into 10 clusters [35]. Cluster centroid was created by the average within the K-mean cluster.

^bLetter following percentages indicate significant difference over time based on general lineal model ANOVA followed by Fisher's Least Significant Difference LSD test $p < 0.05$.

Table S12. Comparison of fungal cluster 2 of OTU abundance over time. Average number of genus-level OTUs per g soil from five plots in a commercial American ginseng *Panax quinquefolius* garden at just prior -5 dph and after harvest 10, 41, 73, 198 and 231 dph. Genus names for OTUs identified based on 97% nt identity of the 220 - 280 bp ITS2 region of the 18S rRNA using QIIME 2 with the UNITE v8.0 database (release 2019.10, <https://QIIME2.org/>).

| Percentage of abundance per OTUs per genera in cluster 2 ^a | | | | | | | |
|---|--------------------|----------------------|---------|---------|---------|---------|---------|
| Phylum | Genus | -5 dph | 10 dph | 41 dph | 73 dph | 198 dph | 231 dph |
| Ascomycota | <i>Trichoderma</i> | 24.6% A ^b | 24.9% A | 20.5% A | 14.4% A | 11.4% A | 17.0% A |

^aCluster was created by K-means clustering algorithm in R separating OTU abundance over dph into 10 clusters [35]. Cluster centroid was created by the average within the K-mean cluster.

^bLetter following percentages indicate significant difference over time based on general lineal model ANOVA followed by Fisher's Least Significant Difference LSD test $p < 0.05$.

Table S13. Comparison of fungal cluster 3 of OTU abundance over time. Average number of genus-level OTUs per g soil from five plots in a commercial American ginseng *Panax quinquefolius* garden at just prior -5 dph and after harvest 10, 41, 73, 198 and 231 dph. Genus names for OTUs identified based on 97% nt identity of the 220 - 280 bp ITS2 region of the 18S rRNA using QIIME 2 with the UNITE v8.0 database (release 2019.10, <https://QIIME2.org/>).

| Percentage of abundance per OTUs per genera in cluster 3 ^a | | | | | | | |
|---|------------------------|---------------------|--------|--------|---------|---------|---------|
| Phylum | Genus | -5 dph | 10 dph | 41 dph | 73 dph | 198 dph | 231 dph |
| Basidiomycota | <i>Subulicystidium</i> | 0.3% C ^b | 0% C | 0.5% C | 11.8% A | 1.1% B | 10.9% A |

^aCluster was created by K-means clustering algorithm in R separating OTU abundance over dph into 10 clusters [35]. Cluster centroid was created by the average within the K-mean cluster.

^bLetter following percentages indicate significant difference over time based on general lineal model ANOVA followed by Fisher's Least Significant Difference LSD test $p < 0.05$.

Table S14. Comparison of fungal cluster 4 of OTU abundance over time. Average number of genus-level OTUs per g soil from five plots in a commercial American ginseng *Panax quinquefolius* garden at just prior -5 dph and after harvest 10, 41, 73, 198 and 231 dph. Genus names for OTUs identified based on 97% nt identity of the 220 - 280 bp ITS2 region of the 18S rRNA using QIIME 2 with the UNITE v8.0 database (release 2019.10, <https://QIIME2.org/>).

| Percentage of abundance per OTUs per genera in cluster 4 ^a | | | | | | | |
|---|----------------------|---------------------|---------|---------|---------|---------|---------|
| Phylum | Genus | -5 dph | 10dph | 41 dph | 73 dph | 198 dph | 231 dph |
| Ascomycota | <i>Acremonium</i> | 4.7% A ^b | 5.6% A* | 3.1% A | 1.9% A | 3.0% A | 2.6% A |
| Ascomycota | <i>Ascomycota_24</i> | 3.9% A | 6.0% A | 5.0% A | 5.5% A | 0.9% A | 2.6% A |
| Ascomycota | <i>Ascomycota_33</i> | 1.2% A | 1.1% A | 4.3% A | 1.7% A | 4.0% A | 3.2% A |
| Ascomycota | <i>Penicillium</i> | 7.2% A | 5.6% A | 6.5% A | 1.7% A | 7.7% A | 5.2% A |
| Ascomycota | <i>Schizothecium</i> | 2.1% B | 0.9% B | 1.1% B | 2.8% AB | 1.5% B | 5.2% A |
| Ascomycota | <i>Talaromyces</i> | 3.2% AB | 2.0% B | 4.3% AB | 3.5% AB | 3.5% AB | 7.6% A |
| Mortierellomycota | <i>Mortierella</i> | 1.3% B | 4.7% A | 2.9% AB | 3.5% AB | 2.3% AB | 3.3% AB |
| Cluster centroid | | 3.4% A | 3.7% A | 3.9% A | 2.9% A | 3.3% A | 4.2 % A |

^aCluster was created by K-means clustering algorithm in R separating OTU abundance over dph into 10 clusters [35]. Cluster centroid was created by the average within the K-mean cluster.

^bLetter following percentages indicate significant difference over time based on general lineal model ANOVA followed by Fisher's Least Significant Difference LSD test $p < 0.05$.

Table S15. Comparison of fungal cluster 5 of OTU abundance over time. Average number of genus-level OTUs per g soil from five plots in a commercial American ginseng *Panax quinquefolius* garden at just prior -5 dph and after harvest 10, 41, 73, 198 and 231 dph. Genus names for OTUs identified based on 97% nt identity of the 220 - 280 bp ITS2 region of the 18S rRNA using QIIME 2 with the UNITE v8.0 database (release 2019.10, <https://QIIME2.org/>).

| Percentage of abundance per OTUs per genera in cluster 5 ^a | | | | | | | |
|---|---------------------------|---------------------|--------|--------|--------|---------|--------|
| Phylum | Genus | -5 dph | 10 dph | 41 dph | 73dph | 198 dph | 231dph |
| Ascomycota | <i>Ascomycota_01</i> | 0.2% A ^b | 0% B | 0% B | 0% B | 0% B | 1.2% A |
| Ascomycota | <i>Ascomycota_16</i> | 0% B | 0.8% A | 0.3% A | 0.4% A | 0.2% A | 1.1% A |
| Ascomycota | <i>Ascomycota_28</i> | 0.3% A | 0% B | 0.3% A | 0.5% A | 0.1% A | 1.6% A |
| Ascomycota | <i>Ascomycota_29</i> | 0% B | 0.7% A | 0.2% A | 1.0% A | 0% B | 0.4% A |
| Ascomycota | <i>Aspergillus</i> | 0.4% A | 0.2% A | 0.4% A | 0% B | 0.5% A | 0.9% A |
| Ascomycota | <i>Eucasphaeria</i> | 0% B | 0.5% A | 0.4% A | 0.1% A | 0.7% A | 0.2% A |
| Ascomycota | <i>Metapochonia</i> | 0.6% A | 0.7% A | 0.3% A | 0.3% A | 0.1% A | 0.4% A |
| Ascomycota | <i>Volutella</i> | 0.3% A | 0.6% A | 0.4% A | 0.3% A | 0.6% A | 0.5% A |
| Chytridiomycota | <i>Sclerostagonospora</i> | 0.1% A | 0.6% A | 1.0% A | 0.5% A | 0.3% A | 0.9% A |
| Chytridiomycota | <i>Spizellomyces_1</i> | 0.5% A | 0.4% A | 0.5% A | 0.1% A | 0.2% A | 0.4% A |
| Rozellomycota | <i>Rozellomycota</i> | 0.7% A | 0.8% A | 0.3% A | 0.3% A | 0.4% A | 0.6% A |
| Cluster centroid | | 0.3% A | 0.5% A | 0.4% A | 0.3% A | 0.3% A | 0.7% A |

^aCluster was created by K-means clustering algorithm in R separating OTU abundance over dph into 10 clusters [35]. Cluster centroid was created by the average within the K-mean cluster.

^bLetter following percentages indicate significant difference over time based on general lineal model ANOVA followed by Fisher's Least Significant Difference LSD test $p < 0.05$.

Table S16. Comparison of fungal cluster 6 of OTU abundance over time. Average number of genus-level OTUs per g soil from five plots in a commercial American ginseng *Panax quinquefolius* garden at just prior -5 dph and after harvest 10, 41, 73, 198 and 231 dph. Genus names for OTUs identified based on 97% nt identity of the 220 - 280 bp ITS2 region of the 18S rRNA using QIIME 2 with the UNITE v8.0 database (release 2019.10, <https://QIIME2.org/>).

| Phylum | Genus | Percentage of abundance per OTUs per genera in cluster 6 ^a | | | | | |
|------------|----------------------|---|--------|--------|---------|---------|---------|
| | | -5 dph | 10 dph | 41 dph | 73 dph | 198 dph | 231 dph |
| Ascomycota | <i>Ascomycota_04</i> | 1.4% AB ^b | 2.1% A | 0.3% C | 0.9% B | 0.8% B | 0.6% B |
| Ascomycota | <i>Ascomycota_26</i> | 2.4% B | 3.0% A | 1.7% B | 3.3% A | 0.5% B | 0.9% B |
| Ascomycota | <i>Ascomycota_27</i> | 2.9% B | 5.1% A | 0.7% B | 1.7% B | 1.1% B | 0.5% C |
| Ascomycota | <i>Ascomycota_30</i> | 1.9% B | 2.7% A | 1.1% B | 1.6% B | 0.9% B | 0.6% B |
| Ascomycota | <i>Ascomycota_34</i> | 1.6% B | 2.6% A | 0% D | 1.6% B | 0.2% C | 0% D |
| Ascomycota | <i>Chaetomium</i> | 1.3% B | 4.1% A | 0.6% B | 1.4% B | 2.5% AB | 0.5% B |
| Ascomycota | <i>Sarocladium</i> | 2.6% A | 2.1% A | 3.9% A | 0.7% A | 1.5% A | 1.0% A |
| | Cluster centroid | 2.0% AB | 3.1% A | 1.2% B | 1.6% AB | 1.1% B | 0.6% B |

^aCluster was created by K-means clustering algorithm in R separating OTU abundance over dph into 10 clusters [35]. Cluster centroid was created by the average within the K-mean cluster.

^bLetter following percentages indicate significant difference over time based on general lineal model ANOVA followed by Fisher's Least Significant Difference LSD test $p < 0.05$.

Table S17. Comparison of fungal cluster 7 of OTU abundance over time. Average number of genus-level OTUs per g soil from five plots in a commercial American ginseng *Panax quinquefolius* garden at just prior -5 dph and after harvest 10, 41, 73, 198 and 231 dph. Genus names for OTUs identified based on 97% nt identity of the 220 - 280 bp ITS2 region of the 18S rRNA using QIIME 2 with the UNITE v8.0 database (release 2019.10, <https://QIIME2.org/>).

| Percentage of abundance per OTUs per genera in cluster 7 ^a | | | | | | | |
|---|----------------------|---------------------|---------|---------|---------|---------|---------|
| Phylum | Genus | -5 dph | 10 dph | 41 dph | 73 dph | 198 dph | 231 dph |
| Ascomycota | <i>Alternaria</i> | 2.4% A ^b | 0% C | 1.2% B | 0.2% B | 0.1% B | 0.5% B |
| Ascomycota | <i>Ascomycota_21</i> | 0.6% B | 0% C | 0% C | 0.4% B | 1.1% A | 0.6% B |
| Ascomycota | <i>Neosetophoma</i> | 1.4% A | 0.8% A | 0.5% A | 0.9% A | 0.7% A | 0.9% A |
| Ascomycota | <i>Oidiodendron</i> | 1.6% A | 0% C | 0.9% AB | 0.3% B | 0.2% B | 0.3% B |
| Ascomycota | <i>Tetracladium</i> | 2.6% A | 0.5% B | 0.2% B | 0.3% B | 0.6% B | 0.5% B |
| | Cluster centroid | 1.7% A | 0.3% AB | 0.6% AB | 0.4% AB | 0.5% AB | 0.5% AB |

^aCluster was created by K-means clustering algorithm in R separating OTU abundance over dph into 10 clusters [35]. Cluster centroid was created by the average within the K-mean cluster.

^bLetter following percentages indicate significant difference over time based on general lineal model ANOVA followed by Fisher's Least Significant Difference LSD test $p < 0.05$.

Table S18. Comparison of fungal cluster 8 of OTU abundance over time. Average number of genus-level OTUs per g soil from five plots in a commercial American ginseng *Panax quinquefolius* garden at just prior -5 dph and after harvest 10, 41, 73, 198 and 231 dph. Genus names for OTUs identified based on 97% nt identity of the 220 - 280 bp ITS2 region of the 18S rRNA using QIIME 2 with the UNITE v8.0 database (release 2019.10, <https://QIIME2.org/>).

| | | Percentage of abundance per OTUs per genera in cluster 8 ^a | | | | | |
|------------------|----------------------|---|--------|---------|--------|---------|---------|
| Phylum | Genus | -5 dph | 10 dph | 41 dph | 73 dph | 198 dph | 231 dph |
| Ascomycota | <i>Ascomycota_11</i> | 0% D ^b | 0.1% C | 2.1% B | 2.9% A | 0.1% C | 0% D |
| Ascomycota | <i>Ascomycota_18</i> | 1.0% B | 1.1% B | 2.3% AB | 2.4% A | 1.5% B | 0.5% B |
| Ascomycota | <i>Ascomycota_23</i> | 1.0% B | 1.1% B | 0.6% BC | 1.9% A | 0.2% C | 0% D |
| Cluster centroid | | 0.7% B | 0.7% B | 1.7% B | 2.4% A | 0.6% B | 0.2% B |

^aCluster was created by K-means clustering algorithm in R separating OTU abundance over dph into 10 clusters [35]. Cluster centroid was created by the average within the K-mean cluster.

^bLetter following percentages indicate significant difference over time based on general lineal model ANOVA followed by Fisher's Least Significant Difference LSD test $p < 0.05$.

Table S19. Comparison of fungal cluster 9 of OTU abundance over time. Average number of genus-level OTUs per g soil from five plots in a commercial American ginseng *Panax quinquefolius* garden at just prior -5 dph and after harvest 10, 41, 73, 198 and 231 dph. Genus names for OTUs identified based on 97% nt identity of the 220 - 280 bp ITS2 region of the 18S rRNA using QIIME 2 with the UNITE v8.0 database (release 2019.10, <https://QIIME2.org/>).

| Percentage of abundance per OTUs per genera in cluster 9 ^a | | | | | | | |
|---|-----------------------|--------|--------|--------|--------|---------|---------|
| Phylum | Genus | -5 dph | 10 dph | 41 dph | 73 dph | 198 dph | 231 dph |
| Ascomycota | <i>Arcopilus</i> | 0% AB | 0.1% A | 0.1% A | 0% A | 0% A | 0.2% A |
| Ascomycota | <i>Arthrinium</i> | 0.3% A | 0% A | 0% A | 0.2% A | 0.1% A | 0% A |
| Ascomycota | <i>Articulospora</i> | 0% A | 0% A | 0.1% A | 0% A | 0.1% A | 0% A |
| Ascomycota | <i>Ascomycota_02</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_06</i> | 0% A | 0% A | 0% A | 0% A | 0.1% A | 0.1% A |
| Ascomycota | <i>Ascomycota_07</i> | 0% A | 0.2% A | 0.0% A | 0% A | 0.0% A | 0.0% A |
| Ascomycota | <i>Ascomycota_08</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_09</i> | 0% A | 0% A | 0.2% A | 0.1% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_10</i> | 0% A | 0% A | 0.0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_12</i> | 0% A | 0% A | 0.2% A | 0.3% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_13</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_14</i> | 0% A | 0% A | 0% A | 0% A | 0.3% A | 0% A |
| Ascomycota | <i>Ascomycota_15</i> | 0% A | 0.2% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_20</i> | 0% A | 0.4% A | 0% A | 0.3% A | 0.1% A | 0.1% A |
| Ascomycota | <i>Ascomycota_31</i> | 0% A | 0% A | 0.0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_32</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_37</i> | 0% A | 0% A | 0% A | 0% A | 0.1% A | 0% A |
| Ascomycota | <i>Ascomycota_38</i> | 0% A | 0.2% A | 0.3% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_39</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_40</i> | 0.1% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_41</i> | 0% A | 0% A | 0% A | 0.1% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_42</i> | 0% A | 0% A | 0.1% A | 0.1% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_43</i> | 0.2% A | 0.3% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_44</i> | 0.0% A | 0% A | 0.0% A | 0% A | 0% A | 0.1% A |
| Ascomycota | <i>Ascomycota_45</i> | 0% A | 0.2% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_46</i> | 0% A | 0% A | 0% A | 0% A | 0.0% A | 0% A |
| Ascomycota | <i>Bipolaris</i> | 0.2% A | 0% B | 0% B | 0% B | 0% B | 0% B |
| Ascomycota | <i>Cercophora</i> | 0% A | 0% A | 0.1% A | 0% A | 0.1% A | 0.1% A |
| Ascomycota | <i>Chaetosphaeria</i> | 0% A | 0% A | 0% A | 0.1% A | 0% A | 0.3% A |
| Ascomycota | <i>Chrysosporium</i> | 0.2% A | 0% A | 0.1% A | 0% A | 0.1% A | 0% A |
| Ascomycota | <i>Cistella</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Colletotrichum</i> | 0% B | 0% B | 0% B | 0% B | 0% B | 0.2% A |
| Ascomycota | <i>Cytospora</i> | 0% A | 0.0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Dactylella</i> | 0% B | 0% B | 0.3% A | 0% B | 0% B | 0% B |
| Ascomycota | <i>Dinemasporium</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Hymenoscyphus</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0.2% A |

| | | | | | | | |
|-----------------|---------------------------|--------|--------|--------|--------|--------|--------|
| Ascomycota | <i>Hymenula</i> | 0% A | 0.1% A | 0.2% A | 0.1% A | 0% A | 0% A |
| Ascomycota | <i>Iodophanus</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Knufia</i> | 0% B | 0% B | 0% B | 0% B | 0.2% A | 0% B |
| Ascomycota | <i>Lecythophora</i> | 0.1% A | 0% A | 0% A | 0.2% A | 0.1% A | 0.1% A |
| Ascomycota | <i>Malbranchea</i> | 0.3% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Murisporia</i> | 0% A | 0% A | 0% A | 0.1% A | 0% A | 0.2% A |
| Ascomycota | <i>Myrmecridium</i> | 0% B | 0% B | 0% B | 0.6% A | 0% B | 0% B |
| Ascomycota | <i>Paraphoma</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Parathyridaria</i> | 0% B | 0% B | 0% B | 0.6% A | 0% B | 0% B |
| Ascomycota | <i>Phialemonium</i> | 0% A | 0% A | 0% A | 0% A | 0.1% A | 0.1% A |
| Ascomycota | <i>Pseudodogymnoacs</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Stachybotrys</i> | 0% A | 0% A | 0% A | 0% A | 0.2% A | 0% A |
| Basidiomycota | <i>Basidiomycota_02</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0.4% A |
| Basidiomycota | <i>Basidiomycota_03</i> | 0% A | 0% A | 0% A | 0.1% A | 0% A | 0% A |
| Basidiomycota | <i>Basidiomycota_07</i> | 0% A | 0% A | 0% A | 0.0% A | 0% A | 0% A |
| Basidiomycota | <i>Basidiomycota_08</i> | 0% A | 0% A | 0% A | 0.3% A | 0% A | 0.1% A |
| Basidiomycota | <i>Basidiomycota_10</i> | 0% A | 0% A | 0% A | 0% A | 0.0% A | 0% A |
| Basidiomycota | <i>Bovista</i> | 0% A | 0% A | 0% A | 0% A | 0.0% A | 0% A |
| Basidiomycota | <i>Conocybe</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Basidiomycota | <i>Crepidotus</i> | 0% A | 0% A | 0% A | 0.1% A | 0% A | 0% A |
| Basidiomycota | <i>Entoloma</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Basidiomycota | <i>Filobasidium</i> | 0.3% A | 0% B | 0% B | 0% B | 0% B | 0% B |
| Basidiomycota | <i>Geminibasidium</i> | 0% B | 0.3% A | 0% B | 0% B | 0% B | 0% B |
| Basidiomycota | <i>Heterocephalacria</i> | 0.1% A | 0.2% A | 0% A | 0.1% A | 0% A | 0% A |
| Basidiomycota | <i>Irpex</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Basidiomycota | <i>Mycena</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Basidiomycota | <i>Peniophora</i> | 0% A | 0% A | 0% A | 0.1% A | 0% A | 0% A |
| Basidiomycota | <i>Phlebia</i> | 0% A | 0% A | 0% A | 0.1% A | 0% A | 0% A |
| Basidiomycota | <i>Piskurozyma</i> | 0% A | 0% A | 0% A | 0.0% A | 0% A | 0% A |
| Basidiomycota | <i>Plicaturopsis</i> | 0% A | 0% A | 0% A | 0.1% A | 0% A | 0% A |
| Basidiomycota | <i>Pluteus</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Basidiomycota | <i>Postia</i> | 0% A | 0% A | 0% A | 0.1% A | 0% A | 0% A |
| Basidiomycota | <i>Psathyrella</i> | 0% A | 0% A | 0.1% A | 0% A | 0% A | 0% A |
| Basidiomycota | <i>Scopuloides</i> | 0% A | 0% A | 0.1% A | 0% A | 0% A | 0% A |
| Basidiomycota | <i>Sistotrema</i> | 0% A | 0% A | 0.2% A | 0.1% A | 0% A | 0% A |
| Basidiomycota | <i>Solicoccozyma</i> | 0.1% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Basidiomycota | <i>Steccherinum</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Basidiomycota | <i>Suillus</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Basidiomycota | <i>Trametes</i> | 0% A | 0% A | 0% A | 0.1% A | 0% A | 0% A |
| Basidiomycota | <i>Udeniozyma</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Basidiomycota | <i>Waitea</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Chytridiomycota | <i>Chytridiomycota_01</i> | 0.2% A | 0.1% A | 0.1% A | 0.1% A | 0.1% A | 0% A |
| Chytridiomycota | <i>Chytridiomycota_02</i> | 0% A | 0% A | 0% A | 0% A | 0.1% A | 0.1% A |

| | | | | | | | |
|------------------|---------------------------|---------|---------|---------|---------|---------|---------|
| Chytridiomycota | <i>Chytridiomycota_03</i> | 0% A | 0% A | 0% A | 0% A | 0.1% A | 0% A |
| Chytridiomycota | <i>Operculomyces</i> | 0.2% A | 0% A | 0.1% A | 0% A | 0% A | 0% A |
| Chytridiomycota | <i>Powellomyces</i> | 0% A | 0% A | 0% A | 0% A | 0.1% A | 0% A |
| Chytridiomycota | <i>Rhizophlyctis</i> | 0.1% A | 0.2% A | 0% A | 0.1% A | 0% A | 0% A |
| Chytridiomycota | <i>Spizellomyces</i> | 0% A | 0.1% A | 0.0% A | 0.1% A | 0.0% A | 0% A |
| Mucoromycota | <i>Umbelopsis</i> | 0% A | 0% A | 0% A | 0.0% A | 0% A | 0% A |
| Zoopagomycota | <i>Zoopagomycota</i> | 0% B | 0% B | 0% B | 0.3% A | 0% B | 0% B |
| Cluster centroid | | 0.003%A | 0.003%A | 0.003%A | 0.005%A | 0.002%A | 0.003%A |

^aCluster was created by K-means clustering algorithm in R separating OTU abundance over dph into 10 clusters [35]. Cluster centroid was created by the average within the K-mean cluster.

^bLetter following percentages indicate significant difference over time based on general lineal model ANOVA followed by Fisher's Least Significant Difference LSD test $p < 0.05$.

Table S20. Comparison of fungal cluster 10 of OTU abundance over time. Average number of genus-level OTUs per g soil from five plots in a commercial American ginseng *Panax quinquefolius* garden at just prior -5 dph and after harvest 10, 41, 73, 198 and 231 dph. Genus names for OTUs identified based on 97% nt identity of the 220 - 280 bp ITS2 region of the 18S rRNA using QIIME 2 with the UNITE v8.0 database (release 2019.10, <https://QIIME2.org/>).

| Phylum | Genus | Percentage of abundance per OTUs per genera in cluster 10 ^a | | | | | |
|------------|----------------------|--|--------|--------|--------|---------|---------|
| | | -5 dph | 10 dph | 41 dph | 73 dph | 198 dph | 231 dph |
| Ascomycota | <i>Arcopilus</i> | 0% A ^b | 0.1% A | 0.1% A | 0% A | 0% A | 0.2% A |
| Ascomycota | <i>Arthrinium</i> | 0.3% A | 0% A | 0% A | 0.2% A | 0.1% A | 0% A |
| Ascomycota | <i>Articulospora</i> | 0% A | 0% A | 0.1% A | 0% A | 0.1% A | 0% A |
| Ascomycota | <i>Ascomycota_02</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_06</i> | 0% A | 0% A | 0% A | 0% A | 0.1% A | 0.1% A |
| Ascomycota | <i>Ascomycota_07</i> | 0% A | 0.2% A | 0.0% A | 0% A | 0.0% A | 0.0% A |
| Ascomycota | <i>Ascomycota_08</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_09</i> | 0% A | 0% A | 0.2% A | 0.1% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_10</i> | 0% A | 0% A | 0.0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_12</i> | 0% A | 0% A | 0.2% A | 0.3% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_13</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_14</i> | 0% A | 0% A | 0% A | 0% A | 0.3% A | 0% A |
| Ascomycota | <i>Ascomycota_15</i> | 0% A | 0.2% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_20</i> | 0% A | 0.4% A | 0% A | 0.3% A | 0.1% A | 0.1% A |
| Ascomycota | <i>Ascomycota_31</i> | 0% A | 0% A | 0.0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_32</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_37</i> | 0% A | 0% A | 0% A | 0% A | 0.1% A | 0% A |
| Ascomycota | <i>Ascomycota_38</i> | 0% A | 0.2% A | 0.3% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_39</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_40</i> | 0.1% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_41</i> | 0% A | 0% A | 0% A | 0.1% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_42</i> | 0% A | 0% A | 0.1% A | 0.1% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_43</i> | 0.2% A | 0.3% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_44</i> | 0.0% A | 0% A | 0.0% A | 0% A | 0% A | 0.1% A |
| Ascomycota | <i>Ascomycota_45</i> | 0% A | 0.2% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Ascomycota_46</i> | 0% A | 0% A | 0% A | 0% A | 0.0% A | 0% A |
| Ascomycota | <i>Bipolaris</i> | 0.2% A | 0% B | 0% B | 0% B | 0% B | 0% B |

| | | | | | | | |
|---------------|--------------------------|--------|--------|--------|--------|--------|--------|
| Ascomycota | <i>Cercophora</i> | 0% A | 0% A | 0.1% A | 0% A | 0.1% A | 0.1% A |
| Ascomycota | <i>Chaetosphaeria</i> | 0% A | 0% A | 0% A | 0.1% A | 0% A | 0.3% A |
| Ascomycota | <i>Chrysosporium</i> | 0.2% A | 0% A | 0.1% A | 0% A | 0.1% A | 0% A |
| Ascomycota | <i>Cistella</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Colletotrichum</i> | 0% B | 0% B | 0% B | 0% B | 0% B | 0.2% A |
| Ascomycota | <i>Cytospora</i> | 0% A | 0.0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Dactylella</i> | 0% B | 0% B | 0.3% A | 0% B | 0% B | 0% B |
| Ascomycota | <i>Dinemasporium</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Hymenoscyphus</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0.2% A |
| Ascomycota | <i>Hymenula</i> | 0% A | 0.1% A | 0.2% A | 0.1% A | 0% A | 0% A |
| Ascomycota | <i>Iodophanus</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Knufia</i> | 0% B | 0% B | 0% B | 0% B | 0.2% A | 0% B |
| Ascomycota | <i>Lecythophora</i> | 0.1% A | 0% A | 0% A | 0.2% A | 0.1% A | 0.1% A |
| Ascomycota | <i>Malbranchea</i> | 0.3% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Murisporia</i> | 0% A | 0% A | 0% A | 0.1% A | 0% A | 0.2% A |
| Ascomycota | <i>Myrmecridium</i> | 0% B | 0% B | 0% B | 0.6% A | 0% B | 0% B |
| Ascomycota | <i>Paraphoma</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Parathyridaria</i> | 0% B | 0% B | 0% B | 0.6% A | 0% B | 0% B |
| Ascomycota | <i>Phialemonium</i> | 0% A | 0% A | 0% A | 0% A | 0.1% A | 0.1% A |
| Ascomycota | <i>Pseudodogymnoasc</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Ascomycota | <i>Stachybotrys</i> | 0% A | 0% A | 0% A | 0% A | 0.2% A | 0% A |
| Basidiomycota | <i>Basidiomycota_02</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0.4% A |
| Basidiomycota | <i>Basidiomycota_03</i> | 0% A | 0% A | 0% A | 0.1% A | 0% A | 0% A |
| Basidiomycota | <i>Basidiomycota_07</i> | 0% A | 0% A | 0% A | 0.0% A | 0% A | 0% A |
| Basidiomycota | <i>Basidiomycota_08</i> | 0% A | 0% A | 0% A | 0.3% A | 0% A | 0.1% A |
| Basidiomycota | <i>Basidiomycota_10</i> | 0% A | 0% A | 0% A | 0% A | 0.0% A | 0% A |
| Basidiomycota | <i>Bovista</i> | 0% A | 0% A | 0% A | 0% A | 0.0% A | 0% A |
| Basidiomycota | <i>Conocybe</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0.0% A |
| Basidiomycota | <i>Crepidotus</i> | 0% A | 0% A | 0% A | 0.1% A | 0% A | 0% A |
| Basidiomycota | <i>Entoloma</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Basidiomycota | <i>Filobasidium</i> | 0.3% A | 0% B | 0% B | 0% B | 0% B | 0% B |
| Basidiomycota | <i>Geminibasidium</i> | 0% B | 0.3% A | 0% B | 0% B | 0% B | 0% B |
| Basidiomycota | <i>Heterocephalacria</i> | 0.1% A | 0.2% A | 0% A | 0.1% A | 0% A | 0% A |
| Basidiomycota | <i>Irpex</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Basidiomycota | <i>Mycena</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |

| | | | | | | | |
|------------------|---------------------------|---------|---------|---------|---------|---------|---------|
| Basidiomycota | <i>Peniophora</i> | 0% A | 0% A | 0% A | 0.1% A | 0% A | 0% A |
| Basidiomycota | <i>Phlebia</i> | 0% A | 0% A | 0% A | 0.1% A | 0% A | 0% A |
| Basidiomycota | <i>Piskurozyma</i> | 0% A | 0% A | 0% A | 0.0% A | 0% A | 0% A |
| Basidiomycota | <i>Plicaturopsis</i> | 0% A | 0% A | 0% A | 0.1% A | 0% A | 0% A |
| Basidiomycota | <i>Pluteus</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Basidiomycota | <i>Postia</i> | 0% A | 0% A | 0% A | 0.1% A | 0% A | 0% A |
| Basidiomycota | <i>Psathyrella</i> | 0% A | 0% A | 0.1% A | 0% A | 0% A | 0% A |
| Basidiomycota | <i>Scopuloides</i> | 0% A | 0% A | 0.1% A | 0% A | 0% A | 0% A |
| Basidiomycota | <i>Sistotrema</i> | 0% A | 0% A | 0.2% A | 0.1% A | 0% A | 0% A |
| Basidiomycota | <i>Solicoccozyma</i> | 0.1% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Basidiomycota | <i>Steccherinum</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Basidiomycota | <i>Suillus</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Basidiomycota | <i>Trametes</i> | 0% A | 0% A | 0% A | 0.1% A | 0% A | 0% A |
| Basidiomycota | <i>Udeniomyces</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0% A |
| Basidiomycota | <i>Waitea</i> | 0% A | 0% A | 0% A | 0% A | 0% A | 0.0% A |
| Chytridiomycota | <i>Chytridiomycota_01</i> | 0.2% A | 0.1% A | 0.1% A | 0.1% A | 0.1% A | 0% A |
| Chytridiomycota | <i>Chytridiomycota_02</i> | 0% A | 0% A | 0% A | 0% A | 0.1% A | 0.1% A |
| Chytridiomycota | <i>Chytridiomycota_03</i> | 0% A | 0% A | 0% A | 0% A | 0.1% A | 0% A |
| Chytridiomycota | <i>Operculomyces</i> | 0.2% A | 0% A | 0.1% A | 0% A | 0% A | 0% A |
| Chytridiomycota | <i>Powellomyces</i> | 0% A | 0% A | 0% A | 0% A | 0.1% A | 0% A |
| Chytridiomycota | <i>Rhizophlyctis</i> | 0.1% A | 0.2% A | 0% A | 0.1% A | 0% A | 0% A |
| Chytridiomycota | <i>Spizellomyces</i> | 0% A | 0.1% A | 0.0% A | 0.1% A | 0.0% A | 0% A |
| Mucoromycota | <i>Umbelopsis</i> | 0% A | 0% A | 0% A | 0.0% A | 0% A | 0% A |
| Zoopagomycota | <i>Zoopagomycota</i> | 0% B | 0% B | 0% B | 0.3% A | 0% B | 0% B |
| Cluster centroid | | 0.003%A | 0.003%A | 0.003%A | 0.005%A | 0.002%A | 0.003%A |

^aCluster was created by K-means clustering algorithm in R separating OTU abundance over dph into 10 clusters [35]. Cluster centroid was created by the average within the K-mean cluster.

^bLetter following percentages indicate significant difference over time based on general lineal model ANOVA followed by Fisher's Least Significant Difference LSD test $p < 0.05$.