1 INTRODUCTION

The occurrence of algal blooms or cyanobacterial blooms not only leads to the asphyxiation of aquatic fauna, but also releases highly toxic compounds, including microcystins, threatening the health of human beings and other organisms (Dai et al., 2018; Sun, Sun, Zhang, Esquivel-Elizondo, & Wu, 2018). Biological methods are known to be simple and efficient to control algal blooms, with less pollution compared with the physical and chemical methods (Hou et al., 2019; Yu et al., 2019; Zhang et al., 2018). In addition to the inhibition of cyanobacterial growth, algicidal bacteria and viruses can affect the water clarity and aquatic ecosystem (Wang et al., 2010). Recently, a new method for the removal of cyanobacteria by fungi was reported (Jia et al., 2010). Further, it has been reported that the mycelia of fungus Trichaptum abietinum 1302BG could enclose and eliminate almost all cocultivated cyanobacterial cells within a short time (Jia et al., 2010), and the color of cyanobacterial medium turned transparent (Han et al., 2011). Other fungi, such as Trametes versicolor F21a, Bjerkandera adusta T1, Lophariaspadicea, Phanerochaete chrysosporium, Trichoderma citrinoviride, and Irpex lacteus T2b have
been reported to exhibit algicidal ability (Han et al., 2011; Shu et al., 2016; Wang et al., 2010; Zeng, Wang, & Wang, 2015; Zeng et al., 2019). Among these, *T. versicolor* F21a and *B. adusta* T1 were considered as the two best algicidal fungi (Dai et al., 2018; Han et al., 2011; Zeng et al., 2015, 2019).

Previous studies have reported that both living and dead cyanobacterial cells first adhere to fungal mycelia before being eliminated by surrounding mycelia (Dai et al., 2018; Jia et al., 2010). It has been further demonstrated that the membranes of cyanobacterial cells and the pyrrole ring of chlorophyll a were extensively disrupted by mycelia of *P. chrysosporium* (Zeng et al., 2015). Transcriptomic and proteomic analyses of the algicidal mechanism of *T. versicolor* F21a showed that several biological processes, such as glucan 1,4-α-glucosidase activity, hydrolase activity, lipase activity, and endopeptidase activity, and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways, including glycolysis/gluconeogenesis, pyruvate metabolism, starch and sucrose metabolism, and amino acids biosynthesis, are involved in the elimination of cyanobacterial cells (Dai et al., 2018; Gao et al., 2017). The expression of all Carbohydrate-Active enZymes (CAZyme) genes significantly increased during the algicidal process in *T. versicolor* F21a (Dai et al., 2018; Gao et al., 2017). Several members of CAZyme, such as AA5, GH18, GH5, GH79, GH128, and PL8, might play key roles in the decomposition of cyanobacterial cells at different eliminating stages (Dai et al., 2018). Although the underlying molecular mechanism of algicidal fungus *T. versicolor* F21a was elucidated, there are no reports on the mechanism of other efficient algicidal fungi.

*B. adusta* is a widely distributed “white rot” fungus, which has been often associated with the decomposition of hardwoods (Moody, Dudley, Hiscox, Boddy, & Eastwood, 2018). The components of wood cell walls, such as cellulose, hemicellulose, and recalcitrant lignin, can be degraded by this fungus (Moody et al., 2018). Besides, this fungus has been reported to decompose a wide range of environmental pollutants (Bouacem et al., 2018; Han et al., 2011; Sugawara, Igeta, Amano, Hyuga, & Sugano, 2019). In our previous study, *B. adusta* T1 was found to be one of the best algicidal fungi (Han et al., 2011). In this study, gene expression in the mycelia of *B. adusta* T1, cocultivated with and without cyanobacterial cells during the algicidal process, was compared by a time-serial transcriptomic analysis. Differentially expressed genes (DEGs) were used to identify key decomposition gene(s) and pathway(s) in *B. adusta* T1, and the results were compared with that of *T. versicolor* F21a reported in a previous study (Dai et al., 2018).

## 2 | MATERIALS AND METHODS

### 2.1 | Fungal and algal strains

The previously isolated fungus *B. adusta* T1 from Zijinshan Mountain was used in this study (Han et al., 2011). Cyanobacterial strain (*Microcystis aeruginosa* PCC7806) was provided by the Institute of Hydrobiology of the Chinese Academy of Sciences (Wuhan, China).

### 2.2 | Cocultivation of fungal mycelia and cyanobacterial cells

The cyanobacterial strain was cultivated at 25°C under 12-hr light and 12-hr dark cycles with ~90 μmol/m² s⁻¹ of photons in BG-11 medium (Jia et al., 2010). Round fungal mycelium (seven mm in diameter) was inoculated onto a nine-cm plate, containing 15 ml of potato liquid medium, and incubated under static conditions for five days. Then, fungal mycelia were taken and transferred into 250-mL Erlenmeyer flasks containing 100 ml of algal solution or medium. The cocultures were incubated at 25°C, 90 μmol photons/m² s⁻¹, and

![Figure 1](image-url)  
**Figure 1** Changes in the algicidal process of *B. adusta* T1. Note: (a) Images of cocultivation after 48 hr; CK, the cyanobacterial cells as control; T1, the cocultivation of cyanobacterial cells and *B. adusta* T1 mycelia; S-T1, the cocultivation of cyanobacterial cells and died fungal mycelia. (b) Changes in chlorophyll a content during the algicidal process.
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120 rpm to investigate differentially expressed fungal genes. Total chlorophyll $a$ was measured according to the Standard Methods for the Examination of Water and Wastewater (Standard Methods for the Examination of Water & Wastewater, 1998).

2.3 RNA isolation and sequencing

Mycelia of $B. adusta$ T1 were collected from cocultures after 6, 12, 24, and 48 hr of incubation. Two biological replicates of each treatment were used for RNA sequencing. Total RNA was extracted from each sample with TRIzol reagent following the manufacturer's instructions (Takara, Dalian, China). Then, crude RNA was digested via 10 U DNase I (TaKaRa, Japan) at 37°C for 30 min, and then, mRNA was isolated using Dynabeads® Oligo (dT) 25 (Life, America) following the manufacturer's instructions.

One hundred ng mRNA of each sample was used to construct a sequencing library using NEBNext® Ultra™ RNA Library Prep Kit (NEB, America). Paired-end sequencing of cDNA fragments (~300 bp) was performed using Illumina HiSeq 4,000 platform at BGI-Shenzhen, China.

2.4 Transcriptomic analysis

In this study, RNA-Seq data of $B. adusta$ T1 at 6, 12, 24, and 48 hr were analyzed. The quality of 150-bp reads was assessed using the FASTQC program (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/). The paired-end raw reads from RNA sequencing were trimmed using the pipeline Trimmomatic (v0.33) with parameters (LEADING:3 TRAILING:3 SLIDINGWINDOW:4:15 HEADCROP:12 MINLEN:36) (Bolger, Lohse, & Usadel, 2014). The clean reads were mapped to the $B. adusta$ genome (v1.0) using STAR software (v2.5.3a) (Binder et al., 2013; Dobin et al., 2013). Expression value in FPKM (fragments per kilobase of exon model per million reads mapped) and DEGs were calculated via Cuffdiff (v2.2.1) using default parameters ($p < .05$, a fold change $\geq$ 2) (Si et al., 2019; Trapnell et al., 2012). Gene function was annotated using BLAST against reference protein-encoding sequences from the Nr database of GenBank, Gene Ontology (GO), and KEGG (Ashburner et al., 2000; Kanehisa, Furumichi, Tanabe, Sato, & Morishima, 2017; Kanehisa & Goto, 2000; Kanehisa, Sato, Kawashima, Furumichi, & Tanabe, 2016). Fisher’s exact test was used to obtain enriched functional terms at $p < .05$.

2.5 CAZyme and Secretome Annotation

All putative protein sequences of $B. adusta$ were annotated with hmmmscan against dbCAN database (Cantarel et al., 2009; Johnson, Eddy, & Portugaly, 2010; Yin et al., 2012) and further classified according to mycoCLAP database (Strasser et al., 2015). Signal information of the proteins was predicted by Target P 1.1 Server (Emanuelsson, Brunak, von Heijne, & Nielsen, 2007).

2.6 Quantitative PCR (qPCR) validation

qPCR was used to validate the gene expression calculated from RNA-Seq data. A few randomly selected lignocellulose-active enzyme genes were used in this study, and the $\beta$-actin gene of $B. adusta$ T1 was used as the endogenous control. The 20 μl reaction mixture consisted of 10 μl SYBR® Fast qPCR Mix (2x), 0.5 μl of each primer (10 μmol/L$^{-1}$), and 120–150 ng cDNA (Table A1). The qRT-PCR program was set as follows: 95°C for 10 min, followed by 40 cycles of 95°C for 15 s, 60°C for 20 s, and 72°C for 30 s. Relative expression levels were calculated using 2$^{-\Delta\Delta C_T}$ method (Livak & Schmittgen, 2001). Three biological replicates were used for qRT-PCR.
3. RESULTS

3.1 | Elimination rate during the algicidal process

The algicidal process of *B. adusta* T1 was monitored via spectrophotometer. As shown in Figure 1, the chlorophyll a content gradually decreased with the increase in incubation time. Approximately 86% of cyanobacterial cells were eliminated within 48 hr. The cyanobacterial cells were almost disappeared in the flask cocultivated with living fungal mycelia while the cyanobacterial cells were almost not affected by dead fungal mycelia compared with the blank control (Figure 1).

3.2 | RNA-Seq data generation and mapping

Mycelia of *B. adusta* T1 that was cocultivated with cyanobacterial cells at 6, 12, 24, and 48 hr were used for RNA sequencing. Fungal mycelia without cyanobacterial cells at the same time point were used as a control. Good quality RNA was isolated and used for RNA sequencing (Figure A1). A total of 63,437,015 pairs of raw reads (SRA accession: PRJNA543936) were generated (Table A2). Approximately 96% of reads were retained after the removal of adaptor and low-quality bases (Table A2). More than 64% of reads were uniquely mapped to the reference genome by pipeline STAR (Table A2), suggesting that the results of mapping can be used for the identification of fungal DEGs.

3.3 | Identification of fungal DEGs involved in the algicidal process

Boxplot of FPKM values across all samples showed the consistency of biological replicates of each treatment (Figure A2). Multi-dimensional scaling (MDS) showed that the gene expression in mycelia cocultured with cyanobacterial cells was distinctly separated from that of mycelia without cyanobacterial cells (Figure 2). The difference became highly apparent with the increase in cocultivation time (Figure 2). A total of 132, 300, 422, and 823 fungal DEGs were identified at 6, 12, 24, and 48 hr in the mycelia cocultivated with cyanobacterial cells compared with the control, respectively (Figure 3). The expression of six randomly selected lignocellulose-active enzyme genes, that is, a gene of esterase family, two genes of hydrolase family, a gene of hydrolase family 5, a radical oxidase encoding gene, a gene of hydrolase family 128, and a gene of hydrolase family 13, were further investigated via qRT-PCR (Table A1). Similar expression patterns were observed between qRT-PCR and transcriptomic analysis (Figure A3), indicating that DEGs identified by the transcriptomic analysis were suitable for further analyses.

3.4 | Annotation and enrichment analyses of fungal DEGs

After the comparison of candidate genes with Nr from NCBI, GO, and KEGG databases, DEGs were used to obtain enriched terms by Fisher's
5.1.2.1.3.5. Composition and expression of CAZyme genes of *B. adusta* T1 and its comparison with that of *T. versicolor* F21a

A total of 401 CAZyme genes were identified in the genome of *B. adusta* by hmmsearch against the dbCAN database (Table 1). The analysis showed that DEGs were enriched on glycerolipid metabolism, starch and sucrose metabolism, metabolism of xenobiotics by cytochrome P450, galactose metabolism, and ascorbate and aldarate metabolism in different stages of the algicidal process (Figure 7).
lignocellulose-active genes can be divided into 77 CAZyme modules (Table 1). Most of the genes belonged to Glycoside Hydrolases (GH) family and Auxiliary Activities (AA) family. About 312 CAZyme genes were identified in the genome of *T. versicolor* F21a (Dai et al., 2018). The number of CAZyme genes in *B. adusta* T1 genome (401 CAZyme genes) was higher than that of *T. versicolor* F21a (312 CAZyme genes). Seventy CAZyme modules were detected in *B. adusta* T1, compared to 43 CAZyme modules in *T. versicolor* F21a in the previous study (Dai et al., 2018). However, the algicidal effects of *T. versicolor* F21a were slightly more efficient than that of *B. adusta* T1 (Han et al., 2011).

The identified 128 differentially expressed CAZyme genes in *B. adusta* T1 were found to belong to 37 modules (Table 1). The genes within the same module exhibited diverse expression profiles during the algicidal process of *B. adusta* T1 (Figure 8). It was observed that module GH128, AA7, AA6, and GH109 had the highest accumulated expression during the algicidal process. The sublocation analysis showed that ~61% (245/401) of lignocellulose-active proteins contained secretory pathway signal peptides that can be secreted outside of fungal mycelia (Table A3). Genes within GH128 that encoded endo-1,3-β-glucanase (EC 3.2.1.39) could decompose xyloglucans and β-1,3-glucans into xylose and glucose, respectively. The enzymes of GH128, AA7, AA6, and GH109 were less efficient in cyanobacterial cell disruption. It is noteworthy that the accumulated expression of Polysaccharide lyases genes, particularly the PL8 module was highly up-regulated during the later stage of the algicidal process of *B. adusta* T1, which was much delayed when compared to *T. versicolor* F21a (Dai et al., 2018).

### 3.6 | Expression of other decomposition genes in *B. adusta* T1 and their comparison with that of *T. versicolor* F21a

Only a few serine-type peptidase, carboxypeptidase, and aspartic-type endopeptidase, with strong ability in cyanobacterial cell disruption, were enriched in the DEGs list during the early stage of the algicidal process (6 hr) (Figure 6). However, no strong decomposition enzyme was enriched during the later stage of the algicidal process until 24 hr (Figure 6). During the later stage (24 hr), proteins
with aspartic-type endopeptidase activity and manganese peroxidase activity were the main decomposition enzymes (Figure 6). Various types of decomposition enzymes, such as threonine-type endopeptidase and serine-type endopeptidase, were induced after 48 hr of cocultivation. In this study, proteases with Protein ID jgi|Bjead1_1|36244|fgenesh1_kg.4_#_443_#_Locus8459v1_medCvg1568.9s and jgi|Bjead1_1|342083|CE153752_10262, and jgi|Bjead1_1|110676|e_gw1.8.836.1 were observed to be the main degradation genes that might be involved in cyanobacterial cells disruption (Figure 9). Thus, these proteases can play significant roles in the algicidal process. The decomposition genes showed delayed expression compared with that of T. versicolor F21a.

**4 | DISCUSSION**

Although several fungi showed a strong algicidal activity (Han et al., 2011), the underlying molecular mechanisms for algicidal capacities are largely less investigated. Interestingly, a few fungi from the Polyporales order of Basidiomycota exhibited a strong algicidal activity (Han et al., 2011). Comparative genome analyses found that the genomes of white rot fungi contain more genes encoding plant cell wall degrading enzymes than that of brown rot and mycorrhizal fungi (Kohler et al., 2015; Tisserant et al., 2013). White rot fungi including the order Polyporales can degrade lignin as well as cellulose (Kohler et al., 2015). In the present study, we observed that the number of CAZyme genes and expressed CAZyme genes of B. adusta T1 was great than that of T. versicolor F21a. However, the algicidal effects of B. adusta T1 were slightly less efficient than that of T. versicolor F21a (Han et al., 2011). More genome sequences of fungi with diverse algicidal abilities are available now, and we also compared the number of CAZyme genes in the genome of different algicidal fungi. No direct correlation was found between algicidal efficiency and several CAZyme genes (Data not shown). A similar result was observed in the study of Pilgaard et al., 2019. This suggested that the high efficiencies of algicidal fungi are not attributed to the number of genes encoding CAZyme in the fungal genome. High lignocellulose degradation ability of white rot fungi, in comparison with that of brown rot fungi and mycorrhizal fungi, can be attributed to the number of genes encoding plant cell wall degrading enzymes in fungal genomes as a result of long-term natural selection (Kohler et al., 2015). The numbers of CAZyme genes were not directly correlated with algicidal abilities, which might be due to the fact that most algicidal fungi were isolated from terrestrial environments and lacked evolution selection pressure in the water system (Han et al., 2011).

Direct contact between fungal mycelia and cyanobacterial cells was required for eliminating cyanobacterial cells by fungi (Han et al., 2011; Jia et al., 2010). Previous studies showed that a few decomposition enzymes might play important roles in eliminating cyanobacterial cells by T. versicolor F21a. In particular, cellulase, β-glucanase, and protease were supposed to efficiently disrupt cyanobacterial cells by T. versicolor F21a (Dai et al., 2018; Gao et al., 2017). In the present study, a large number of decomposition enzymes belonging to 37 modules were observed during the algicidal process of B. adusta T1. Among them, GH128, AA7, AA6, and GH109 were the highest accumulated
| Enzyme classes | CAZyme module | No. of decomposition enzymes in the genome | No. of decomposition enzymes detected by RNA-Seq | No. of decomposition enzymes in DEGs by RNA-Seq |
|----------------|---------------|------------------------------------------|-----------------------------------------------|-----------------------------------------------|
| Auxiliary activities | AA1 | 1 | 1 | |
| | AA2 | 21 | 19 | 10 |
| | AA3 | 38 | 30 | 12 |
| | AA4 | 1 | | |
| | AA5 | 7 | 8 | 6 |
| | AA6 | 5 | 4 | 3 |
| | AA7 | 10 | 6 | 3 |
| | AA8 | 2 | 2 | |
| | AA9 | 27 | 20 | 7 |
| Carbohydrate esterases | CE1 | 18 | 11 | 3 |
| | CE10 | 42 | 31 | 6 |
| | CE12 | 3 | 2 | |
| | CE14 | 1 | 1 | |
| | CE15 | 2 | 2 | |
| | CE16 | 14 | 6 | 3 |
| | CE2 | 1 | 1 | |
| | CE3 | 1 | 1 | |
| | CE4 | 5 | 3 | 3 |
| | CE8 | 2 | 2 | 1 |
| | CE9 | 1 | | |
| | GH1 | 2 | 2 | 1 |
| Glycoside hydrolases | GH10 | 4 | 5 | 4 |
| | GH105 | 3 | 3 | 1 |
| | GH109 | 8 | 8 | 5 |
| | GH115 | 2 | 2 | 1 |
| | GH12 | 2 | 1 | |
| | GH125 | 1 | 1 | |
| | GH127 | 1 | 1 | |
| | GH128 | 5 | 3 | 2 |
| | GH13 | 9 | 9 | 6 |
| | GH131 | 3 | | |
| | GH15 | 2 | 2 | |
| | GH16 | 19 | 17 | 5 |
| | GH17 | 1 | 1 | |
| | GH18 | 13 | 10 | 3 |
| | GH2 | 3 | 2 | 2 |
| | GH20 | 4 | 2 | |
| | GH23 | 1 | | |
| | GH24 | 1 | 1 | |
| | GH25 | 1 | 1 | |
| | GH27 | 3 | 3 | 1 |
| | GH28 | 6 | 4 | |
| | GH3 | 8 | 8 | 4 |
| | GH30 | 1 | 1 | |

(Continues)
expression module. However, the enzymes of GH128, AA7, AA6, and GH109 were not able to efficiently disrupt the macromolecules (Ekstrom, Taujale, McGinn, & Yin, 2014; Yin et al., 2012), such as cellulose in the cell wall of cyanobacterial cells. This suggested that lignocellulose-active proteins of *B. adusta* T1 might not be the key enzymes for the breakdown of cyanobacterial cells.

Previous studies showed that chondroitin ABC lyase (EC 4.2.2.1) of PL8 and alginate lyase (EC 4.2.2.3) of PL14 were able to decompose peptidoglycan and alginate (Lombard, Golaconda Ramulu, Drula, Coutinho, & Henrissat, 2014), and the expression level was also significantly up-regulated during the algicidal process of *T. versicolor* F21a (Dai et al., 2018; Gao et al., 2017). Chondroitin AC lyase (chondroitin sulfate) and alginate lyase were unique to a known saprophytic marine fungus *Paradendryphiella salina* in the breakdown of dried brown algae in the medium compared with its terrestrial counterparts (Pilgaard et al., 2019). Recombinant expression of Chondroitin AC lyase of the marine fungus *P. salina* reveals that alginate lyase can degrade several types of brown algae polysaccharides (Pilgaard et al., 2019). A putative PL8 of *P. salina* with a similar sequence should also decompose brown macroalgae (Pilgaard et al., 2019). Proteomic analysis of the secretome of *P. salina* grown on three species of brown algae and under carbon limitation implied that the basic CAZyme repertoire of saprobic fungi

| Enzyme classes | CAZyme module | No. of decomposition enzymes in the genome | No. of decomposition enzymes detected by RNA-Seq | No. of decomposition enzymes in DEGs by RNA-Seq |
|----------------|---------------|------------------------------------------|---------------------------------------------|---------------------------------------------|
| GH31           | 4             | 5                                        | 3                                           |
| GH35           | 4             | 4                                        |                                             |
| GH37           | 2             | 1                                        | 1                                           |
| GH38           | 1             |                                          |                                             |
| GH43           | 6             | 6                                        | 4                                           |
| GH47           | 6             | 3                                        |                                             |
| GH5            | 20            | 16                                       | 8                                           |
| GH51           | 2             | 2                                        | 1                                           |
| GH53           | 1             | 1                                        |                                             |
| GH55           | 3             | 3                                        | 1                                           |
| GH6            | 1             | 1                                        | 1                                           |
| GH63           | 2             | 1                                        |                                             |
| GH7            | 5             | 4                                        | 1                                           |
| GH71           | 3             | 3                                        | 1                                           |
| GH72           | 1             | 1                                        |                                             |
| GH74           | 3             | 3                                        |                                             |
| GH76           | 2             | 1                                        |                                             |
| GH78           | 2             | 2                                        |                                             |
| GH79           | 7             | 9                                        | 6                                           |
| GH85           | 1             | 1                                        |                                             |
| GH88           | 1             | 1                                        |                                             |
| GH89           | 1             | 1                                        |                                             |
| GH9            | 1             | 1                                        |                                             |
| GH92           | 3             | 3                                        | 1                                           |
| GH95           | 1             | 1                                        |                                             |
| GH99           | 1             |                                          |                                             |

**Polysaccharide lyases**

| Polysaccharide lyases | PL1  | PL12 | PL14 | PL3  | PL4  | PL5  | PL8  | Total |
|-----------------------|------|------|------|------|------|------|------|-------|
|                       | 1    | 1    | 5    | 2    | 1    | 2    | 1    | 401   |
|                       | 1    | 1    | 1    | 2    | 1    | 1    | 1    | 324   |
|                       | 1    | 1    | 1    | 1    | 1    | 1    | 1    | 128   |

**TABLE 1** (Continued)
belongs to ascomycetes, with the addition of PL7 alginate lyases, provide *P. salina* with sufficient enzymatic capabilities to degrade several types of brown algae polysaccharides (Pilgaard et al., 2019). In the present study, the total expression level of PL14 was down-regulated during the algicidal process of *B. adusta* T1, while no gene, belonging to PL7, was detected in the genome of *B. adusta*. The accumulated
expression level of PL8 was highly up-regulated in the later stage of the algicidal process of B. adusta T1, which was much delayed when compared with T. versicolor F21a (Dai et al., 2018). All the evidence indicated that enzymes of PL8 with strong peptidoglycan and alginate decomposition abilities might be a vital genetic factor for the determination of the algicidal ability of T. versicolor F21a as well as B. adusta T1.

Analysis of the enriched GO terms and KEGG pathways showed that several types of peptidases were enriched during the algicidal process of B. adusta T1. In particular, proteases (protein ID jgi|Bjead1_1|36244|fgenesh1_kg.4_#_443_#_Locus8459v1_med-Cvg1568.9s, jgi|Bjead1_1|342083|CE153752_10262, and jgi|Bjead1_1|110676|fgenesh1_kg.7_#_39_#_Locus4370v1_med-Cvg1568.9s) were highly up-regulated during the later stages of cocultivation. Proteomic analysis of P. salina also implied that the PL7 and PL8 enzymes, abundantly secreted together with enzymes of P. salina, were necessary for degradation of laminarin, cellulose, lipids, and peptides of brown algae (Pilgaard et al., 2019). Different types of peptides were detected in P. salina grown on three species of brown algae (Pilgaard et al., 2019). Additionally, several fungal proteins belonging to peptidase were also up-regulated during the algicidal process of T. versicolor F21a (Gao et al., 2017). Besides, four homologous decomposition enzymes of other species with endo-glycosidase and endopeptidase activities were selected to investigate their effects on cyanobacterial cells, and one type of protease was found to effectively disrupt cyanobacterial cells (Dai et al., 2018).

Comparison of the gene expression during the algicidal process of B. adusta T1 and T. versicolor F21a demonstrated that majority of decomposition genes with endopeptidase and endo-glycosidase activities in B. adusta T1 were expressed in the later stage of cocultivation, while the similar genes in T. versicolor F21a were induced in the early stage (Dai et al., 2018). Thus, protease together with enzymes of PL8 might play a key role in the elimination of cyanobacterial cells both by B. adusta T1 and T. versicolor F21a. The expression of enzymes of PL8 and peptidases in B. adusta T1 was little delayed compared with that of T. versicolor F21a, which should be the reason why the algicidal efficiency of T. versicolor F21a is better than that of B. adusta T1.

The production of microcystins (MC) by cyanobacterial blooms often severely threatens human and ecosystems health (Li, Li, & Li, 2017). Biodegradation is an efficient and sustainable biological strategy for MC removal (Li et al., 2017). A large number of bacteria and several fungi were reported with MC removal or degrading capabilities (Dziga, Wasylewski, Wadyla, Nybom, & Meriluoto, 2013; Jia, Du, Song, Zhao, & Tian, 2012; Li et al., 2017; Mohamed, Hashem, & Alami, 2014; Qin et al., 2019). Four mlr genes (i.e., mlrC, A, D, and B) located sequentially in a gene cluster in the genome of Sphingomonas sp. ACM-3962 strain were identified for MC bio-degradation (Bourne et al., 1996; Bourne, Riddles, Jones, Smith, & Blakeley, 2001). The enzymatic pathway involves at least three intracellular enzymes and two intermediate products (Li et al., 2017). Heterologous expression of the mlrA gene originated from Novosphingobium sp. THN1 showed that the recombinant MlrA hydrolyzed microcystin-RR into a linear intermediate product by cleaving the peptide bond between Adda and arginine residue, which is also the first step involved in MC degradation pathway (Wang et al., 2017). Site-directed mutants of MlrA suggested that MlrA is likely not a metalloprotease but a glutamate protease belonging to type II CAAX prenyl endopeptidases (Xu et al., 2019).

FIGURE 9 Time-course change of protease genes expression level of T1 cocultivation with cyanobacteria. Note: 6h_c, control sample at 6h; 6h_T, treatment sample at 6 h; 12h_c, control sample at 12 h; 12h_T, treatment sample at 12 h; 24h_c, control sample at 24 h; 24h_T, treatment sample at 24 h; 48h_c, control sample at 48 h; 48h_T, treatment sample at 48 h
these from T. versicolor F21a, reported in our previous study. The identified DEGs were enriched in endopeptidase activity, cellulose catabolic process, and transmembrane transporter activity. Endopeptidases together with enzymes of PL8 might play a key role in the elimination of cyanobacterial cells by both algicidal fungi, B. adusta T1 and T. versicolor F21a.

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CONFLICTS OF INTEREST
None declared.

AUTHOR CONTRIBUTION
Guomin Han: Conceptualization (equal); Software (lead); Writing-original draft (equal). Hui Ma: Investigation (equal). Shenrong Ren: Investigation (supporting). Xueyan Gao: Investigation (supporting). Xiaolong He: Investigation (supporting). Suwen Zhu: Resources (equal); Validation (supporting). Ruining Deng: Validation (supporting). Shihua Zhang: Conceptualization (equal); Writing-review & editing (equal).

ETHICS STATEMENT
None required.

DATA AVAILABILITY STATEMENT
The raw paired-end sequences from the Bjerkandera adusta isolate T1 are available at https://www.ncbi.nlm.nih.gov/bioproject/PRJNA543936. The genome annotations of Bjerkandera adusta and Trametes versicolor can be found at the JGI MycoCosm: https://mycocosm.jgi. doe.gov/Bjead1_1/Bjead1_1.home.html and https://mycocosm.jgi. doe.gov/Trave1/Trave1.home.html, respectively.

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### APPENDIX 1

#### Table A1

| Protein ID | Annotation                        | Primer                                      |
|------------|-----------------------------------|---------------------------------------------|
| jgi|Bjead1_1|459664|MIX10988_17319_14 | Radical oxidase | GTCAAGCGGGTGTTCTTTAA |
|          |                                   |                                             | CCTCTCCTGTTGCCGTTT |
| jgi|Bjead1_1|34143|fgenes1_kg.1.954_945.1 | Esterase family 1 protein | CCTCCCTGCAAAACCTTCACA |
|          |                                   |                                             | GGAGACGTGTCGGGAAAGAG |
| jgi|Bjead1_1|172436|gm1.8875_g | Hydrolase family 5 protein | TACGAGGGCGACGATTGG |
|          |                                   |                                             | CTCACC GGACACGTAACCA |
| jgi|Bjead1_1|35099|fgenes1_kg.2.711_711.1 | Hydrolase family 5 protein | CTCGTTGACCCGCCACACAAC |
|          |                                   |                                             | GGGAAATACGTGAGGCTCGTT |
| jgi|Bjead1_1|355947|CE167616_517 | Hydrolase family 128 protein | AGCGCGGTGTGTCATACAAC |
|          |                                   |                                             | TGTGTCCGGCATCGGTATT |
| jgi|Bjead1_1|38229|fgenes1_kg.7.551_551.1 | Hydrolase family 13 protein | CACGCCCGACTATTCGAAGT |
|          |                                   |                                             | GTCGGGTTTCCGTGTCAG |

#### Table A2

| Sample  | Raw reads | Number of input reads | Cleaned length | Uniquely mapped reads number | Uniquely mapped reads (%) |
|---------|-----------|-----------------------|----------------|-----------------------------|--------------------------|
| 6h_ck1  | 3,713,910 | 3,531,468             | 129.69         | 2,491,981                   | 70.57                    |
| 6h_ck2  | 3,618,291 | 3,416,852             | 129.055        | 2,205,290                   | 64.54                    |
| 6h_T1   | 3,644,390 | 3,577,152             | 128.745        | 2,802,466                   | 78.34                    |
| 6h_T2   | 4,379,858 | 4,280,639             | 128.835        | 3,282,569                   | 76.68                    |
| 12h_ck1 | 3,832,620 | 3,691,873             | 129.505        | 2,706,111                   | 73.30                    |
| 12h_ck2 | 3,806,801 | 3,651,869             | 129.09         | 2,603,461                   | 71.29                    |
| 12h_T1  | 3,493,777 | 3,325,461             | 125.865        | 2,458,201                   | 73.92                    |
| 12h_T2  | 4,020,571 | 3,899,676             | 128.9          | 2,967,516                   | 76.53                    |
| 24h_ck1 | 3,609,635 | 3,388,118             | 128.875        | 2,326,955                   | 68.68                    |
| 24h_ck2 | 3,684,973 | 3,497,767             | 129.655        | 2,466,212                   | 70.51                    |
| 24h_T1  | 4,831,627 | 4,684,474             | 128.62         | 3,554,342                   | 75.87                    |
| 24h_T2  | 4,567,295 | 4,436,833             | 128.9          | 3,395,508                   | 76.53                    |
| 48h_ck1 | 3,638,776 | 3,456,573             | 129.255        | 2,500,095                   | 72.33                    |
| 48h_ck2 | 3,594,592 | 3,405,731             | 128.51         | 2,473,909                   | 72.64                    |
| 48h_T1  | 4,499,718 | 4,347,471             | 128.275        | 3,264,957                   | 75.10                    |
| 48h_T2  | 4,500,181 | 4,353,762             | 128.58         | 3,277,084                   | 75.27                    |

1 Note: The number of reads were expressed in pairs.
| Protein ID  | Len   | mTP  | SP   | Other  | Loc | RC |
|------------|-------|------|------|--------|-----|----|
| 39948      | 1,041 | 0.095| 0.093| 0.844  | _   | 2  |
| 170203     | 646   | 0.083| 0.105| 0.872  | _   | 2  |
| 229483     | 319   | 0.049| 0.917| 0.053  | S   | 1  |
| 113359     | 295   | 0.045| 0.95  | 0.032  | S   | 1  |
| 40021      | 320   | 0.081| 0.908| 0.028  | S   | 1  |
| 40040      | 465   | 0.053| 0.942| 0.029  | S   | 1  |
| 230253     | 1,024 | 0.014| 0.966| 0.07   | S   | 1  |
| 230354     | 1,005 | 0.342| 0.705| 0.024  | S   | 4  |
| 183239     | 385   | 0.671| 0.027| 0.355  | M   | 4  |
| 62585      | 305   | 0.147| 0.104| 0.761  | _   | 2  |
| 113961     | 604   | 0.534| 0.055| 0.439  | M   | 5  |
| 452849     | 310   | 0.077| 0.037| 0.944  | _   | 1  |
| 170455     | 322   | 0.091| 0.068| 0.894  | _   | 1  |
| 237378     | 316   | 0.042| 0.949| 0.058  | S   | 1  |
| 40461      | 244   | 0.054| 0.954| 0.043  | S   | 1  |
| 183509     | 612   | 0.558| 0.024| 0.588  | _   | 5  |
| 240122     | 301   | 0.092| 0.873| 0.031  | S   | 2  |
| 40615      | 587   | 0.037| 0.159| 0.919  | _   | 2  |
| 241975     | 605   | 0.068| 0.073| 0.901  | _   | 1  |
| 52811      | 537   | 0.063| 0.913| 0.03   | S   | 1  |
| 40743      | 377   | 0.103| 0.892| 0.017  | S   | 2  |
| 170929     | 704   | 0.088| 0.048| 0.937  | _   | 1  |
| 170934     | 551   | 0.063| 0.897| 0.086  | S   | 1  |
| 244200     | 674   | 0.027| 0.93  | 0.065  | S   | 1  |
| 244246     | 669   | 0.018| 0.971| 0.054  | S   | 1  |
| 62986      | 499   | 0.058| 0.906| 0.041  | S   | 1  |
| 71431      | 617   | 0.491| 0.658| 0.014  | S   | 5  |
| 245049     | 604   | 0.442| 0.655| 0.01   | S   | 4  |
| 40812      | 611   | 0.087| 0.044| 0.906  | _   | 1  |
| 245297     | 598   | 0.061| 0.81  | 0.11   | S   | 2  |
| 171002     | 606   | 0.196| 0.68  | 0.028  | S   | 3  |
| 84503      | 373   | 0.101| 0.05  | 0.922  | _   | 1  |
| 171059     | 593   | 0.14  | 0.872| 0.019  | S   | 2  |
| 156054     | 596   | 0.044| 0.887| 0.074  | S   | 1  |
| 114954     | 574   | 0.084| 0.115| 0.897  | _   | 2  |
| 40886      | 614   | 0.079| 0.052| 0.904  | _   | 1  |
| 136631     | 614   | 0.123| 0.045| 0.86   | _   | 2  |
| 114902     | 593   | 0.423| 0.556| 0.029  | S   | 5  |
| 52983      | 613   | 0.052| 0.044| 0.95   | _   | 1  |
| 52991      | 597   | 0.044| 0.914| 0.052  | S   | 1  |
| 183896     | 599   | 0.014| 0.93  | 0.089  | S   | 1  |
| 53087      | 1,011 | 0.036| 0.969| 0.05   | S   | 1  |
| 41108      | 696   | 0.159| 0.081| 0.841  | _   | 2  |
| 41113      | 573   | 0.093| 0.207| 0.634  | _   | 3  |
| 171368     | 478   | 0.069| 0.079| 0.9    | _   | 1  |
| Protein ID | Len | mTP | SP | Other | Loc | RC |
|------------|-----|-----|----|-------|-----|----|
| 41241      | 396 | 0.274 | 0.84 | 0.018 | S   | 3  |
| 454703     | 402 | 0.63  | 0.021 | 0.452 | M   | 5  |
| 41251      | 337 | 0.075 | 0.736 | 0.21  | S   | 3  |
| 41305      | 371 | 0.11  | 0.094 | 0.754 |     | 2  |
| 41306      | 538 | 0.094 | 0.099 | 0.816 |     | 2  |
| 256509     | 423 | 0.468 | 0.891 | 0.004 | S   | 3  |
| 184224     | 600 | 0.103 | 0.101 | 0.838 |     | 2  |
| 41490      | 303 | 0.052 | 0.147 | 0.93  |     | 2  |
| 260893     | 199 | 0.086 | 0.089 | 0.914 |     | 1  |
| 184394     | 582 | 0.803 | 0.053 | 0.115 | M   | 2  |
| 157149     | 768 | 0.029 | 0.956 | 0.036 | S   | 1  |
| 41596      | 266 | 0.069 | 0.929 | 0.046 | S   | 1  |
| 171769     | 774 | 0.021 | 0.96  | 0.057 | S   | 1  |
| 261859     | 808 | 0.085 | 0.06  | 0.922 |     | 1  |
| 116111     | 281 | 0.069 | 0.143 | 0.873 |     | 2  |
| 263236     | 400 | 0.054 | 0.958 | 0.066 | S   | 1  |
| 29758      | 400 | 0.043 | 0.995 | 0.011 | S   | 1  |
| 263252     | 398 | 0.053 | 0.98  | 0.022 | S   | 1  |
| 41686      | 427 | 0.307 | 0.369 | 0.337 | S   | 5  |
| 41708      | 649 | 0.18  | 0.862 | 0.014 | S   | 2  |
| 41754      | 647 | 0.053 | 0.182 | 0.858 |     | 2  |
| 41763      | 404 | 0.094 | 0.768 | 0.13  | S   | 2  |
| 53682      | 693 | 0.255 | 0.759 | 0.029 | S   | 3  |
| 41854      | 517 | 0.021 | 0.968 | 0.058 | S   | 1  |
| 41863      | 491 | 0.11  | 0.913 | 0.016 | S   | 1  |
| 41869      | 336 | 0.222 | 0.908 | 0.016 | S   | 2  |
| 41896      | 447 | 0.713 | 0.025 | 0.412 | M   | 4  |
| 138203     | 774 | 0.05  | 0.127 | 0.857 |     | 2  |
| 184697     | 372 | 0.085 | 0.874 | 0.045 | S   | 2  |
| 116816     | 362 | 0.078 | 0.863 | 0.061 | S   | 2  |
| 172102     | 377 | 0.068 | 0.887 | 0.051 | S   | 1  |
| 41961      | 329 | 0.044 | 0.92  | 0.064 | S   | 1  |
| 456042     | 328 | 0.038 | 0.942 | 0.045 | S   | 1  |
| 268970     | 386 | 0.025 | 0.953 | 0.056 | S   | 1  |
| 29957      | 283 | 0.019 | 0.958 | 0.067 | S   | 1  |
| 116945     | 203 | 0.143 | 0.062 | 0.889 |     | 2  |
| 157771     | 401 | 0.037 | 0.944 | 0.045 | S   | 1  |
| 157775     | 304 | 0.039 | 0.933 | 0.056 | S   | 1  |
| 63838      | 343 | 0.015 | 0.974 | 0.051 | S   | 1  |
| 41982      | 373 | 0.156 | 0.807 | 0.026 | S   | 2  |
| 172152     | 362 | 0.046 | 0.927 | 0.051 | S   | 1  |
| 269481     | 367 | 0.124 | 0.787 | 0.049 | S   | 2  |
| 269524     | 373 | 0.13  | 0.823 | 0.028 | S   | 2  |
| 41997      | 618 | 0.09  | 0.958 | 0.02  | S   | 1  |
| 172246     | 372 | 0.117 | 0.854 | 0.028 | S   | 2  |
| Protein ID | Len | mTP  | SP  | Other | Loc | RC |
|------------|-----|------|-----|-------|-----|----|
| 157924     | 374 | 0.155| 0.857| 0.027 | S   | 2  |
| 117149     | 396 | 0.013| 0.496| 0.863 |     | 4  |
| 184935     | 309 | 0.034| 0.944| 0.061 | S   | 1  |
| 138704     | 475 | 0.096| 0.071| 0.887 |     | 2  |
| 172436     | 486 | 0.083| 0.049| 0.928 |     | 1  |
| 42291      | 347 | 0.056| 0.938| 0.021 | S   | 1  |
| 81341      | 141 | 0.059| 0.274| 0.852 |     | 3  |
| 158334     | 414 | 0.237| 0.054| 0.674 |     | 3  |
| 42434      | 421 | 0.05 | 0.914| 0.051 | S   | 1  |
| 54172      | 363 | 0.017| 0.977| 0.039 | S   | 1  |
| 185179     | 452 | 0.09 | 0.805| 0.059 | S   | 2  |
| 117666     | 259 | 0.056| 0.913| 0.05  | S   | 1  |
| 42534      | 327 | 0.084| 0.883| 0.031 | S   | 2  |
| 42539      | 270 | 0.19 | 0.044| 0.855 |     | 2  |
| 296151     | 848 | 0.178| 0.112| 0.76  |     | 3  |
| 185311     | 397 | 0.037| 0.706| 0.59  | S   | 5  |
| 42617      | 504 | 0.024| 0.239| 0.872 |     | 2  |
| 42631      | 975 | 0.141| 0.86 | 0.023 | S   | 2  |
| 117772     | 330 | 0.454| 0.018| 0.718 |     | 4  |
| 54399      | 313 | 0.027| 0.948| 0.043 | S   | 1  |
| 172925     | 348 | 0.068| 0.979| 0.031 | S   | 1  |
| 172926     | 355 | 0.031| 0.968| 0.045 | S   | 1  |
| 158817     | 338 | 0.037| 0.936| 0.087 | S   | 1  |
| 158842     | 1,102| 0.131| 0.059| 0.88  |     | 2  |
| 185485     | 287 | 0.099| 0.149| 0.826 |     | 2  |
| 118319     | 648 | 0.118| 0.832| 0.057 | S   | 2  |
| 139564     | 387 | 0.947| 0.041| 0.047 | M   | 1  |
| 42889      | 285 | 0.055| 0.192| 0.895 |     | 2  |
| 302552     | 344 | 0.191| 0.044| 0.811 |     | 2  |
| 305292     | 253 | 0.084| 0.889| 0.033 | S   | 1  |
| 43095      | 366 | 0.129| 0.816| 0.031 | S   | 2  |
| 306404     | 366 | 0.113| 0.849| 0.032 | S   | 2  |
| 43114      | 348 | 0.099| 0.818| 0.057 | S   | 2  |
| 306863     | 366 | 0.041| 0.901| 0.056 | S   | 1  |
| 118718     | 363 | 0.052| 0.884| 0.049 | S   | 1  |
| 119037     | 314 | 0.05 | 0.91 | 0.069 | S   | 1  |
| 43329      | 364 | 0.143| 0.843| 0.03  | S   | 2  |
| 173495     | 364 | 0.337| 0.782| 0.013 | S   | 3  |
| 311850     | 437 | 0.082| 0.904| 0.031 | S   | 1  |
| 54893      | 416 | 0.149| 0.835| 0.047 | S   | 2  |
| 185921     | 568 | 0.19 | 0.847| 0.046 | S   | 2  |
| 459664     | 777 | 0.052| 0.777| 0.257 | S   | 3  |
| 43446      | 386 | 0.099| 0.882| 0.061 | S   | 2  |
| 313682     | 859 | 0.047| 0.95 | 0.031 | S   | 1  |
| 173673     | 260 | 0.015| 0.968| 0.041 | S   | 1  |

(Continues)
| Protein ID | Len | mTP | SP  | Other | Loc | RC |
|-----------|-----|-----|-----|-------|-----|----|
| 119350    | 399 | 0.033 | 0.941 | 0.062 | S  | 1  |
| 119522    | 575 | 0.095 | 0.042 | 0.13  | M  | 2  |
| 119593    | 1,000 | 0.12 | 0.864 | 0.207 | S  | 2  |
| 43812     | 1,034 | 0.027 | 0.834 | 0.427 | S  | 3  |
| 43892     | 615  | 0.019 | 0.971 | 0.047 | S  | 1  |
| 323280    | 369  | 0.239 | 0.763 | 0.019 | S  | 3  |
| 43929     | 258  | 0.026 | 0.965 | 0.084 | S  | 1  |
| 186344    | 320  | 0.122 | 0.849 | 0.039 | S  | 2  |
| 120002    | 362  | 0.08  | 0.87  | 0.048 | S  | 2  |
| 55334     | 249  | 0.034 | 0.907 | 0.075 | S  | 1  |
| 43966     | 742  | 0.024 | 0.946 | 0.05  | S  | 1  |
| 324420    | 819  | 0.032 | 0.934 | 0.049 | S  | 1  |
| 186388    | 434  | 0.136 | 0.879 | 0.039 | S  | 2  |
| 44047     | 495  | 0.025 | 0.966 | 0.045 | S  | 1  |
| 44072     | 557  | 0.412 | 0.595 | 0.018 | S  | 5  |
| 302659    | 470  | 0.38  | 0.617 | 0.062 | S  | 4  |
| 141290    | 460  | 0.062 | 0.147 | 0.889 | _  | 4  |
| 120399    | 298  | 0.117 | 0.362 | 0.535 | _  | 5  |
| 344867    | 663  | 0.092 | 0.927 | 0.021 | S  | 4  |
| 141539    | 663  | 0.101 | 0.904 | 0.022 | S  | 1  |
| 306714    | 804  | 0.294 | 0.842 | 0.009 | S  | 3  |
| 44370     | 571  | 0.236 | 0.777 | 0.041 | S  | 3  |
| 44376     | 532  | 0.037 | 0.964 | 0.029 | S  | 1  |
| 44391     | 385  | 0.022 | 0.964 | 0.048 | S  | 1  |
| 141648    | 466  | 0.369 | 0.686 | 0.046 | S  | 4  |
| 55696     | 466  | 0.59  | 0.689 | 0.03  | S  | 5  |
| 462628    | 730  | 0.223 | 0.087 | 0.657 | _  | 3  |
| 120968    | 1,020 | 0.018 | 0.966 | 0.057 | S  | 1  |
| 161363    | 452  | 0.052 | 0.912 | 0.047 | S  | 1  |
| 174734    | 531  | 0.054 | 0.857 | 0.206 | S  | 2  |
| 161500    | 326  | 0.05  | 0.927 | 0.032 | S  | 1  |
| 353490    | 284  | 0.807 | 0.044 | 0.166 | M  | 2  |
| 353489    | 254  | 0.422 | 0.051 | 0.632 | _  | 4  |
| 44803     | 1,134 | 0.105 | 0.028 | 0.928 | _  | 1  |
| 355947    | 264  | 0.021 | 0.946 | 0.08  | S  | 1  |
| 73811     | 287  | 0.489 | 0.745 | 0.016 | S  | 4  |
| 121664    | 369  | 0.079 | 0.874 | 0.033 | S  | 2  |
| 31936     | 332  | 0.211 | 0.783 | 0.03  | S  | 3  |
| 73869     | 357  | 0.123 | 0.12  | 0.842 | _  | 2  |
| 463744    | 931  | 0.029 | 0.972 | 0.025 | S  | 1  |
| 45029     | 958  | 0.016 | 0.969 | 0.057 | S  | 1  |
| 187270    | 615  | 0.044 | 0.957 | 0.029 | S  | 1  |
| 56225     | 960  | 0.166 | 0.202 | 0.582 | _  | 4  |
| 32051     | 406  | 0.186 | 0.073 | 0.732 | _  | 3  |
| 361367    | 713  | 0.08  | 0.063 | 0.949 | _  | 1  |

(Continues)
| Protein ID | Len | mTP | SP   | Other | Loc | RC |
|------------|-----|-----|------|-------|-----|----|
| 73972      | 481 | 0.159 | 0.698 | 0.092 | S   | 3  |
| 175283     | 521 | 0.208 | 0.945 | 0.004 | S   | 2  |
| 45135      | 778 | 0.166 | 0.895 | 0.011 | S   | 2  |
| 121936     | 537 | 0.043 | 0.918 | 0.053 | S   | 1  |
| 45153      | 588 | 0.043 | 0.845 | 0.111 | S   | 2  |
| 122105     | 500 | 0.097 | 0.128 | 0.838 |     |    |
| 56307      | 208 | 0.323 | 0.115 | 0.412 |     |    |
| 45281      | 340 | 0.341 | 0.59  | 0.036 | S   | 4  |
| 45314      | 601 | 0.082 | 0.12  | 0.844 |     |    |
| 465711     | 611 | 0.071 | 0.279 | 0.729 |     |    |
| 175513     | 700 | 0.052 | 0.367 | 0.644 |     |    |
| 143000     | 604 | 0.101 | 0.128 | 0.746 |     |    |
| 56449      | 403 | 0.04  | 0.96  | 0.034 | S   | 1  |
| 175536     | 379 | 0.127 | 0.872 | 0.031 | S   | 2  |
| 74164      | 587 | 0.144 | 0.145 | 0.649 |     |    |
| 162505     | 587 | 0.081 | 0.165 | 0.796 |     |    |
| 56499      | 798 | 0.368 | 0.808 | 0.011 | S   | 3  |
| 56525      | 330 | 0.449 | 0.653 | 0.023 | S   | 4  |
| 45516      | 850 | 0.067 | 0.891 | 0.081 | S   | 1  |
| 162602     | 215 | 0.09  | 0.086 | 0.866 |     |    |
| 384658     | 698 | 0.142 | 0.879 | 0.033 | S   | 2  |
| 45570      | 1,468 | 0.018 | 0.965 | 0.042 | S   | 1  |
| 187728     | 605 | 0.116 | 0.157 | 0.718 |     |    |
| 45647      | 404 | 0.1   | 0.692 | 0.179 | S   | 3  |
| 66377      | 626 | 0.158 | 0.64  | 0.062 | S   | 3  |
| 66400      | 890 | 0.144 | 0.023 | 0.921 |     |    |
| 122937     | 361 | 0.08  | 0.919 | 0.03  | S   | 1  |
| 66493      | 204 | 0.046 | 0.304 | 0.687 |     |    |
| 143585     | 374 | 0.045 | 0.094 | 0.947 |     |    |
| 123323     | 650 | 0.114 | 0.295 | 0.801 |     |    |
| 45905      | 313 | 0.127 | 0.925 | 0.028 | S   | 2  |
| 403554     | 339 | 0.262 | 0.075 | 0.74  |     |    |
| 56859      | 320 | 0.081 | 0.863 | 0.059 | S   | 2  |
| 176420     | 458 | 0.019 | 0.972 | 0.037 | S   | 1  |
| 46260      | 847 | 0.035 | 0.189 | 0.908 |     |    |
| 188241     | 862 | 0.038 | 0.161 | 0.94  |     |    |
| 33215      | 801 | 0.067 | 0.777 | 0.182 | S   | 3  |
| 101267     | 513 | 0.022 | 0.946 | 0.089 | S   | 1  |
| 33263      | 449 | 0.021 | 0.9   | 0.099 | S   | 1  |
| 102985     | 338 | 0.067 | 0.974 | 0.027 | S   | 1  |
| 448899     | 540 | 0.413 | 0.042 | 0.616 |     |    |
| 177450     | 748 | 0.043 | 0.939 | 0.031 | S   | 1  |
| 196330     | 544 | 0.05  | 0.961 | 0.019 | S   | 1  |
| 33636      | 717 | 0.168 | 0.175 | 0.701 |     |    |
| 125362     | 239 | 0.358 | 0.042 | 0.545 |     |    |

(Continues)
| Protein ID | Len | mTP | SP | Other | Loc | RC |
|------------|-----|-----|----|-------|-----|----|
| 100935     | 396 | 0.091 | 0.352 | 0.583 | _   | 4  |
| 164180     | 836 | 0.303 | 0.845 | 0.012 | S   | 3  |
| 102479     | 750 | 0.243 | 0.06  | 0.721 | _   | 3  |
| 199563     | 388 | 0.678 | 0.27  | 0.052 | M   | 3  |
| 145317     | 557 | 0.044 | 0.799 | 0.201 | S   | 3  |
| 95645      | 99  | 0.09  | 0.193 | 0.743 | _   | 3  |
| 33906      | 312 | 0.19  | 0.087 | 0.732 | _   | 3  |
| 201958     | 607 | 0.826 | 0.018 | 0.328 | M   | 3  |
| 33959      | 594 | 0.708 | 0.032 | 0.35  | M   | 4  |
| 33963      | 340 | 0.025 | 0.921 | 0.133 | S   | 2  |
| 203296     | 422 | 0.12  | 0.923 | 0.024 | S   | 1  |
| 34143      | 292 | 0.061 | 0.079 | 0.934 | _   | 1  |
| 47402      | 390 | 0.028 | 0.942 | 0.071 | S   | 1  |
| 164550     | 682 | 0.506 | 0.434 | 0.072 | M   | 5  |
| 126363     | 785 | 0.226 | 0.14  | 0.716 | _   | 3  |
| 34175      | 506 | 0.937 | 0.026 | 0.099 | M   | 1  |
| 126440     | 419 | 0.058 | 0.137 | 0.91  | _   | 2  |
| 207338     | 523 | 0.042 | 0.926 | 0.053 | S   | 1  |
| 34226      | 479 | 0.071 | 0.086 | 0.922 | _   | 1  |
| 207890     | 208 | 0.042 | 0.926 | 0.053 | S   | 1  |
| 24753      | 992 | 0.257 | 0.036 | 0.723 | _   | 3  |
| 101242     | 366 | 0.165 | 0.049 | 0.851 | _   | 2  |
| 209426     | 255 | 0.073 | 0.226 | 0.761 | _   | 3  |
| 47558      | 367 | 0.035 | 0.916 | 0.062 | S   | 1  |
| 164740     | 337 | 0.048 | 0.798 | 0.118 | S   | 2  |
| 47647      | 744 | 0.034 | 0.946 | 0.075 | S   | 1  |
| 103882     | 413 | 0.153 | 0.052 | 0.854 | _   | 2  |
| 24940      | 781 | 0.104 | 0.077 | 0.907 | _   | 1  |
| 34577      | 474 | 0.223 | 0.03  | 0.844 | _   | 2  |
| 24950      | 374 | 0.049 | 0.978 | 0.015 | S   | 1  |
| 275330     | 650 | 0.465 | 0.629 | 0.023 | S   | 5  |
| 34622      | 607 | 0.147 | 0.12  | 0.719 | _   | 3  |
| 34651      | 526 | 0.127 | 0.039 | 0.875 | _   | 2  |
| 34705      | 653 | 0.061 | 0.067 | 0.905 | _   | 1  |
| 165147     | 577 | 0.063 | 0.086 | 0.896 | _   | 1  |
| 34805      | 391 | 0.914 | 0.035 | 0.118 | M   | 2  |
| 280856     | 545 | 0.204 | 0.073 | 0.755 | _   | 3  |
| 104675     | 505 | 0.097 | 0.869 | 0.039 | S   | 2  |
| 282706     | 466 | 0.089 | 0.952 | 0.038 | S   | 1  |
| 34945      | 466 | 0.261 | 0.722 | 0.022 | S   | 3  |
| 35099      | 397 | 0.034 | 0.957 | 0.044 | S   | 1  |
| 35123      | 603 | 0.73  | 0.055 | 0.209 | M   | 3  |
| 35255      | 335 | 0.09  | 0.869 | 0.039 | S   | 2  |
| 128174     | 279 | 0.124 | 0.95  | 0.01  | S   | 1  |
| 331356     | 251 | 0.066 | 0.79  | 0.195 | S   | 3  |

(Continues)
| Protein ID | Len | mTP | SP  | Other | Loc | RC |
|------------|-----|-----|-----|-------|-----|----|
| 35327      | 233 | 0.037 | 0.887 | 0.112 | S   | 2  |
| 35330      | 235 | 0.04  | 0.881 | 0.096 | S   | 2  |
| 104983     | 435 | 0.365 | 0.084 | 0.512 | _   | 5  |
| 165879     | 280 | 0.063 | 0.095 | 0.909 | _   | 1  |
| 165993     | 546 | 0.072 | 0.707 | 0.106 | S   | 2  |
| 338580     | 678 | 0.048 | 0.947 | 0.019 | S   | 1  |
| 35711      | 528 | 0.089 | 0.177 | 0.79  | _   | 2  |
| 105145     | 362 | 0.361 | 0.72  | 0.031 | S   | 4  |
| 48723      | 546 | 0.07  | 0.964 | 0.021 | S   | 1  |
| 35742      | 516 | 0.053 | 0.457 | 0.796 | _   | 4  |
| 340063     | 377 | 0.193 | 0.176 | 0.709 | _   | 3  |
| 105469     | 346 | 0.204 | 0.051 | 0.772 | _   | 3  |
| 105723     | 203 | 0.124 | 0.097 | 0.841 | _   | 2  |
| 48765      | 461 | 0.582 | 0.076 | 0.307 | M   | 4  |
| 105560     | 432 | 0.053 | 0.904 | 0.049 | S   | 1  |
| 68408      | 564 | 0.03  | 0.956 | 0.04  | S   | 1  |
| 25772      | 321 | 0.025 | 0.966 | 0.043 | S   | 1  |
| 106998     | 404 | 0.052 | 0.172 | 0.887 | _   | 2  |
| 35876      | 325 | 0.046 | 0.921 | 0.085 | S   | 1  |
| 35880      | 488 | 0.054 | 0.182 | 0.909 | _   | 2  |
| 106046     | 321 | 0.103 | 0.937 | 0.018 | S   | 1  |
| 106351     | 275 | 0.118 | 0.059 | 0.875 | _   | 2  |
| 59360      | 863 | 0.079 | 0.83  | 0.127 | S   | 2  |
| 25843      | 321 | 0.303 | 0.882 | 0.013 | S   | 3  |
| 166233     | 323 | 0.181 | 0.857 | 0.033 | S   | 2  |
| 35905      | 325 | 0.061 | 0.937 | 0.04  | S   | 1  |
| 129150     | 325 | 0.167 | 0.909 | 0.032 | S   | 2  |
| 364963     | 340 | 0.055 | 0.899 | 0.036 | S   | 1  |
| 365447     | 826 | 0.077 | 0.893 | 0.039 | S   | 1  |
| 365822     | 509 | 0.036 | 0.921 | 0.071 | S   | 1  |
| 106230     | 542 | 0.345 | 0.068 | 0.679 | _   | 4  |
| 464718     | 327 | 0.1   | 0.856 | 0.041 | S   | 2  |
| 49096      | 474 | 0.051 | 0.961 | 0.044 | S   | 1  |
| 129655     | 389 | 0.274 | 0.187 | 0.411 | _   | 5  |
| 49205      | 779 | 0.028 | 0.954 | 0.046 | S   | 1  |
| 166629     | 301 | 0.351 | 0.134 | 0.447 | _   | 5  |
| 180053     | 292 | 0.4   | 0.1   | 0.395 | M   | 5  |
| 107081     | 1,018 | 0.021 | 0.962 | 0.059 | S   | 1  |
| 106859     | 396 | 0.04  | 0.484 | 0.631 | _   | 5  |
| 387673     | 192 | 0.127 | 0.115 | 0.864 | _   | 2  |
| 107229     | 219 | 0.14  | 0.06  | 0.876 | _   | 2  |
| 107188     | 503 | 0.053 | 0.868 | 0.154 | S   | 2  |
| 108447     | 882 | 0.021 | 0.947 | 0.069 | S   | 1  |
| 36572      | 867 | 0.082 | 0.087 | 0.879 | _   | 2  |
| 389256     | 583 | 0.057 | 0.958 | 0.017 | S   | 1  |

(Continues)
| Protein ID | Len | mTP | SP  | Other | Loc | RC |
|-----------|-----|-----|-----|-------|-----|----|
| 49473     | 238 | 0.019 | 0.964 | 0.071 | S   | 1  |
| 180279    | 701 | 0.433 | 0.747 | 0.012 | S   | 4  |
| 107702    | 742 | 0.189 | 0.042 | 0.841 | _   | 2  |
| 150151    | 257 | 0.413 | 0.059 | 0.588 | _   | 5  |
| 49748     | 386 | 0.015 | 0.906 | 0.209 | S   | 2  |
| 150399    | 588 | 0.123 | 0.817 | 0.031 | S   | 2  |
| 36985     | 453 | 0.051 | 0.294 | 0.694 | _   | 4  |
| 36994     | 589 | 0.045 | 0.917 | 0.036 | S   | 1  |
| 130948    | 590 | 0.038 | 0.942 | 0.053 | S   | 1  |
| 36996     | 588 | 0.066 | 0.925 | 0.036 | S   | 1  |
| 37005     | 203 | 0.044 | 0.261 | 0.726 | _   | 3  |
| 37023     | 753 | 0.068 | 0.477 | 0.496 | _   | 5  |
| 396825    | 410 | 0.022 | 0.966 | 0.049 | S   | 1  |
| 37051     | 681 | 0.056 | 0.101 | 0.905 | _   | 1  |
| 167339    | 723 | 0.081 | 0.047 | 0.918 | _   | 1  |
| 108031    | 840 | 0.039 | 0.298 | 0.854 | _   | 3  |
| 60306     | 510 | 0.96  | 0.018 | 0.089 | M   | 1  |
| 94900     | 199 | 0.349 | 0.054 | 0.575 | _   | 4  |
| 150787    | 929 | 0.174 | 0.491 | 0.328 | S   | 5  |
| 108631    | 254 | 0.7   | 0.029 | 0.417 | M   | 4  |
| 151004    | 587 | 0.056 | 0.645 | 0.36  | S   | 4  |
| 408988    | 1,119| 0.13  | 0.887 | 0.023 | S   | 2  |
| 37467     | 467 | 0.03  | 0.984 | 0.031 | S   | 1  |
| 131760    | 370 | 0.03  | 0.705 | 0.316 | S   | 4  |
| 412878    | 510 | 0.049 | 0.888 | 0.057 | S   | 1  |
| 109222    | 337 | 0.086 | 0.929 | 0.02  | S   | 1  |
| 420841    | 296 | 0.43  | 0.109 | 0.29  | M   | 5  |
| 167984    | 273 | 0.256 | 0.065 | 0.614 | _   | 4  |
| 37832     | 314 | 0.294 | 0.736 | 0.057 | S   | 3  |
| 181255    | 402 | 0.021 | 0.96  | 0.068 | S   | 1  |
| 37882     | 458 | 0.034 | 0.945 | 0.064 | S   | 1  |
| 168122    | 772 | 0.03  | 0.949 | 0.05  | S   | 1  |
| 132435    | 597 | 0.138 | 0.364 | 0.28  | S   | 5  |
| 424941    | 446 | 0.025 | 0.965 | 0.038 | S   | 1  |
| 69748     | 2,350| 0.114 | 0.907 | 0.026 | S   | 2  |
| 38169     | 565 | 0.021 | 0.958 | 0.058 | S   | 1  |
| 38189     | 796 | 0.115 | 0.147 | 0.695 | _   | 3  |
| 109757    | 566 | 0.908 | 0.033 | 0.094 | M   | 1  |
| 38208     | 806 | 0.057 | 0.966 | 0.015 | S   | 1  |
| 50823     | 892 | 0.053 | 0.066 | 0.95  | _   | 1  |
| 38229     | 528 | 0.123 | 0.923 | 0.014 | S   | 2  |
| 69931     | 375 | 0.044 | 0.99  | 0.027 | S   | 1  |
| 61232     | 400 | 0.265 | 0.256 | 0.365 | _   | 5  |
| 38397     | 558 | 0.019 | 0.947 | 0.08  | S   | 1  |
| 133171    | 563 | 0.194 | 0.78  | 0.019 | S   | 3  |
| Protein ID | Len | mTP | SP   | Other | Loc | RC |
|-----------|-----|-----|------|-------|-----|----|
| 38406     | 253 | 0.17| 0.863| 0.026 | S   | 2  |
| 38407     | 253 | 0.12| 0.822| 0.058 | S   | 2  |
| 110758    | 322 | 0.172| 0.383| 0.274 | S   | 5  |
| 152728    | 384 | 0.062| 0.798| 0.143 | S   | 2  |
| 110978    | 740 | 0.279| 0.141| 0.526 | _   | 4  |
| 168656    | 547 | 0.041| 0.97 | 0.032 | S   | 1  |
| 111162    | 528 | 0.041| 0.316| 0.851 | _   | 3  |
| 434943    | 523 | 0.146| 0.921| 0.011 | S   | 2  |
| 61366     | 344 | 0.068| 0.951| 0.018 | S   | 1  |
| 38562     | 579 | 0.048| 0.961| 0.032 | S   | 1  |
| 61437     | 560 | 0.053| 0.951| 0.021 | S   | 1  |
| 111196    | 150 | 0.118| 0.118| 0.85  | _   | 2  |
| 38632     | 752 | 0.11 | 0.714| 0.134 | S   | 3  |
| 38673     | 589 | 0.045| 0.9  | 0.09  | S   | 1  |
| 38796     | 890 | 0.051| 0.889| 0.068 | S   | 1  |
| 111761    | 408 | 0.065| 0.959| 0.023 | S   | 1  |
| 441800    | 339 | 0.362| 0.212| 0.32  | M   | 5  |
| 169026    | 714 | 0.062| 0.987| 0.015 | S   | 1  |
| 153331    | 307 | 0.041| 0.53 | 0.552 | _   | 5  |
| 153350    | 869 | 0.293| 0.063| 0.66  | _   | 4  |
| 111954    | 463 | 0.02 | 0.981| 0.054 | S   | 1  |
| 61758     | 254 | 0.03 | 0.337| 0.811 | _   | 3  |
| 51514     | 257 | 0.043| 0.288| 0.734 | _   | 3  |
| 111348    | 534 | 0.03 | 0.978| 0.038 | S   | 1  |
| 169283    | 531 | 0.071| 0.944| 0.017 | S   | 1  |
| 39120     | 460 | 0.039| 0.139| 0.91  | _   | 2  |
| 153798    | 467 | 0.061| 0.158| 0.896 | _   | 2  |
| 182393    | 468 | 0.038| 0.133| 0.935 | _   | 1  |
| 112304    | 545 | 0.154| 0.113| 0.64  | _   | 3  |
| 39290     | 605 | 0.079| 0.129| 0.844 | _   | 2  |
| 214618    | 503 | 0.081| 0.056| 0.926 | _   | 1  |
| 39296     | 269 | 0.061| 0.915| 0.031 | S   | 1  |
| 39375     | 890 | 0.055| 0.865| 0.069 | S   | 2  |
| 51842     | 588 | 0.112| 0.122| 0.793 | _   | 2  |
| 51888     | 475 | 0.314| 0.663| 0.039 | S   | 4  |
| 182705    | 511 | 0.053| 0.883| 0.083 | S   | 1  |
| 219817    | 369 | 0.317| 0.328| 0.142 | S   | 5  |
| 219843    | 336 | 0.45 | 0.866| 0.004 | S   | 3  |
| 182872    | 668 | 0.034| 0.956| 0.057 | S   | 1  |
| 39816     | 471 | 0.021| 0.96 | 0.064 | S   | 1  |
| 227734    | 617 | 0.118| 0.049| 0.865 | _   | 2  |

Abbreviation: cTP, chloroplast transit peptide; Len, Sequence length; Loc, prediction of localization; M, Mitochondrion; RC, Reliability class; S, secretory pathway; SP, signal peptide.
FiguRe A1  Total RNAs extracted from mycelia co-cultivated with cyanobacterial cells (Treatment) and without cyanobacterial cells (Control) of 6, 12, 24, and 48 hr samples

FiguRe A2  Boxplots showing the distribution of the FPKM values of each sample. Note: 6h_c_k, control sample at 6 hr; 6h_T, treatment sample at 6 hr; 12h_c_k, control sample at 12 hr; 12h_T, treatment sample at 12 hr; 24h_c_k, control sample at 24 hr; 24h_T, treatment sample at 24 hr; 48h_c_k, control sample at 48 hr; 48h_T, treatment sample at 48 hr. "_0" and "_1" represent repeat samples

FiguRe A3  Comparison of expression changes between Real-time PCR and RNA-Sequencing. Note: A, jgi|Bjead1_1|34143|fgenesh1_kg.1#_945#_Locus732v1_medCvg1115.6s (a protein of esterase family 1); B, jgi|Bjead1_1|35099|fgenesh1_kg.2#_711#_Locus118v3_medCvg9284.2s (a protein of hydrolase family 5); C, jgi|Bjead1_1|172436|gm1.8875_g (a protein of hydrolase family 5); D, jgi|Bjead1_1|459664|MIX10988_17319_14 (a radical oxidase); E, jgi|Bjead1_1|355947|CE167616_517 (a protein of hydrolase family 128); F, jgi|Bjead1_1|38229|fgenesh1_kg.7#_551#_Locus8080v1_medCvg1578.8s (a protein of hydrolase family 13)