
Departments of ¹Biology and ²Medicine, Duke University, PO box 90338, Biological Sciences Building, Durham, NC 27708, USA.
³Department of Plant and Microbial Biology, University of California, Berkeley, CA, USA.
⁴Department of Biology, Stanford University, Stanford, CA, USA.

Summary

Ectomycorrhizal (EM) fungi form symbiotic associations with plant roots that regulate nutrient exchange between forest plants and soil. Environmental metagenomics approaches that employ next-generation sequencing show great promise for studying EM symbioses; however, metatranscriptomic studies have been constrained by the inherent difficulties associated with isolation and sequencing of RNA from mycorrhizae. Here we apply an optimized method for combined DNA/RNA extraction using field-collected EM fungal–pine root clusters, together with protocols for taxonomic identification of expressed ribosomal RNA, and inference of EM function based on plant and fungal metatranscriptomics. We used transcribed portions of ribosomal RNA genes to identify several transcriptionally dominant fungal taxa associated with loblolly pine including Amphinema, Russula and Piloderma spp. One taxon, Piloderma croceum, has a publically available genome that allowed us to identify patterns of gene content and transcript abundance. Over 1500 abundantly expressed Piloderma genes were detected from mycorrhizal roots, including genes for protein metabolism, cell signalling, electron transport, terpene synthesis and other extracellular activities. In contrast, Piloderma gene encoding an ammonia transporter showed highest transcript abundance in soil samples. Our methodology highlights the potential of metatranscriptomics to identify genes associated with symbiosis and ecosystem function using field-collected samples.

Introduction

The symbiotic activities of ectomycorrhizal (EM) fungi are essential for pine forest establishment and sustainability (Hasselquist et al., 2005; Wang and Qiu, 2006; Smith and Read, 2008). The composition of EM fungal communities can be affected by environmental factors (Cullings and Makhija, 2001; Cullings et al., 2003; Wolfe et al., 2008). The EM symbiosis is characterized by a hyphal mantle that forms over root tips (Bonfante and Genre, 2010) where both epidermal and cortical root cells are colonized by intercellular hyphae (the Hartig net). EM fungi, through cell–cell interaction of their hyphal network with root cells, enjoy direct access to their plant host’s carbon and compensate the plant host by stimulating plant growth (Sung et al., 1995), mineral nutrient uptake (Van den Driessche, 1991), water absorption (Smith and Read, 2008) and disease resistance (Zhao et al., 2008).

Genomic studies of EM fungi are providing novel insights into mechanisms of symbiosis. In Laccaria bicolor (the first EM fungus to have its genome sequenced), approximately 20 000 protein-encoding genes were identified including ammonia transporters, GTPase and small-secreted proteins involved in symbiosis establishment (Martin et al., 2008). Genome sequencing of the black truffle (Tuber melanosporum) has also revealed many genes that play a role in EM–fungal–plant interaction including plant cell adhesion, plant defence evasion, and plant cell wall modifications (Martin et al., 2010).

Molecular dissection of mycorrhizal symbiosis is complicated by many challenges, including the difficulty of culturing most EM fungi and the requirements for inoculation and successful EM colonization of living plant roots. For most EM fungi, in vitro gene expression analyses are still not practical or possible. Fortunately, metagenomic...
methods that follow gene expression in field-collected samples show much promise for understanding the mechanisms by which different EM fungal lineages respond to their natural environment. Next-generation DNA sequencing studies using high-throughput amplicon sequencing especially show great promise for functional studies of EM fungal communities (Gottel et al., 2011; Gugerli et al., 2013; Shakya et al., 2013; Talbot et al., 2014). For example, a recent study of the North American pine soil ‘mycobiome’ showed strong geographic patterning of EM fungal communities but high degrees of functional convergence across these communities (Talbot et al., 2014). However, only few methods have been applied to study EM function and they are based on relatively coarse measures of community enzyme production or gross hyphal morphology (Courty et al., 2005; Moeller et al., 2014). Consequently, application of finer resolution metagenomic approaches shows great potential to advance the study of EM functional ecology. While transcriptomic tools are well developed for some model systems in vitro (Laccaria, Tuber) (Martin et al., 2008; 2010; Plett et al., 2011), metatranscriptomics has not been widely applied to study the function of ectomycorrhizae in the natural environment. This is due to the difficulty of obtaining high-quality RNA from a small amount of field tissues and the challenge of assembling and analysing metatranscriptomic data. To study the functional distribution of EM fungal hyphal network in both root and soil systems, we collected root clusters and soils from two Pinus taeda native forests. Here we propose a methodology to study the metatranscriptome of EM fungi–pine root symbiotic associations from small samples (pine root clusters) using next-generation sequencing technology and advanced assemblers that use data from the rapidly growing number of transcriptomic sequence databases. To test our methodology, we used the Pinus–Piloderma system because of the large amount of publicly available transcriptomic data from these two species (Grigoriev et al., 2012; NCBI). Our methodology identifies a core set of Piloderma genes expressed under a variety of developmental/environmental conditions.

Results

Sampling and RNA extraction for field-collected samples

To study EM fungal–Pinus interactions in situ, we sampled at least 12 replicates of EM root clusters and soils from two P. taeda native forests 10 mile apart (Fig. S1). The organic soil horizons were collected using soil cores. In each plot, two soil cores were collected from two points 50 m apart from each other (i.e. four soil cores were collected in total). Intact root clusters containing fresh root tips were collected using forceps under a dissection microscope. Soil samples were also collected from the same soil core from which roots were collected. At least three individual root and soil samples were collected from a single core as subreplicates.

Application of metagenomic approaches presents challenges due to the difficulty of obtaining high-quality RNA from a small amount of field tissues, especially from plant roots (Chang et al., 1993; Martin et al., 2004), and the challenge of assembly of whole-metatranscriptomic data. Because initial attempts to isolate RNA from single mycorrhizal root tip yielded insufficient RNA for HiSeq, we chose to focus on EM root clusters, which are larger and more suitable for obtaining high-quality RNA, next-generation sequencing and comparative metatranscriptomics at the single-species level. Because high-quality mRNA is critical for transcriptomics, choosing the right extraction method is critical for field-collected root cores with small amounts of usable tissue. Of the methods we compared (Table S1), including kit-based and conventional methods, the best results were obtained using a cetyltrimethyl ammonium bromide (CTAB)/chloroform extraction with LiCl precipitation of RNA. The CTAB/LiCl method described by Chang and colleagues (1993) was able to recover good quality RNA from root samples of P. taeda; however, the quantity of recovered RNA was relatively low (6 ng RNA mg⁻¹ root cluster). Several CTAB methods modified from Chang and colleagues (1993) or Liao and colleagues (2004) were applied to extract RNA from larger amount of pine tissues (1–4 g) (Joosen et al., 2006; Lorenz et al., 2009; 2010; Canales et al., 2011). In this study, we modified the RNA extraction method from Chang and colleagues (1993) combined with genome grinding/beading strategy to homogenize small amounts of root tissue. The improved methods enabled us to obtain good quantity of DNA and RNA from the same extraction in a single root cluster (100 ng RNA mg⁻¹ tissues). RNA isolation from single root clusters yielded of 0.5 μg high-quality RNA, sufficient for the production of quality reads by Illumina RNAseq. Except RNA PowerSoil kit (MoBio, Carlsbad, CA, USA), all of the RNA extraction methods we examined were not adopted for soil samples collected in the field (Table S1).

Integrative assembly of cDNA sequences

We performed Illumina HiSeq sequencing to analyse the transcriptomic activity for individual root clusters and soil samples respectively. We recovered an average of 40 million reads that passed quality control from a single EM root cluster (Table S2). The computational workflow sorted out the reads representing fungal ribosomal RNA (rRNA) using fungal rRNA databases (Fig. 1). De novo assembly using the Velvet package (Zerbino and Birney, 2008) was applied to assemble and identify the variable region (divergent domain 2, D2) of rRNA large subunit
regions (LSUs) of fungal species. The assembled contigs containing D2 regions were used as a database for fungal rRNA reads aligning to calculate the abundance of particular fungi. Short rRNA reads representing the LSU D2 region (around 180 bp) were extracted, paired and normalized using RPKM (reads per kilobase per million). The fungal taxonomic identity (at the genus level) was determined using BLAST (Bayesian classifier and NCBI) and dominant fungal lineages identified. The unmapped reads were subsequently mapped to bacterial 16S rRNA and P. taeda transcript database (NCBI). Of the transcriptionally active EM fungi, Piloderma spp. were most often detected from root samples we collected (the details were described in the following sections). Thus, the Piloderma croceum database (Pilcr1 F 1598; Grigoriev et al., 2012) was used to extract reads representing Piloderma genes from Piloderma dominated root clusters and soil samples. De novo assembly using Trinity package was applied to recover the fungal genes for the samples that are dominated by the fungal species without publicly available databases.

The distribution of reads in individual root clusters

Figure 2 shows the percentage of reads within a typical EM root cluster associated with different metatranscripts. Our approach was able to recover reads from functional genes, with 35% from fungi and 42% from P. taeda. In addition, smaller amounts of ribosomal DNA reads generated during cDNA synthesis were obtained which could be attributed to fungi (0.9%), P. taeda (0.8%) and bacteria (0.1%), as well as 0.007% reads that mapped to the fungal internal transcribed spacer (ITS) region. Similar ratios were observed between the biological replicates in

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**Fig. 1.** Computational flowchart used to analyse Illumina HiSeq RNA reads of EM root clusters.

**Fig. 2.** Percent of read associated with fungal, bacterial and pine transcripts in EM root clusters detected by Illumina HiSeq. Numbers in parentheses indicate the number of reads (in millions) recovered from total reads for each group. (n = 16, total number of reads after quality trimming = 35 million).
all root samples (Table S2), which also contained an average of 9% unknown sequences, and 14% unqualified and unassembled reads.

Identification of fungal taxa within individual root clusters
To identify active fungi in EM root clusters, we recovered total DNA and RNA from the same extraction, and then compared fungi detected from stable DNA with those detected from more labile RNA, using the logic that the rRNA of active fungi would be overrepresented (Baldrían et al., 2012; Liu et al., 2012). Using total DNA with 454 amplicon sequencing of the ribosomal ITS region, we detected from 27 to 52 fungal operational taxonomic units (OTUs) per root cluster (Fig. 3A; Table S3A). In contrast, fungal transcripts coding for rRNA (LSU D2 region) from individual root clusters were dominated by only one to several fungal OTUs belonging to Piloderma, Amphinema, Russulaceae and Cenococcum, Thelephoraceae and Mycena sp. (Fig. 3; Table S3). With exception of Mycena, all are known to be EM taxa. Of these, the most transcriptionally active EM fungi were Piloderma spp. that were detected in 7 of 16 root samples, comprising up to 93% of total LSU D2 reads from a single root cluster. Phylogenetic analysis revealed the presence of three distinct Piloderma species with 93–98% similarity in their D2 region (Figs S2 and S3). Comparison with sequences from the UNITE database identified these OTUs as Piloderma byssinum, P. croceum and a third unidentified Piloderma species (Fig. S3). In addition, two lineages of Amphinema and three lineages of Russulaceae were also detected with 85–98% sequence identity within the D2 region of each OTU respectively.

Mapping Piloderma-specific functional reads in soil and root clusters
To investigate Piloderma transcriptional activity in soil and root samples, we used genomic and transcriptomic data for P. croceum (Picr1 F 1598 v 1.0; Grigoriev et al., 2012) to identify functional genes. Aligning all RNA-Seq reads against the P. croceum F 1598 transcript dataset (v1.0), we obtained an average of 100 000 and 1 000 000 reads in individual soil and root samples respectively. The most highly expressed transcripts could be readily assigned to Gene Ontology (GO) categories (Fig. 4). Most of the identified transcripts are related to gene functions in protein translation, protein degradation, protein folding, cell signalling, mitochondrial activity, terpene synthesis or to unknown proteins.

Functional category analysis reveals that Piloderma genes for nutrient transportation were predominantly expressed in soil samples, while genes for terpene biosynthesis were significantly expressed in root samples (Fig. 4). Sets of highly expressed genes (with percentage of reads >0.02%) were identified using BLASTX (Fig. 5; Table S4). Of 141 highly expressed functional-related gene groups, 124 gene groups were commonly expressed in both root and soil samples and are assumed to be directly associated with response of Piloderma hyphae to its environment (Fig. 5A). Only 17 unique gene groups were determined by comparison with false discovery rate < 0.1 (Fig. 5B). Eight Piloderma gene groups were found to be upregulated in soil compared with the EM root and nine gene groups displayed significantly higher expression within the EM root compared with soil. Figure 5B shows that similar patterns of differential gene expression in root versus soil Piloderma transcripts were observed across all sample locations.

Genomic and transcriptomic identification of Piloderma small secreted proteins
The small proteins secreted by plant pathogenic fungi or plant symbiotic fungi have been implicated in playing an important role in host compatibility (Chisholm et al., 2006; Plett et al., 2011). Four highly expressed genes encoding small secreted proteins were detected from Piloderma, and investigated further (Figs 5 and S4). These small secreted proteins included PiCr, PiBas, PiSs1 and PiEsp, which had sequences homologous to the cysteine-rich protein (gi392569350), fungal biotrophy-associated secreted protein (gi471559611), small secreted protein (gi328860126) and EM-associated small secreted protein (gi170100116). These small-secreted proteins have distinct primary and tertiary protein structures (Figs S4 and S5) indicating their functional independence. Like many other effectors associated with fungal virulence (Saunders et al., 2012), these four small secreted proteins share at least one of the following properties: a signal polypeptide, small protein size and cysteine rich, implying their involvement in Piloderma–host symbiosis.

All the small secreted proteins encode a small polypeptide of less than 215 amino acids and were predicted as non-cytoplasmic proteins with no transmembrane domains (data not shown). PiCr, PiBas and PiSs1 contain a signal peptide at their N-terminals. A distinct sequence pattern was found in PiCr, which contains six cysteine residues arranged in an inverted symmetrical repeat. No specific domains and motifs were predicted from those small secreted proteins (data not shown). All four small secreted proteins show high sequence identities (over 99%) with representative contigs in P. croceum genome. Sequence analysis of the P. croceum genome contigs indicated that the several highly expressed genes encoding functionally associated proteins are clustered with
either PiCr, PiBas and PiSs1 respectively. Most genes belonging to the same individual clusters also shared similar RNA transcript levels (% reads >0.01) (Fig. 6). Based on time course analyses for individual root samples, it was determined that the genes in the clusters were induced along with the small, secreted proteins (data not shown). Transcriptomic analysis shows that genes in the clusters of PiCr, PiBas and PiSs1 are most likely involved in membrane trafficking. A set of genes encodes extracellular activity including secreted
phospholipase C, laccase and phospholipase-dependent transferases were also found located adjacent to the PiBas gene.

Identification of P. taeda functional genes in mycorrhizal root clusters

In addition to fungal genes, metatranscriptomic analysis of root clusters recovered over 40% of the reads representing functional plant genes from P. taeda that allowed us to study the function of both organisms from the same sample (Fig. 2). A total of 212,500 functional contigs from P. taeda were identified from EM root clusters. Of those, 2,600 highly expressed contigs representing over 50 gene groups were shared among different sampled EM roots (Table S5).

Discussion

Simultaneous identification of active fungal and plant transcriptomes using next-generation sequencing

To study EM root function in situ, we applied improved methodologies for obtaining high-quality DNA/RNA (from the same extraction), poly-A enrichment, cDNA construction, data assembly and comparative metatranscriptomic analyses at the single-species level. A workflow for bioinformatic analysis using advanced and popular software packages allowed us to sort and assemble the RNA-seq data (Fig. 1). The cDNA construction methods using poly-T primers were appropriate for isolating eukaryotic mRNAs and cDNA libraries, such that mRNA accounted for more than 80% of the total number of reads. This methodology still yields up to 1% rRNA, sufficient to taxonomically EM fungal species and other microbes that are present. Our method sorted and extracted the reads represent D2 regions from environmental samples for fungal identification, while at the same time, quantifying their abundance at the transcriptomic level (Fig. 1; Fig. S6). Based on LSU D2 RNA analysis, we found that most root clusters are dominated by a single fungal species (Fig. 3); in contrast, a much higher diversity of fungal taxa (>5) was observed from the same root samples using 454-sequencing of ITS amplicons (Fig. 3A), suggesting that only one or very few species of EM fungi are actively functioning within a given root cluster at the same time. A higher diversity of dominant fungal taxa (>5) was observed from soil samples (data not shown); however, RNA-seq again revealed that
Fig. 5. Cross-comparative expression of (A) highly expressed and (B) unique Piloderma gene groups in soil and root samples. The gene groups highly expressed at least in an individual sample (% reads >0.02 from all Piloderma reads were selected for clustering and heat map visualization). The color key represents RPKM normalized log2 transformed counts of the genes. Wilcoxon signed-rank test (Bauer, 1972) was used to filter the data. Each gene family was significantly overexpressed in one of the group as determined by comparisons with false discovery rate (FDR) <0.1 using Benjamini-Hochberg test.

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these transcripts were also dominated by one or only a few fungal taxa.

Analysis of the EM metatranscriptome using poly-A selection following by gene mapping and de-novo assembly identified functional ‘symbiosis’ genes from both EM fungus and its plant host *P. taeda*. *Piloderma* spp. are consistently the dominant EM fungal taxon in root and soil samples from over 50 pine forests across 10 states in North America (Talbot *et al*., 2014). By using the publically available *Piloderma* genome database, we focused on how genomic machinery operates in dominant taxa (*Piloderma*) in the investigated natural environment. The representative genes of interests and their functions are discussed in the following sections.

Previous studies on the *Piloderma*–Quercus EM symbioses identified a set of premycorrhiza-related host genes (*Quercus robur*) (Krüger *et al*., 2004; Herrmann and Buscot, 2007). Because HiSeq provides much larger numbers of RNA reads (up 30 million reads per lane), efficient mapping of transcript reads (Fig. 1) enables simultaneous analysis of metagenome expression even when multiple fungal and plant species are present.

**Unique metabolic genes are highly expressed in symbiotic tissues**

EM fungi develop communication networks using their hyphae as functional units. At the cellular level, EM hyphae that form the Hartig net establish the physical interaction with hosts; in contrast, hyphae that extend outward into the soil mostly contribute to resource uptake or interaction with biotic factors in the environment (Nehls, 2007). In addition to root clusters, we also collected soils from the same soil cores where the root samples were collected and generated the metatranscriptomic data to study microbial function in the soil samples. Regardless of which collecting site we sampled, comparative functional profiles for several gene groups differed significantly.
Aspergillus Fig. S7) that shares high amino acid identity (61%) with ammonium transporter (PiAMT; amino acid sequence in nutrient exchange (Fig. 5A). One type of high-affinity permease, indicating the great activation of fluxes for two for monosaccharides, one for inorganic phosphate, one for choline (ammonium salts), two for amino acids, transporters, including one gene for ammonium (PiAMT), groups we detected for C/N/P-associated proteins are of the rhizosphere (EM roots versus soil). Nine of 18 gene samples, suggesting that ammonium may be a preferential source of nitrogen in soil. Similarly, a high level of gene expression for glutamine synthase and glutamate-related transporters in both free mycelium and EM roots implies that glutamine pathway is the main biogeochemical pathway for ammonium assimilation and nitrogen utilization in Piloderma. Glutamine could be assimilated using ammonium, or directly imported from soil and serve as the major molecule translocated to the roots.

Current studies showed that at least 44 of 132 glycoside hydrolases (GHS) contribute to plant cell wall degradation (Gilbert, 2010; http://www.cazy.org/). Of 141 highly expressed gene families (Fig. 5A), we detected only two GHS (GH12 and GH16); no other enzymes involved in degradation of cellulose, hemicellulose and pectin were identified by our metatranscriptome studies, suggesting adaptation of Piloderma to the EM symbiotic lifestyle. As with other EM fungi, we infer that Piloderma mainly absorbs monosaccharides from the host and environment via its monosaccharide/sugar transporter families.

Several other extracellular enzymes were highly expressed in both root and soil samples. These include fungal chitosanase (GH75), which is involved in modification of fungal cell wall structure, and may be required for fungal development or to make cell more accessible for colonization. Ricin B-like lectin could activate fungal signal transduction through binding and clustering specific carbohydrates on fungal cell surfaces. Cupredoxin is involved in electron transfer. High expression of the gene for glycoamidase indicates active regulation of glycoprotein maturation (Suzuki et al., 1994). Overall, these common extracellular enzymes are most likely involved in basic biological processes of fungal development and adaption to environment.

Fungal small secreted proteins present in EM pine roots

Secreted effector-like proteins are involved in a variety of pathogenic and symbiotic fungal–host interactions (Martin et al., 2008; Lowe and Howlett, 2012). However, the mechanisms for delivery and function of the effectors are less known. In general, effectors are often highly divergent in plant-pathogenic fungi and lack similarity in their sequences to proteins in most databases. Our study identified four highly expressed effector-like genes (PiCr, PiBas, PiSs1 and PiEsp) that share high sequence similarity with other effector-like proteins. This implies that these proteins are likely to be involved in communication between Piloderma and pine roots. However, more studies on functional analysis are needed to determine the role of these small secreted proteins in Piloderma symbiosis.

Four sets of Piloderma genes for secretory pathway are also clustered in the genome with these four effector-like genes involved in the EM symbiotic interface (Fig. 6). The six cysteines of PiCr protein are arranged in a symmetrical structure, likely form three disulphide bridges. The disulphide bridges could contribute to protein stability.
during secretion. There is no direct evidence to link such a structure with their function on symbiosis, though many small secreted proteins of fungi that contain four to eight cysteine residues have found function inside the plant cells to induce plant defence system (Rep, 2005; Stergiopoulos and de Wit, 2009). Gene expression analysis by mapping the transcriptomic reads to genome sequence of the PiCr cluster revealed a set of five genes including genes for cysteine-rich protein (PiCr), two motor proteins (K1 and K2), ER-to-Golgi transport (Vsp) and cis-Golgi transport (Trs) are induced exclusively in symbiotic tissues. One motor protein (K1) contains the multifunctional domains for kinesin heavy chain (KIsCo), transmembrane channel (MscS), protein kinase (HrpJ), RNA-binding (Pumilio), vesicle coat trafficking (Sec1) and a coatomer element (COP II) using conserved domain prediction server in NCBI (data not shown). Those results indicate the mediation of organelle-to-organelle secretory pathway is involved in PiCr secretion and fungal–host recognition. PiBas encodes a protein with high homology to the fungal biotrophy-associated secreted protein (Bas), a small protein secreted into plant cells during compatible mycorrhizal interactions (Mosquera et al., 2009). Genomic features related to the biotrophic lifestyle in PiBas clustered genes include plant cell wall and membrane manipulation [e.g. laccase, phospholipase C and pyridoxal phosphate (PLP)-dependent transferases]. Expression analysis showed that most of the genes selected contained in the PiBas cluster were induced in root tissues and soil samples, suggesting that PiBas clusters could be involved in manipulating host cell structures and cell processes during EM symbiosis; the same gene cluster could play a role during growth in soil.

PiSs1 and PiEsp are homologous to effector-type small secreted proteins with unknown function. PiSs1 cluster encode proteins for transcription, translation, protein translocation and ER-to-Golgi transport (YOS1), indicating that a specific synthetic and delivery pathway is involved in function of PiSs1, whereas no functionally documented genes were detected adjacent to PiEsp (data not shown).

In this study, we developed an effective approach for studying EM fungal metatranscriptomes to identify specific molecular mechanisms operating to regulate fungal–plant interactions and fungal fitness. We were able to identify Piloderma spp. as the main functional EM fungal player in pine forest environments. Availability of publically available genome resources for P. croceum also made it also possible for us to identify key sets of genes which were expressed within ectomycorrhizae and soil. Unfortunately, genome data were not yet available at the present time for several other fungi identified by our study (Russula, Amphinema, Thelephora). Given the increasing availability of fungal genome assemblies and annotations, exploitation of metatranscriptomic analysis shows great promise for profiling lineage-specific transcriptomics in situ in other systems and contribute for a better understanding of the functional roles fungi play in nature.

**Experimental procedures**

**Sampling**

Organic soil horizons were collected from two *P. taeda* plots located in the Duke Forest, Durhamco, NC, USA in April 2012 using soil cores (10 cm diameter; 15 cm height) (Fig. S1). At the time of sampling, the average temperature in these forests was 21°C. Root and soil samples were stored on ice and frozen in liquid nitrogen or dry ice within an hour after collection, and stored at −80°C prior to RNA extraction.

**RNA preparation and cDNA construction**

Total RNA was isolated from root samples using a CTAB/ chloroform extraction and LiCl precipitation method modified according to Chang and colleagues (1993). Frozen roots were ground using ten 2 mm zirconia beads (BSP, Bartlesville, OK, USA) in a GenoGrinder 2000 (OPS Diagnostics, Lebanon, NJ, USA) at 1500 strokes min⁻¹ for 30 s. Immediately after grinding, 1 ml DEPC/CTAB solution (2% CTAB and PVP; 100 mM Tris-HCl, pH 8.8; 25 mM EDTA, pH 8.0; 2 M NaCl; 2% fresh beta-mercaptoethanol and 1% DEPC, v/v) was added to the ground roots. The sample was then homogenized by vortexing and incubated at 65°C for 10 min. Equal volumes of a chloroform : isoamy alcohol mixture (24:1) were added to the samples, mixed by vortex and centrifuged at 9000 g for 10 min. The supernatant was recovered and RNA in the supernatant precipitated with 2:1 LiCl precipitation step was treated with 1 unit RNase at 37°C for 16 h. After centrifugation at 9000 g for 5 min, the supernatant was collected for DNA extraction and the pellet (RNA) was washed using 70% EtOH and eluted in DNase/RNase-free water. The supernatant collected in LiCl precipitation step was treated with 1 unit RNase at 37°C for 30 min, then precipitated with equal volumes of ice cold isopropanol. After centrifugation at 9000 g for 10 min, the pellet (DNA) was washed using 70% EtOH and eluted in DNase/RNase-free water.

RNA from soil was extracted using the RNA PowerSoil kit (MoBio, Carlsbad, CA, USA) as indicated in the manufacturer’s instructions. Total RNA quality was quantified using a 2100 bioanalyzer (Agilent, Santa Clara, CA, USA) and Qubit 2.0 fluorometer (Invitrogen, Grand Island, NY, USA) following the supplier’s protocols. Only RNA with high integrity (RIN > 8.0) and showing well-defined peaks for 18S and 28S rRNAs on an electropherogram (RNA 6000 Nano LabChip, Agilent) was used for cDNA library construction. The 0.5 μg RNA was used for cDNA library construction using TruSeq RNA Sample Prep v2 (Illumina, San Diego, CA, USA) and poly-T primers to enrich poly-A containing mRNA. The cDNA samples were sequenced using HiSeq 2000 (Illumina) in Institute for Genome Sciences and Policy at Duke University. Twelve samples were sequenced using a lane of Illumina run to generate 38 Gb of data. The raw reads were submitted to Sequence Read Archive (http://trace.ncbi.nlm.nih.gov/Traces/sra/) (Accession No. SRP041643).
Packages and databases used for bioinformatics analysis

The bioinformatic packages used for assembling and annotating the datasets were: the Galaxy web-based package (https://main.g2.bx.psu.edu/) to check the quality of reads, FastQC for sequence trimming and quality filtering (cut-off with quality scores <28; Blankenberg et al, 2010), Bowtie for reference-based mapping (http://bowtie-bio.sourceforge.net/index.shtml), Velvet (Zerbino and Birney, 2008) and Trinity (Grabherr et al, 2011) for de novo assembly and a combination of Blastx (Tao, 2010), GO (Ashburner et al., 2000), Kyoto Encyclopedia of Genes and Genomes (KEGG) (Kanehisa et al., 2012) and NCBI eukaryotic orthologous groups (KOG) (Tatusov et al., 2003) for gene annotation. Amino acids predicted from nucleotide sequences was performed using ExPASy (http://web.expasy.org/translate/). EMBL-EBI and Signal-3L were used for signal-peptide prediction (http://www.csbio.sjtu.edu.cn/bioinf/Signal-3L/). NCBI (Marchler-Bauer et al, 2011) and Myhits were applied for production of conserved domains and motifs (http://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi). In general, default parameters were applied for the bioinformatics analysis.

Databases used for mapping including: Fungal rRNA (~400 000 contigs; NCBI); Bacterial 16S (~2 1000 000 contigs; Ribosomal Database Project, http://rdp.cme.msu.edu/); P. taeda (~320 000 contigs; NCBI), P. croceum (~340 000 contigs; Pilcr1 F 1598 v 1.0, Grigoriev et al., 2012). The annotated sequences of coding genes downloaded from NCBI for over 30 fungal species (mostly EM fungi of trees or wood rot fungi) that were assumed to be best hits for the sequences of Pinus-associated EM fungi were pooled and used as references for fungal gene annotation using Blastx (Tao, 2010), including S. lacrymans (12 925 genes), Coniophora puteana (13 898 genes), Laccaria bicolor (18 315 genes), Dichomitius squalens (12 511 genes), Gloeophyllum trabeum (11 889 genes), Stereum hirsutum (14 455 genes) and others. The annotated sequences of coding genes downloaded from NCBI for 15 plant species were pooled and used as references for P. taeda gene annotation, including Populus trichocarpa (62 211 genes), Glycine max (62 511 genes), Vitis vinifera (56 152 genes), Zea mays (33 490 genes), Rcinus communis (32 094 genes) and others. The databases were quality filtered using FASTA manipulation of Galaxy web-based package.

Statistical analysis

In total, nine root and nine soil samples that contain RNA-Seq reads of Piloderma taxa were analysed for Figs 4 and 5. In Fig. 4, we tested for statistical differences between factors using a Tukey test. Differences were considered significant at \( P < 0.05 \). The data of each sample were the mean for the biological replicates. The functional categories (Fig. 4) and heat map (Fig. 5) were generated using R package(s) (R Development Core Team, 2011).

Acknowledgements

We would like to thank Igor Grigoriev, Francis Martin and François Buscot for access to genome data for Piloderma croceum. Genome sequence data were produced by the US Department of Energy Joint Genome Institute http://www.jgi.doe.gov/ in collaboration with the user community. We also thank members of the Vigalys, Peay and Bruns lab for assistance with soil/root sampling and Mr. Chih-Ming Hsu for help with bioinformatics data. This work is supported by NSF grant DBI-10–46052 to RV, DBI-10–45658 to KGP and DBI 10–46115 to TDB (http://www.stanford.edu/~kpeay/DOB_Home.html).

References


Supporting information

Additional Supporting Information may be found in the online version of this article at the publisher’s web-site:

Fig. S1. Location of the collection sites.

Fig. S2. Partial large-subunit ribosomal RNA sequences (D2 region, ∼180 bp) for the most dominant fungal taxa detected from mycorrhizal root clusters (Fig. 3).

Fig. S3. Phylogenetic placement of LSU RNA sequences for three Piloderma spp. based on ribosomal large-subunit D2 region. Sequences were aligned against taxonomically identified reference sequences of Piloderma spp. from GenBank with ClustalW; phylogenetic analyses performed using parsimony criterion in PAUP 3.0. Bootstrap tree (‘fast bootstrap’ with 300 replicates) shows placement of three Piloderma spp.

Fig. S4. Nucleotide and peptide sequences of Piloderma effectors: (A) PiCr1, (B) PiBas, (C) PiSs1 and (D) PiEsp. The putative signal sequences are shown in the peptide sequence (Bold and underlined). In (A), the symmetrical arrangement of cysteine (C) residues is shown in boldface.

Fig. S5. Ribbon diagrams showed the predicted-tertiary structures for (A) PiCr, (B) PiBas, (C) PiSs1 and (D) PiEsp. The helix (pink) and sheet structures (yellow) were shown. N and C terminal are labelled. The protein tertiary structures were predicted using I-TASSER v 3.0 (Zhang 2008; Roy et al., 2010; Roy et al., 2012). C-score is a confidence score for estimating the quality of predicted models by I-TASSER. It is calculated based on the significance of threading template alignments and the convergence parameters of the structure assembly simulations. C-score is in the range from −5 to 2, where a C-score of higher value signifies a model with a high confidence.

Fig. S6. Partial images of visualization for reads of root samples Bowtie-mapped to a 28S rRNA reference (gi300394395, Piloderma falax) using Integrative Genomics Viewer 2.2x (Thorvaldsdottir et al. 2013). Fewer and variable sequences were found in variable regions (D1 and D2) compared with the conserved regions of 28S. The red box indicates the region (∼180 bp) where the reads were extracted for fungal taxa identification in this study. Mapped bars in blue indicate the inferred insert size on the reference gene is smaller than expected given the actual insert size; red is the inferred insert size on the reference gene is larger than expected given the actual insert size.

Fig. S7. Predicted amino acid sequence of PiAMT.

Table S1. Comparison of RNA extraction methods for pine roots (EM) and needles.

Table S2. Read and Percent of read associated with fungal, bacterial and pine transcripts in EM root clusters detected by Illumina HiSeq.

Table S3. Taxonomic composition of EM root clusters based on (A) ITS DNA amplicon sequences (B) trancribed ITS RNA sequences, and (C) ribosomal RNA (LSU D2 region). (A–C) The absolute counts (read counts) and relative value (% reads) are shown.

Table S4. Highly expression of Piloderma gene groups in soil and root samples. The gene families with >0.02 in at least a sample were selected. Table S4A showed the number of reads of individual gene families obtained from root and soil samples. Table S4B showed the list Piloderma protein ID from PilCr1 database for each gene group.

Table S5. Relative expression of Pinus taeda genes of mycorrhizal root clusters. Deseq 1.14.0 package (Anders and Huber, 2010) was applied to normalize the reads mapped to Pinus taeda EST database (Deseq > 100 cutoff). Simon Anders and Wolfgang Huber (2010); Differential expression analysis for sequence count data. Genome Biology 11:R106.