Effect of choline-phosphate cytidylyltransferase gene (*pcyt-1*) expression on departure of pine wood nematode, *Bursaphelenchus xylophilus* (Nematoda: Aphelenchoididae), from *Monochamus alternatus* (Coleoptera:Cerambycidae)

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Abstract

In order to study the causes of pine wood nematodes (PWN), *Bursaphelenchus xylophilus* departure from its vector beetle, *Monochamus alternatus*, we collected PWNs which were extracted from the newly emerged *M. alternatus* and the 7d after emergence beetles. The total RNAs of the two groups of PWNs were extracted and transcriptomes sequencing were performed, and the genes expression differences between the two groups of PWN were analyzed. It was found that expression of choline-phosphate cytidylyltransferase gene (*pcyt-1*) markedly up-regulated. After inhibition of *pcyt-1*expression by RNA interference, the rate of lipid degradation in PWN decreased significantly, and the motility of PWN also decreased significantly. Analysis identified that phosphatidylcholine can promote the emulsification and degradation of lipid droplets in PWN, which provide energy for PWN departure from *M. alternatus*. The up-regulation of gene *pcyt-1* is an important internal trigger for PWN departure from the beetles.

1 Introduction

Pine wilt disease (PWD) constitutes one of the most serious conifer diseases

worldwide, affecting *Pinus* spp. from the Far East forestlands (Japan, China, Korea)

[1, 2], and from Europe (Portugal and Spain) [3-6]. PWD is caused by the pine wood

nematode (PWN), *Bursaphelenchus xylophilus* (Steiner & Buhrer) Nickle, with PWN

transmission being dependent on a vector insect, such as *Monochamus alternatus*

Hope, the main vector in East Asia [7, 8]. The feeding period of *M. alternatus* is an

important stage in the life cycle of beetles, as well as a key step in PWN transmission

[9, 10]. After emergence, *M. alternatus* feed on healthy pine trees, a process

accompanied by the spread of PWN.

PWN has two developmental forms in its life cycle, namely the propagative and

dispersive forms. Under favorable conditions, PWN molt into their propagative form,

and then reproduce rapidly [11, 12]. However, under unfavorable conditions, e.g. high

temperature, starvation, or high population density, PWN (as propagative

second-stage juveniles) will molt to produce the dispersive third-stage juveniles,

which will aggregate around the pupal chamber of the beetles [13, 14]. The dispersal

third-stage juveniles molt to produce fourth-stage juveniles, which enter the tracheal

system of the vector as the beetles emerge [13-16], the fourth-stage juveniles to be

transmitted to the healthy pine trees through wounds caused by the vector [17-20].

There is no unified view on the mechanism of PWN departure from vector.

However, it has been found that some volatile chemicals play an important role in this

process of PWN exit from the vector. It was found that the monoterpenes released

from healthy pine trees, such as β - myrcene and α-pinene, had the strongest attraction

to PWN, these chemicals playing an important role in the process of PWN departure

from vector and the invasion of healthy host trees, as well as in the movement of

PWN within pine trees [21, 22]. Ishkawa et al. found that β - myrcene on the agar

plate held obvious attraction for dispersive third-stage juveniles [23]. Enda et al. dried

Pinus twigs at 70°C to remove volatile substances, then treated twigs with β-myrcene

and fed them to the beetles. It was found that these twigs greatly promoted the

departure of PWN from *M. alternatus*[24]. Stamps et al. showed that various volatile

pine chemicals did not significantly affect PWN departure from the vector and the

departure of PWN is a spontaneous act [25]. Aikawai et al. fed beetles were fed with

fresh pine twigs and with twigs treated with high temperature (121°C, 40min, to

remove volatiles from the pine twigs), respectively, and found that the pine twigs

without volatile chemicals were more likely to cause PWN departure from vector,

while twigs with volatiles had inhibitory effects [26].

The departure of PWN may depend on the nematode's own factors, or it may be

environmental factors, or a combination of the two. Stamps et al. suggested that the

level of lipids in PWN may be the switch that determines whether they depart from

the vector [20]. When PWN had low neutral storage lipid content, departure is

induced by the pine volatile β-myrcene, whereas, when PWN had a high content of

neutral lipids, they continued to be retained within the beetle [20]. Previous studies

shown that intrinsic factors play an important role in regulating the PWN departure,

whereas β-myrcene is a directional signal that attracts PWN escape from the vector

insects [25]. Yang et al. there was no difference in the time of PWN departure from *M.*

alternatus which between fed after starvation and fed directly, and the motility of

PWN carried by the beetles one week after emergence being greater than the PWN

carried by newly emerged (almost resting) beetles [27]. It was speculated that PWN

departure was related to the motility, and the increased motility required energy which

might come from the degradation of neutral lipids [20, 27].

The emulsification of lipid droplets can increase the contact area between lipases

and lipids, which greatly promote lipids degradation[28]. In the present study,

transcriptome sequencing was performed on the PWN which carried by new emerged

M. alternatus and beetles one week after their emergence. Inhibition of expression of

the *pcyt-1* gene, encoding choline-phosphate cytidylyltransferase (EC 2.7.7.15), was

carried out by RNA interference (RNAi), and the effect on lipid degradation and

motility of PWNs was determined.

2 Materials and methods

2.1 PWN collection and RNA extraction

In April 2019, dead specimens *Pinus massoniana* trees, infested by *M. alternatus*

larvae and PWN, were collected at Bocun Forest Farm, Huangshan City, Anhui

Province in China. The trees were cut into logs and maintained in outdoor insect

cages (**Fig. 1A**). *M. alternatus* were collected daily (every 8 h) during the period of

adult beetles emergence. The collected *M. alternatus* were divided into two groups,

and one of which PWN was extracted immediately with Baermann funnel method[29],

whereas another was fed (with fresh pine twigs) for seven days (**Fig. 1B**), before the

PWN was extracted. Extraction of total RNAs from the two groups (each group was

represented by three independent biological replicates) of PWN by Trizol method

[30].

Fig. 1 Collection and feeding of *Monochamus alternatus*

A: Pine trees were cut into logs and maintained in outdoor insect cages, *Monochamus alternatus* were collected daily (every 8 h) during the period of adult beetle emergence. B: The collected *Monochamus alternatus* were put into small bottles and fed with fresh twigs of pine.

2.2 Transcriptome sequencing and analysis (Data provided by Biomarker Technologies, Beijing, China)

RNA quantification and qualification

RNA degradation and contamination was monitored on 1% agarose gels. RNA

purity was checked using the NanoPhotometer® spectrophotometer (IMPLEN, CA,

USA). RNA concentration was measured using Qubit® RNA Assay Kit in Qubit®2.0

Flurometer (Life Technologies, CA, USA). RNA integrity was assessed using the

RNA Nano 6000 Assay Kit of the Agilent Bioanalyzer 2100 system (Agilent

Technologies, CA, USA).

Library preparation for Transcriptome sequencing

A total amount of 1 μg RNA per sample was used as input material for the RNA

sample preparations. Sequencing libraries were generated using NEBNext®Ultra^{TM}

RNA Library Prep Kit for Illumina® (NEB, USA) following manufacturer's

recommendations and index codes were added to attribute sequences to each sample.

Briefly, mRNA was purified from total RNA using poly-T oligo-attached magnetic

beads. Fragmentation was carried out using divalent cations under elevated

temperature in NEBNext First Strand Synthesis Reaction Buffer (5X). First strand

cDNA was synthesized using random hexamer primer and M-MuLV Reverse

Transcriptase (RNase H-). Second strand cDNA synthesis was subsequently

performed using DNA Polymerase I and RNase H. Remaining overhangs were

converted into blunt ends via exonuclease/polymerase activities. After adenylation of

3' ends of DNA fragments, NEBNext Adaptor with hairpin loop structure were ligated

to prepare for hybridization. In order to select cDNA fragments of preferentially

200-250 bp in length, the library fragments were purified with AMPure XP system

(Beckman Coulter, Beverly, USA). Then 3 μl USER Enzyme (NEB, USA) was used

with size-selected, adaptor-ligated cDNA at 37°C for 15 min followed by 5 min at

95°C before PCR. Then PCR was performed with Phusion High-Fidelity DNA

polymerase, Universal PCR primers and Index (X) Primer. At last, PCR products were

purified (AMPure XP system) and library quality was assessed on the Agilent

Bioanalyzer 2100 system.

Clustering and sequencing

The clustering of the index-coded samples was performed on a cBot Cluster

Generation System using TruSeq PE Cluster Kit v4-cBot-HS (Illumia) according to

the manufacturer's instructions. After cluster generation, the library preparations were

sequenced on an Illumina Hiseq x-ten platform at Biomarker Technologies (Beijing,

China) and paired-end reads were generated.

Quality control

Raw data (raw reads) of fastq format were firstly processed through in-house perl

scripts. In this step, clean data(clean reads) were obtained by removing reads

containing adapter, reads containing ploy-N and low quality reads from raw data. At

the same time, Q20, Q30, GC-content and sequence duplication level of the clean data

were calculated. All the downstream analyses were based on clean data with high

quality.

Comparative analysis, and Gene functional annotation

The adaptor sequences and low-quality sequence reads were removed from the

data sets. Raw sequences were transformed into clean reads after data processing.

These clean reads were then mapped to the reference genome sequence. Only reads

with a perfect match or one mismatch were further analyzed and annotated based on

the reference genome.

Gene function was annotated based on the following databases: Nr (NCBI

non-redundant protein sequences); Nt (NCBI non-redundant nucleotide sequences);

Pfam (Protein family); KOG/COG (Clusters of Orthologous Groups of proteins);

Swiss-Prot (A manually annotated and reviewed protein sequence database); KO

(KEGG Ortholog database); GO (Gene Ontology).

Differential expression analysis

Differential expression analysis of two conditions/groups was performed using

the DESeq R package (1.10.1). DESeq provide statistical routines for determining

differential expression in digital gene expression data using a model based on the

negative binomial distribution. The resulting P values were adjusted using the

Benjamini and Hochberg's approach for controlling the false discovery rate. Genes

with an adjusted P-value <0.05 found by DESeq were assigned as differentially

expressed.

KEGG pathway enrichment analysis

KEGG is a database resource for understanding high-level functions and utilities

of the biological system, such as the cell, the organism and the ecosystem, from

molecular-level information, especially large-scale molecular datasets generated by

genome   sequencing   and   other   high-throughput   experimental   technologies

(http://www.genome.jp/kegg/). We used KOBAS software to test the statistical

enrichment of differential expression genes in KEGG pathways.

2.3 RNA interference (RNAi) and qPCR (quantitative real-time PCR) of PWN

(pine wood nematodes) after pcyt-1 interference

To interfere with the choline-phosphate cytidylyltransferase gene (***pcyt-1***) (DNA

sequence: **Supplemental 1**), the interfering gene fragment was

5'-GGTGGACTTTATCGCTCAT-3', and negative control sequence is

5'-GGTGG**G**CTTTA**A**CGCTCAT-3', and designed the antisense strand [31]. To

prepare the double-stranded RNA (dsRNA), which was digested by ribozyme to

obtain the small interfering RNA (siRNA) (dissolved in 20 μl of RNAase-free water),

the *in vitro* Transcription T7 Kit (for siRNA Synthesis) (Takara Bio Inc., Shiga, Japan)

was used.

The PWN was cultured using the *Botrytis cinerea* medium [32], as shown in **Fig.**

2. After 48 h of culture, PWN was extracted (for 2 h) by the Baermann funnel method

[29]. Extracted PWN was soaked in 0.05% (w/v) streptomycin sulfate for 10 min

and washed three times with diethyl pyrocarbonate (DEPC)-treated water. PWNs

(10000 individuals) were soaked in the siRNA solution for 48 h (**Fig. 2E**), and then

washed three times with RNAase-free water. The total RNAs (one preparation per

replicate per group) were extracted by the Trizol method [30]. Synthesis of cDNA was

carried out using HiScript[®] II Q RT SuperMIX for Qpcr (+gDNA wiper) (Vazyme,

Nanjing, China). qPCR was carried out with SYBR[®] Green I chimeric fluorescence,

using ChamQ[TM] SYBR[®] qPCR Master Mix (Low ROX Primixed) (Vazyme, Nanjing,

China). Then q-PCR validation was performed using the 7500 Real-Time PCR

System (SeqGen, Inc. Torrance, CA, USA) and analyzed differences in gene

expression. The reference gene primer was

F: 5'-GCAACACGGAGTTCGTTGTA-3', R: 5'-GTATCGTCACCAACTGGGAT-3'.

Target primer: F: 5'-AGGCCTACAACAACTCAGCC-3', R:

5'-TCAACTGATTCGCGTGTCCA-3'.

199
200   **Fig. 2 PWN culture and RNAi**

A: PWN suspension was placed in a dish, and the eggs adhering to the bottom of the dish were
collected every 6 h. B: Eggs adhering to the bottom of the dish. C: The collected PWN eggs were
placed in a Eppendorf tube and incubated at 25 ° C for 36 h. All the eggs hatched into
second-stage PWN. D: The second-stage PWN juvenile suspension was inoculated into the
freshly grown *Botrytis cinerea* medium and cultured for 48 h (when the majority of nematodes
were 4th stage juvenile).

Notes: 1. Freshly cultured *Botrytis cinerea* medium was used. Aging medium is not conducive to
208   PWN growth.
209   2. Experiment was performed using PWN of the same stage. Mixed ages can cause large
210   errors.
211   3. The time taken to extract PWN should not be too long, with 2-4 h being suitable.
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2.4 Comparison of the difference in motility and lipids content of

PWN after *pcyt-1* RNAi

After 24 h of RNAi (at which time, there was a great difference in motility

between the two PWN groups), the differences of PWN motility were observed, with

videos being taken under a microscope (Zeiss Axio lmager.M2, Carl Zeiss, Gottingen,

Germany). After 72 h of RNAi (at which time, the lipids contents of the two PWN

groups were markedly different.), the lipids of PWN were stained with oil red O [33].

PWN was washed into a 1.5ml eppendorf tube with M9 buffer (standing for 10min at

4°C, discarding the supernatant and repeating it once). The lipids of PWN were fixed

with 4% paraformaldehyde at 4°C for 30 minutes, then frozen in a - 80°C refrigerator

for 15 minutes, then thawed rapidly in 43°C water bath. The sample was centrifuged

for 1 min with 2000 × g, and the supernatant was discarded. Wash three times with 1

× phosphate-buffered saline (PBS) (pH 7.2-7.4), after which the PBS was discarded,

and soaked in 1% Triton X-100 and isopropanol oil red O saturated solution (ratio 2:3)

for 30min. Wash three times with PBS (1x), useing 60% isopropanol to differentiate

clearly under the microscope, and photos were taken (Zeiss Axio lmager. M2, Carl

Zeiss, Gottingen, Germany).

3 Results

3.1Comparison of transcriptome results

The expression level of choline-phosphate cytidylyltransferase gene (*pcyt-1*) of

PWN carried by *M. alternatus*, 7 d after of emergence, was significantly up-regulated

(log2 FC=9.5) relative to PWN from newly emerged beetles, as shown in

supplementary material 2 (Ko00564, EC:2.7.7.15).

3.2 **q-PCR gene experession studies**

After RNAi to *pcyt-1* was carried out in PWN, q-PCR was used for verification of

transcript abundance and the results are shown in Fig. 3, indicating that, after RNAi,

the expression level of *pcyt-1* was significantly down-regulated.

Fig. 3 Relative expression of *pcyt-1* in control pine wood nematodes (PWN) (CK) and PWN
exposed to RNA interference (RNAi).

3.3 **Observation on the motility and lipids content of PWN**.

After RNAi, the motility of PWN decreased significantly, as shown in supplement

material 3 (videos 1 and 2). After RNAi, the lipids content of PWN was significantly

higher than that in the control nematodes (Fig. 2).

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Figure 4 Pine wood nematode lipid content as shown by staining with Oil Red O in the presence
and absence of RNA interference (RNAi) for *pcyt-1*.
Red spots are lipid drops. A: Nematodes after RNAi for 72 h. B: The control nematodes after
culture 72 h. There were still many lipid droplets in the nematodes of the experimental group,
while the number of lipid droplets in the control group was markedly less.

4 Discussion

PWN did not departure immediately after the emergence of *M. alternatus*, but

started to departure after a period of time. There have been reports that PWN start to

departure from *M. alternatus* at different times, such as 7–12 d after the emergence of

beetles [34], at 3–5 d after adult beetle emergence [35], at 7 d after emergence [36], at

5 d after emergence [27, 37], at 10 d after emergence [38]. During the period between

the emergence of *M. alternatus* and the start of the departure of PWN, the

physiological characteristics of PWN may have changed, or it may be continuously

stimulated by certain signaling hemicals. Different studies have different conclusions

on the causes of PWN departure from *M. alternatus*.

Ishkawa et al. examined the attractant effect of volatile chemicals from *Pinus*

densiflora towards the dispersive PWN that leave *M. alternatus*, and showed that

β-myrcene played an important role in the transmigration of the PWN from the vector

to the pine tree and for the movement of the PWN inside the pine wood [23]. To

clarify the effect of the volatiles of *Pinus densiflora* on the departure of PWN from *M.*

alternatus, Aikawa et al. fed *M. alternatus* with normal twigs and with twigs without

volatiles after heating, and consequently suggested that PWN had a trait of

spontaneous departure from *M. alternatus* [26]. Stamps et al. found that lipid content

of PWN gradually decreased with the prolongation after the emergence of *M.*

alternatus, and suggested that the concentration of neutral storage lipids was

correlated with the date at which PWN started to leave their vector [18, 20].

In order to study the effect of feeding behavior of *M. alternatus* on PWN

departure. Wang et al. found that there was no significant difference in the start time

of PWN departure from *M. alternatus* direct feeding and feeding after starvation after

emergence[27]. However, it was found that PWN carried by the newly emerged

beetles was less motility than the PWN carried by the beetles at 7 d after emergence,

and believed that the increase of motility is an important cause of PWN departure[27].

The increased motility requires a lot of energy (in the form of ATP). The degradation

of neutral storage (NS) lipid in PWN can provide energy[20]. Therefore, it is

concluded that the degradation of lipid may be an important endogenous cause of

PWN departure. In the present study, we also found that the lipid content of PWN

after RNAi of *pcyt-1* was markedly higher than that of the control, whereas the

motility of PWN in the RNAi-treated group was lower than the control. This indicates

that lipid degradation is a necessary pre-condition for PWN departure from *M.*

alternatus.

Not all PWN that carried by *M. alternatus* can leave the beetles. About 70% of

PWN failing to leave the vector [34]. Aikawa et al. showed that the percentage of

PWN departure form vector was higher in thick tracheae than in thin tracheae [39].

And considered that PWN in the thin trachea cannot get enough oxygen, so they can't

produce enough energy (ATP) to power their exit, and eventually cause they staying

in the trachea for a long time [39]. After the emergence of *M. alternatus*, the energy

resource (represented by the limited lipid store) of PWN carried by beetles is

gradually exhausted [20]; at this time, even if getting sufficient oxygen, it would not

generate enough energy to drive PWN to move. Wang et al. showed that greater

motility was necessary for PWN to departure from the vector [27]. It is vital for PWN

departure to get sufficient oxygen to degrade lipids and produce enough energy (ATP)

over a limited period, enabling the PWN to achieve high motility.

Lipid droplets (triacylglycerol) are the main energy store in PWN, with lipid

being insoluble in water whereas the enzymes that digest the lipid are water-soluble,

with lipid digestion occurring only at the lipid–water interface [28]. The

emulsification of lipid can increase the lipid-water interface, which can greatly

accelerate its digestion. Phosphatidylcholine (PC) has hydrophilic and hydrophobic

groups, making it a powerful "detergent" conducive to emulsifying lipid and

promoting lipid catabolism [28, 40-42]. Choline-phosphate cytidylyltransferase (CCT)

has high specificity and is the rate-limiting enzyme of phosphatidylcholine synthesis,

controlling the synthesis of phosphatidylcholine [43-45]. In the present study, the

results of transcriptome sequencing revealed that gene *pcyt-1* expression level was

significantly up-regulated in PWN in beetles 7 d after emergence, relative to those

extracted from beetles immediately after emergence ((supplementary 2: ko00564, EC:

2.7.7.15). Following RNAi with the gene *pcyt-1*, the level of lipid catabolism

decreased significantly (**Fig. 4**) and the motility of PWN decreased significantly

(supplementary 3). The results showed that PC emulsification of lipid in PWN is an

important route of lipid emulsification, with the level of *pcyt-1* expression having a

significant effect on nematode departure.

In the present study, the results showed that no eggs were laid in the

experimental group (after RNAi), unlike the situation in the control group

(supplementary 3). This indicates that the expression level of gene *pcyt-1* affects the

development of PWN, suggesting that PWN in the trachea of *M. alternatus* may have

some development, which may promote the departure of PWN from the vector.

However, this development process also needs amount of energy. Therefore, the

degradation of Lipids is still an important factor for PWN departure from *M.*

alternauts.

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