**Supplementary Materials**

**S1.Materials and Methods**

Sample collection of Panax plants

The composition and structure of endophytic microbial communities, as well as their interactions with host plants, are strongly influenced by local environmental conditions[26]. Consequently, all samples of *P. ginseng*, *P. quinquefolium*, and *P. notoginseng* were sourced from their respective core production areas, which are the regions where plant-endophyte co-evolution occurs, as detailed described in a previous study[27]. Simply, sampling was conducted in mid-September 2019 in Baishan City, Jilin Province, for *P. ginseng* and *P. quinquefolius*, and in late October 2019 in Wenshan Prefecture, Yunnan Province, for *P. notoginseng*. All plants were sampled at the late root thickening stage. To capture the growth year-dependent microbial variations, three independent fields, each planted with 2-year-old (2y), 3-year-old (3y), or 4-year-old (4y) *Panax* plants, were selected per species. From each field, nine samples (biological replicates) were collected, and each sample consisted of 10 healthy plants. A total of 81 plant samples (3 *Panax* species × 3 growth year × 9 replicates) were obtained. After collection, plant leaf and root samples were rinsed, surface-disinfected, pulverized in liquid nitrogen to a fine powder, and subsequently archived at -80 ℃, respectively.

Identification of keystone fungal taxa in plant tissues

Genomic DNA was extracted from leaf and root tissues. The fungal internal transcribed spacer (ITS) region was amplified using the host-blocking primer pair ITS1F/ITS2R and sequenced on an Illumina MiSeq platform[28]. After quality filtering and chimera removal, operational taxonomic units (OTUs) were clustered at 97% similarity and taxonomically assigned against the UNITE database[29–31]. Ecological networks for leaf and root communities were constructed separately based on robust Spearman correlations (|ρ| > 0.7, FDR < 0.001) among OTUs with relative abundance > 0.01%[32, 33]. Keystone taxa within each network were defined as nodes exhibiting both high connectivity (degree > 20) and high centrality (betweenness centrality > 5000)[9, 34].

Isolation of keystone fungal taxa and verification of their saponin conversion capability

Since amplicon analysis identified both Plec and Clad in all three *Panax* species, we only selected *P. notoginseng* (a representative species) for subsequent strain isolation experiments, with specific sample collection years detailed in Section 2.1. Based on the amplicon results, P. notoginseng was selected for fungal isolation[28]. Specifically, surface-sterilized leaf or root segments were placed on PDA plates containing 1% streptomycin. The colonies growing from the edges of plant tissues were transferred to new PDA plates. This transfer step was repeated at least three times to obtain pure strains. The isolated strains were identified by molecular marker with the ITS1F/ITS2R primer pair. Subsequently, the strains exhibiting the highest average sequence identity to the molecular marker of the pre viously identified keystone taxa (Plectosphaerella and Cladosporium) were chosen for further functional analyses[28].

The saponin-transforming ability of the potential keystone fungal strains was evaluated by co-culturing the fungi with a mixed saponin substrate including ginsenoside Rb1, Rb2, Rc, Rd, Rg1, Re, and notoginsenoside R1 (NR1). In detail, each culture flask containing 10 mL of PDB medium was inoculated with one of the two fungal keystone strains. This was followed by the addition of 100 μL of a mixed saponin solution. The flasks were then incubated at 25 ℃ with shaking at 160 rpm for 7 days. For the control group, no strains were inoculated. After incubation, the culture broth was snap-frozen, freeze-dried, and the lyophilized residue was subsequently extracted by sonication in methanol. The resulting extract was filtered, and the saponin content in the supernatant was quantified by High-Performance Liquid Chromatography (HPLC) according to Zhang et al[28].

Evaluation of β-glucosidase activity of keystone fungal strains

The β-glucosidase activity of two fungal keystone strains was determined using the pNPG method[35]. A 10 mM pNPG solution was prepared with sodium acetate buffer (pH 5.5). Fungal culture broths were collected at 72 h, 96 h, 120 h, and 144 h after incubation in PDB medium (25°C, 160 rpm). The broths were centrifuged at 10,000×g for 10 min at 4°C, and 1 ml of the supernatant was mixed with 1 ml of 10 mM pNPG solution. The mixture was incubated in a 50°C water bath for 30 min, followed by the addition of 2 ml of 0.25 M sodium carbonate solution to terminate the reaction. After standing at room temperature for 5 min, the absorbance was measured at 405 nm using the culture broth without strain inoculation as a blank control.

DNA, RNA extraction and sequencing of keystone fungal strains

For DNA extraction, the HP Fungal DNA Midi Kit (Omega Biotek, USA) was used to isolate genomic DNA from fungal hyphae according to the instructions. After extraction, the quality and concentration of DNA were detected by a micro-spectrophotometer, which was then used for genomic sequencing. The whole genome was sequenced on the Illumina platform and PacBio Sequel System by Biozeron (Shanghai, China). Hybrid assembly of second and third-generation sequencing data was performed using MaSuRCA v3.4.3to combine Illumina short reads and PacBio long reads, while Canu v2.1.1was used to assemble PacBio reads independently[36, 37]. MUMer v4.0 integrated the MaSuRCA and Canu assemblies and removed redundancy[38]. The integrated genome was polished with Racon for three rounds and further corrected with Pilon for at least three rounds to ensure 99.9% accuracy[39, 40].

Since β-glucosidase can hydrolyze the glycosidic bonds of disaccharides or polysaccharides, the two fungal strains were cultured in YPD (Yeast Extract-Peptone-Dextrose Medium) and Cel-YPD (with glucose replaced by cellobiose only) respectively. After 5 to 7 days of cultivation until sufficient mycelia were obtained, total RNA was extracted using the Fungal Total RNA Isolation Kit (Sangon, China), and RNA sequencing was performed by Biozeron (Shanghai, China). In addition, the remaining mycelia from the above two culture media were mixed with the mycelia filtered from the PDB medium, and the mixture was used as materials for third-generation full-length transcriptome sequencing, which can correct the gene structure annotation information of the fungal genome and transcriptome.

Genomic analysis

The protein sequences of the predicted genes were respectively subjected to blastp alignment with Nr, Swiss-Prot, eggNOG, KEGG and GO databases (BLAST+ 2.8.1, alignment criteria: E-value ≤ 1e-5)[41–45]. Only the best alignment result was retained as the database alignment information for the geneiji. EVenn was used to statistically analyze and visualize the annotation results[46]. The hidden Markov models related to GH1 and GH3 families provided by Pfam were used to perform HMMER alignment with the sequenced fungal genomes to obtain sequences highly related to GH1 and GH3 families[47, 48]. FastTree 2.1.11 was used to construct a phylogenetic tree of these sequences and the GH1 and GH3 gene family sequences reported in the literature[49]. Motif prediction was conducted using MEME Suite 5.5.5[50], and visualization was performed using tvBOT[51]. The sequences with signal peptides in the genome were identified using SignalP 6.0, and then these sequences were analyzed by DeepTMHMM to obtain the secreted protein sequences with signal peptides[52, 53]. TBtools-II was used for GO functional enrichment analysis, and ChiPlot (https://www.chiplot.online/) was used for visualization. The secondary metabolite gene clusters in the genomes of Cladosporium and Plectosphaerella genera were predicted using antiSMASH 7.1[54], and data comparison and visualization of the number of predicted secondary metabolite gene clusters were performed using ChiPlot (https://www.chiplot.online/).

Since there are few species of *Plectosphaerella* and *Cladosporium* genera with genome annotation information uploaded on NCBI, their raw genomes were downloaded, and the Funannotate v1.8.15 pipeline was used for genome structure annotation[55]. The gene families and single-copy orthologous genes were analyzed using OrthoFinder v2.5.5 software[56]. FastTree 2.1.11 was used to construct a phylogenetic tree of the identified tandem single-copy orthologous genes, and tvBOT was employed for visualization. Using r8s based on the results of OrthoFinder, TimeTree was used to determine the divergence years of reference species pairs[57, 58]. Ultrametric trees were constructed for single Plec and Clad species versus outgroup species, as well as for *Plectosphaerella* and *Cladospsorium* genera versus outgroup species. Divergence times among various species and ancestral nodes were calculated. CAFE 5 was employed to analyze gene family expansion and contraction[59]. For significantly expanded gene families, TBtools-II was used for GO enrichment, and the enrichment results were visualized using tvBOT.