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Phylogenetic analysis of *Ganoderma australe* complex in a Bornean tropical rainforest and implications for mechanism of coexistence of various phylogenetic types

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Abstract

We hypothesized that different phylogenetic types of the *Ganoderma australe* complex can coexist and that their coexistence is promoted by resource partitioning among them. Our field survey and phylogenetic analysis revealed six phylogenetic types coexisting within a 3 ha primary forest plot in a Bornean tropical rainforest. Two of the six have been reported previously, whereas the remaining four are new. Fruit bodies of all dominant phylogenetic types appeared more frequently from fresh coarse woody debris than expected. Comparison of resource use patterns between the observed fungal community and the null community did not provide significant evidence of niche partitioning. Although we found high genetic diversity within the plot, the phylogenetic types at the site share resources. Resource partitioning on phylogenetic types of host trees or stochastic processes during colonization of pieces of coarse woody debris might play an important role in forming the community structure of phylogenetic types of *G. australe*.

Keywords: coarse woody debris; coexistence mechanism; niche partitioning; null community; saproxylic fungi; wood-decaying fungi

Introduction

Wood-decaying fungi compete with each other within pieces of coarse woody debris (CWD) (Boddy 2000), and there is substantial fungal diversity at the forest stand level. Different resource use patterns among polypore species have been observed in relation to tree phylogenetic type, size, decay stage, and condition of CWD (e.g., stump or fallen logs) in the temperate and boreal zones (Heilmann-Clausen et al. 2005; Yamashita et al. 2010). As a result, in tropical rainforests with a hyperdiversity of fungi (Lodge 1997; Yamashita et al. 2015a), niche partitioning is expected to play an important role in the maintenance of diversity (Lodge and Cantrell 1995).

Ganoderma australe is a cosmopolitan white rot fungus of tropical regions (Ryvarden and Johansen 1980; Corner 1983). It is a dominant wood-decaying fungus in primary forest of East Malaysia (Yamashita et al. 2009). The species is morphologically and phylogenetically closely related to *Ganoderma applanatum*, which is distributed in northern temperate regions (Ryvarden and Johansen 1980; Corner 1983; Smith and Sivasithamparam 2000). The *G. australe* species complex, which includes *Ganoderma applanatum*, contains at least eight phylogenetic types: the Malaysia group, the Thailand group, the Asia group, the Southern Hemisphere and Asia group, and another four groups (Moncalvo and Buchanan 2008). Multiple phylogenetic types may coexist within small areas.

Because the strength of competition is expected to increase as phylogenetic

relatedness increases (Violle et al. 2011), competition is expected to be stronger within the *G. australe* complex than between it and other species. At our study site, members of the *G. australe* complex have been reported from CWD ranging from thin twigs (≤5 cm) to thick stems (≥40 cm) (25.7 ± 31.9 cm, mean ± s.d.), as well as in logs with intact bark and partly decayed logs (Yamashita et al. 2009). However, the degree to which different phylogenetic types of the complex coexist at this site, and the ecological traits of the individual phylogenetic types is not currently known.

In this study, we hypothesized that some phylogenetic types of the *G. australe* complex coexist in primary Bornean tropical rainforest and that their coexistence is promoted by resource partitioning among them. We conducted a field survey within a 3 ha plot in the Lambir Hills National Park and analyzed molecular data from samples. We compared the resource use patterns of the phylogenetic types of the observed *G. australe* complex community with those of a null community.

Materials and methods

Study site

Our study site is located in a tropical rainforest in the Lambir Hills National Park, Sarawak, Malaysia (4.2°N, 113.5°E; 150–250 m a.s.l.). This park is covered mostly by dipterocarp-dominated primary forest. A 4 ha plot was established in the park in 2000 (Yumoto and Nakashizuka 2005).

A field survey was conducted from 29 May to 27 June 2009. All the CWD with a diameter of >10 cm was inspected for the appearance of fresh fruit bodies of *G. australe* within a 3 ha plot within the 4 ha plot. If we found any, we collected up to three from each piece of CWD; if four or more were present, we collected fruit bodies from the two endpoints and the middle. The decay stage and diameter at the center of the CWD were recorded. We defined the decay stage as (1) fresh, (2) medium, or (3) old (for further description, see Yamashita et al. 2009). The diameter was classified into size classes of 10–19, 20–29, 30–39 cm, 40–49 cm, and ≥50 cm. Fruit bodies of *G. australe* appeared from pieces of CWD at decay stages 1 and 2. We also recorded the number of pieces of CWD with a diameter of >10 cm at stages 1 or 2.

Specimens

The fruit bodies were used for molecular study. We cut each into several pieces and removed context tissue using flame-sterilized forceps and preserved it in 99% ethanol. We dried the rest of the material for 48 h and deposited it at the Research, Development, and Innovation Division of the Forest Department Sarawak, Kuching, Malaysia (see list of specimens in Supplementary Appendix 1). We identified fruit bodies by the color of the pileus and context from keys provided by Ryvarden and Johansen (1980). After molecular study, we measured the size of spore samples in aqueous 1% KOH by microscopy and confirmed that the size ranged from 7.7 to 12.5 × 3.7 to 7.5 μm, which is

close to the size of this species reported by Ryvarden and Johansen (1980).

Molecular experiments

Genomic DNA was extracted from the context tissue with a DNeasy Plant Mini Kit (Qiagen, Hilden, Germany). The rDNA internal transcribed spacer (ITS) region was amplified using the primer pair ITS1-F/ITS4-B (Gardes and Bruns 1993). Polymerase chain reaction (PCR) was performed using a HotStarTaq Plus Master Mix (Qiagen). Each PCR reaction contained a 50 µL mixture (16 µL of distilled water, 25 µL of master mix, 3 µL of ~0.5 ng/µL template DNA, 5 µL of Coral Load PCR buffer, and 0.5 µL of each primer (final, 0.25 µM)). Each DNA fragment was amplified in a PCR thermal cycler (PTC-0200 DNA Engine Cycler; Bio-Rad, Hercules, CA, USA) using an initial 5 min at 94 °C; 35 cycles of 30 s at 94 °C, 30 s at 54 °C, and 1 min at 72 °C; and a final 10 min at 72 °C. The reaction mixture was then held at 4 °C for 5 min. PCR products were purified with a QIAquick PCR Purification Kit (Qiagen) according to the manufacturer's instructions.

The purified PCR products were then sequenced by Macrogen Japan Inc. (Tokyo, Japan) in a PTC-225 Peltier Thermal Cycler (MJ Research, Waltham, MA, USA) using ABI PRISM BigDye Terminator Cycle Sequencing kits with AmpliTaqR DNA polymerase (FS enzyme) (Applied Biosystems, Carlsbad, CA, USA) according to the manufacturers' protocols. The Fluorescent-labelled fragments were purified from the

unincorporated terminators with an ethanol precipitation protocol. The samples were then resuspended in distilled water and electrophoresed in an ABI 3730xl sequencer (Applied Biosystems).

Our PCR amplifications always resulted in a single discrete band, but clear sequencing data of a few PCR products could not be obtained owing to intra-strain polymorphism or faint PCR bands. These products were cloned into the vector pCR4-TOPO using the TOPO TA cloning kit (Invitrogen, Waltham, MA, USA) following the manufacturer's instructions. Recombinant One Shot DH5α-T1 *Escherichia coli* colonies were randomly picked and screened directly for inserts by colony PCR with primers for the vector. The PCR products of positive clones were purified and sequenced as described above.

The sequences determined in this study were deposited in DDBJ (accession nos. LC084660–751; http://getentry.ddbj.nig.ac.jp/top-e.html) and used for phylogenetic analysis.

Phylogenetic analysis

In addition to the sequences obtained in this study, 39 sequences used by Moncalvo and Buchanan (2008) were included in the phylogenetic analysis. Phylogenetic analyses of the rDNA ITS sequences were conducted using the neighbor-joining method (Saitou and Nei 1987). MAFFT v. 6 software (Katoh and Toh 2008) was used for preliminary

multiple alignments of nucleotide sequences, and final alignments were manually adjusted in BioEdit software (Hall 1999). Alignment gaps were treated as missing data, and ambiguous positions were excluded from the analysis. The best-fit evolutionary model was selected on the basis of the Bayesian Information Criterion scores generated in MEGA 6 software (Tamura et al. 2013). We chose the Kimura two-parameter model (Kimura 1980) of nucleotide substitution with a discrete gamma distribution (shape parameter = 1) to allow for non-uniformity of rates among sites, and neighbor joining was performed in MEGA 6. Node support was evaluated by bootstrap analysis (Felsenstein 1985) using 1000 replications.

Statistical analysis

The *G. australe* complex was divided into several phylogenetic types on the basis of the phylogenetic analysis. The number of CWD samples from which fungal fruit bodies belonging to each phylogenetic type appeared was used as an index of abundance. To reveal the resource use patterns among the phylogenetic types, we compared frequency distributions of the size classes and decay stages of CWD samples from which fruit bodies appeared among phylogenetic types by chi-squared test. The frequency distribution of decay stages of CWD samples with fruit bodies was also compared with that of pieces of CWD in the plot.

Overlap in resource use among phylogenetic types was quantitatively evaluated by

Pianka's niche overlap index (Pianka 1973), which ranges from 0 for complete difference in resource use to 1 for complete overlap. The observed resource use pattern was compared with that of a randomly assembled community to test the effect of competition. The null community was created by two randomization algorithms: RA3 retains the number of resource types available for each phylogenetic type but randomizes which resource types are used, and RA4 retains the number of resource types available for each fungal species and assigns 0 to resource types without records. These two methods were recommended by Gotelli and Ellison (2013). For each pair, 10 000 random Monte Carlo permutations were generated and the observed value was compared with the expected value in EcoSimR software (Gotelli and Ellison 2013).

Results

Phylogenetic analysis

We collected 101 fruit bodies of *G. australe*, and successfully sequenced 92 of these. The phylogenetic tree based on our data and that of Moncalvo and Buchanan (2008) divided the 92 samples into six phylogenetically different groups (Types 1–6) with moderate to high bootstrap support (58–100; Fig. 1). There were differences in the lengths of the ITS region including 5.8S rRNA between the types: Type 1, 556 bp except for 5 samples (555 bp in 1 sample, 557 bp in 3 samples, and 525 bp in 1 sample, in each of which we were not able to read the complete ITS2 region); Type 2, 535–538 bp; Type 3, 552–554 bp;

Type 4, 546 bp; Type 5, 556 bp; and Type 6, 561 bp. The numbers of fruit bodies by type were (in descending order) 60 of Type 1, 10 of Type 5, 9 of Type 3, 8 of Type 2, 3 of Type 6, and 2 of Type 4. Types 1–3 were not closely related to the phylogenetic types reported by Moncalvo and Buchanan (2008), although they were closely related to each other. Type 4 was related to samples from North America and Europe (Northern Hemisphere group of Moncalvo and Buchanan 2008), but they were different phylogenetic types. Type 5 was grouped with a Thai sample (Thailand group of Moncalvo and Buchanan 2008). Type 6 was grouped with Asian and Southeast Asian samples (Asia group of Moncalvo and Buchanan 2008). All phylogenetic types collected at our site were classified as members of the *G. australe* complex (Fig. 1).

Resource use pattern

In total, 966 logs were surveyed for the fruit bodies in the 3 ha plot, and the 92 fruit bodies were collected from 44 CWD samples. Type 1 was the most dominant (34/44, 77.2%), followed by Type 5 (6/44, 13.6%) and Type 3 (5/44, 11.4%), based on the number of CWD samples from which fruit bodies appeared. Nine CWD samples hosted two or three phylogenetic types: two pairs each of Types 1 and 2, Types 1 and 3, Types 1 and 5, and Types 1 and 6, and one trio of Types 1, 3, and 5.

Fruit bodies appeared from younger CWD more frequently than expected from the frequency of CWD samples at each decay stage: from 18 CWD samples at stage 1

(18/113, 15.9%) and from 26 samples at stage 2 (26/853, 3.0%) (no fruit bodies were collected from CWD samples at stage 3). The frequency distribution of the decay stage of CWD samples used by the various phylogenetic types differed significantly from that of CWD at the site (Fig. 2; CWD vs. Type 1, $\chi^2 = 14.632$, d.f. = 1, $P = 0.0001$; CWD vs. Type 3, $\chi^2 = 6.919$, d.f. = 1, $P = 0.008$; CWD vs. Type 5, $\chi^2 = 12.221$, d.f. = 1, $P < 0.0001$). Nearly 60% of Type 1 fruit bodies appeared from CWD at stage 2, and more than 60% of Type 3 and Type 5 fruit bodies appeared from CWD at stage 1 (Fig. 2), yet 11.7% (113/966) of CWD belonged to stage 1 and 88.3% (853/966) to stage 2.

Our observations did not support niche partitioning among phylogenetic types of *G. australe*. The three dominant phylogenetic types did not differ significantly in decay stage (Fig. 2) or diameter class (Fig. 3) of CWD from which their fruit bodies appeared (decay stage, $\chi^2 = 2.786$, d.f. = 2, $P = 0.248$; diameter class, $\chi^2 = 1.779$, d.f. = 8, $P = 0.987$). The observed value of Pianka's index for CWD diameter in the 3 ha plot (0.954), based on the two randomization algorithms, was significantly larger than that obtained for the null community: RA3, $P(obs \leq null) = 1.000$, $P(obs \geq null) = 0.003$, $P(obs = null) = 0.003$; RA4, $P(obs \leq null) = 1.000$, $P(obs \geq null) = 0.016$, $P(obs = null) = 0.016$. The observed value of Pianka's index for the CWD decay stage in the 3 ha plot (0.900) was not significantly different from that of the null community: RA3, $P(obs \leq null) = 0.502$, $P(obs \geq null) = 0.750$, $P(obs = null) = 0.252$; RA4, $P(obs \leq null) = 0.502$, $P(obs \geq null) = 0.750$, $P(obs = null) = 0.252$.

Discussion

Our phylogenetic tree clearly shows that six phylogenetic types of the *G. australe* complex coexisted in a small area of tropical rainforest. This is half of the 12 known phylogenetic types of the complex (4 new phylogenetic types from this study and 8 reported by Moncalvo and Buchanan 2008). Moncalvo and Buchanan (2008) noted that some pairs of phylogenetic types show mycelial compatibility. Our sequencing without the need for cloning of most samples suggests a low possibility that different phylogenetic types coexist within a fruit body. Morphological traits seemed to differ among some phylogenetic types. For example, both young and mature fruit bodies of Type 5 had pale green surface pores, whereas those of other phylogenetic types had a pale to dark brown surface. Type 5 has a thin context with long tubes, whereas Types 1 and 2 have a thick context with short tubes (S. Yamashita, personal observation). We need to examine intercompatibility experimentally among phylogenetic types.

We did not detect any evidence of niche partitioning, although we assumed that interactions among phylogenetic types of the *G. australe* complex were so severe that niche partitioning would occur. Data from the 3 ha plot show that all phylogenetic types used fresh CWD (stage 1) more frequently than expected on the basis of its availability at the site. Furthermore, the observed phylogenetic types did not differ in the size classes of pieces of CWD. Thus, the phylogenetic types at the study site share a resource defined by CWD decay stage and size.

Resource partitioning among fungal species within functional groups is commonly known and is still a possible mechanism allowing the coexistence of phylogenetic types. Closely related species of soil fungi occupied clearly different niche positions in relation to vegetation and soil horizon (Taylor et al. 2014). In wood-decaying fungal communities, dominant species divide their resource types according to size and decay stage of CWD (Allen et al. 2000; Heilmann-Clausen 2001; Rajala et al. 2011). In a previous study at our site, for example, fruit bodies of *G. australe* appeared from thick and young CWD samples, whereas those of *Phellinus lamaensis* appeared from thick and old pieces (Yamashita et al. 2009). Thus, differential resource use would be an important mechanism for maintaining fungal species diversity among phylogenetically divergent species. It is also possible that the definitions of size class and decay stage of CWD in this study were too broad to evaluate niche partitioning of the *G. australe* complex. Although we did not evaluate the effect of the phylogenetic type of host trees, differences in host tree species or family among phylogenetic types is a possible mechanism underlying speciation (Bergemann et al. 2009). Among the *G. australe* complex recorded from 15 tree families in a tropical primary rainforest (Hattori et al. 2012), the use of different host phylogenetic types may occur among fungal phylogenetic types, but further research is needed to clarify this issue.

The community structure of wood-decaying fungi on CWD is affected by the dispersal process and environmental filtering (Jönsson et al. 2008), as well as by

interspecific interactions among fungi (Holmer and Stenlid 1997; Heilmann-Clausen and Boddy 2005; Hiscox et al. 2015) after they reach a piece of CWD. Because spores of *Ganoderma* cf. *applanatum* are most probably dispersed by wind (Kadowaki et al. 2011), the dispersal of *G. australe* complex spores probably also depends on wind dispersal. This stochastic process might promote the coexistence among phylogenetic types of the *G. australe* complex with the same environmental demands, as seen in tree species of tropical rainforest (Hubbell and Foster 1986). Related species of the litter fungus *Tricholoma*, with similar niches, colonized open spaces randomly and used antibiotics to defend their territories (Widden and Abitbol 1980). The same process might work among phylogenetic types of *G. australe* at this site.

Resource partitioning on host trees or stochastic processes during colonization might play important roles in forming the community structure of phylogenetic types of *G. australe*. It is also possible, however, that the small sample size made it difficult to statistically detect niche partitioning from the field data. In our study, Type 3 and Type 5 appeared from only five and six pieces, respectively, of CWD. Because fruit bodies of Type 5 sometimes appear on dead standing trees (S. Yamashita, personal observation) and the others mostly on fallen logs, Type 5 may favor younger CWD than the other phylogenetic types. In addition, host preference might differ among fungal populations, as is the case for *Fomes fomentarius* in temperate and boreal regions (Yamashita et al. 2010). Conducting field surveys in several primary forests far from each other will help

us to reveal geographic variation in host use patterns.

Species with a wide distribution generally tend to have high genetic diversity due to isolation and recolonization. In the case of *Datronia caperata*, a polypore species that inhabits mangroves throughout Central America, genetic isolation between populations has likely occurred owing to expansion of certain populations (Bergemann et al. 2009). Genetic diversity in the *G. australe* complex is thought to be driven by an allopatric divergence process (Moncalvo and Buchanan 2008). Our samples contained both widespread phylogenetic types (Types 5 and 6) and more restricted ones (Types 1–4). In an evolutionary time, Borneo Island has come to harbor an extraordinary diversity of plants and animals as a result of immigration to and diversification in the Island (De Bruyn et al. 2014). Because sympatric divergence might be promoted by differential resource use (Giraud et al. 2008) and because diversity in resource types (plant species) is high on Borneo, it would be worth testing endemism of the more restricted phylogenetic types.

The dominant phylogenetic type of the *G. australe* complex appeared mostly on fresh CWD, suggesting that it is an early colonizer. Because fungal species composition affects the decomposition process (Kubartová et al. 2015; Yamashita et al. 2015b), and early colonizers play a key role in subsequent fungal succession (Ottosson et al. 2014; Hiscox et al. 2015) in temperate and boreal regions, *G. australe* might have a large effect on decomposition process as a possible early colonizer in tropical rainforest. Further

ecological research on the association of wood-decaying fungi in CWD is needed to elucidate the relationship between fungal community structure and decomposition process in tropical regions.

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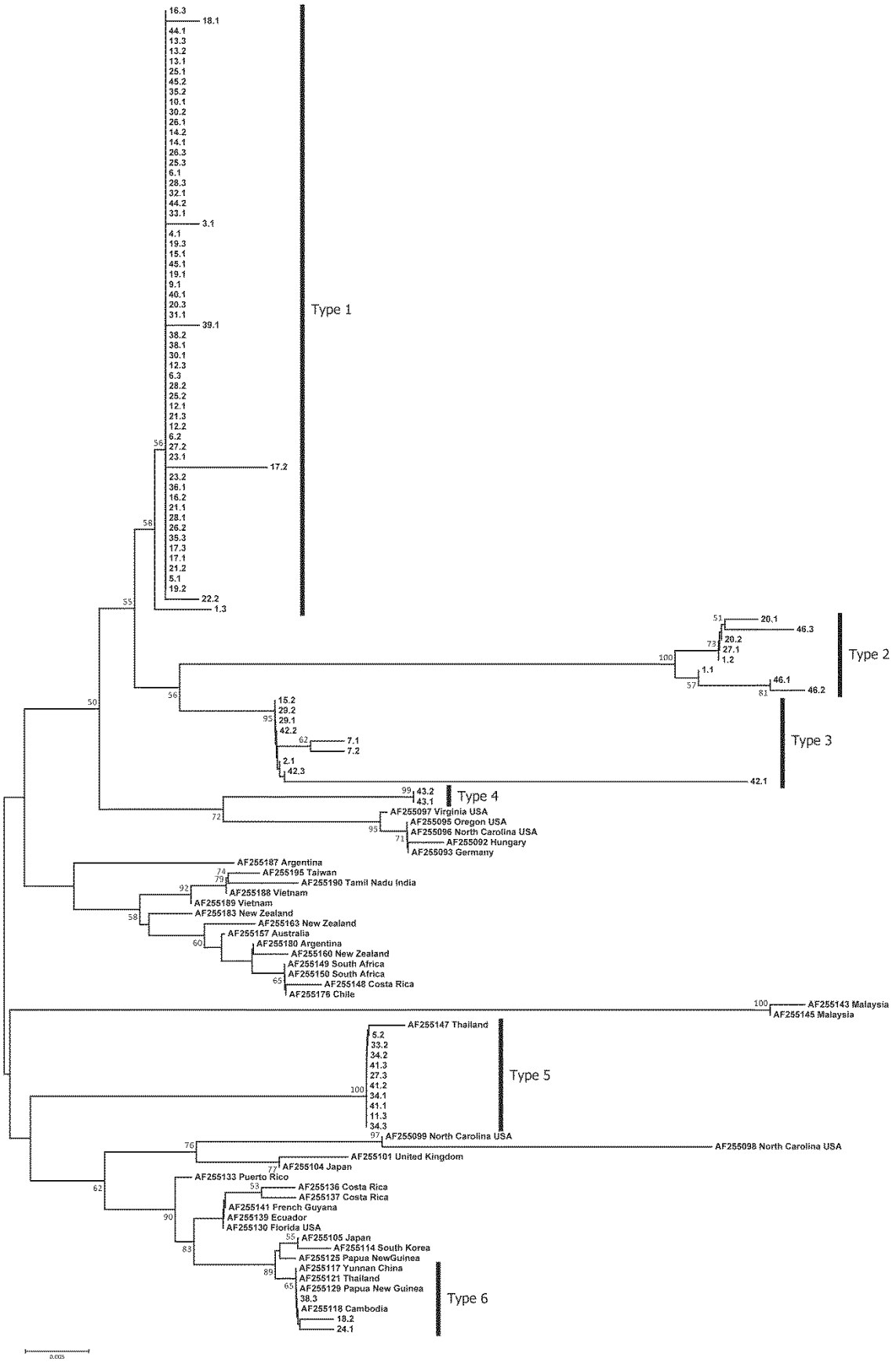
Figure legends

Fig. 1. Neighbor-joining phylogenetic tree derived from rDNA ITS sequences of *Ganoderma australe* complex collected at the Lambir Hills National Park and 39 worldwide sequences reported by Moncalvo and Buchanan (2008). Bootstrap values are shown near nodes.

Fig. 2. Relative proportions of pieces of CWD (numbers above bars) from which fruit bodies of each phylogenetic type appeared at each decay stage. The frequency distribution of the decay stage of CWD samples used by each phylogenetic type differed significantly from that of CWD at the site (χ^2 test, $P < 0.05$). The three dominant phylogenetic types did not differ significantly in decay stage (χ^2 test, $P > 0.05$).

Fig. 3. Numbers of coarse woody debris (CWD) samples from which fruit bodies of the three dominant phylogenetic types appeared in each diameter class in the plot.

Fig. 1


16.3
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17.2
23.2
36.1
16.2
21.1
28.1
26.2
35.3
17.3
17.1
21.2
5.1
19.2
22.2
1.3
Type 1
20.1
46.3
20.2
27.1
1.2
1.1
46.1
46.2
Type 2
15.2
29.2
29.1
42.2
7.1
7.2
2.1
42.3
42.1
Type 3
43.2
43.1
Type 4
AF255097 Virginia USA
AF255095 Oregon USA
AF255096 North Carolina USA
AF255092 Hungary
AF255093 Germany
AF255187 Argentina
AF255195 Taiwan
AF255190 Tamil Nadu India
AF255188 Vietnam
AF255189 Vietnam
AF255183 New Zealand
AF255163 New Zealand
AF255157 Australia
AF255180 Argentina
AF255160 New Zealand
AF255149 South Africa
AF255150 South Africa
AF255148 Costa Rica
AF255176 Chile
AF255143 Malaysia
AF255145 Malaysia
AF255147 Thailand
5.2
33.2
34.2
41.3
27.3
41.2
34.1
41.1
11.3
34.3
Type 5
AF255099 North Carolina USA
AF255098 North Carolina USA
AF255101 United Kingdom
AF255104 Japan
AF255133 Puerto Rico
AF255136 Costa Rica
AF255137 Costa Rica
AF255141 French Guyana
AF255139 Ecuador
AF255130 Florida USA
AF255105 Japan
AF255114 South Korea
AF255125 Papua NewGuinea
AF255117 Yunnan China
AF255121 Thailand
AF255129 Papua New Guinea
38.3
AF255118 Cambodia
18.2
24.1
Type 6
0.005

Fig. 2

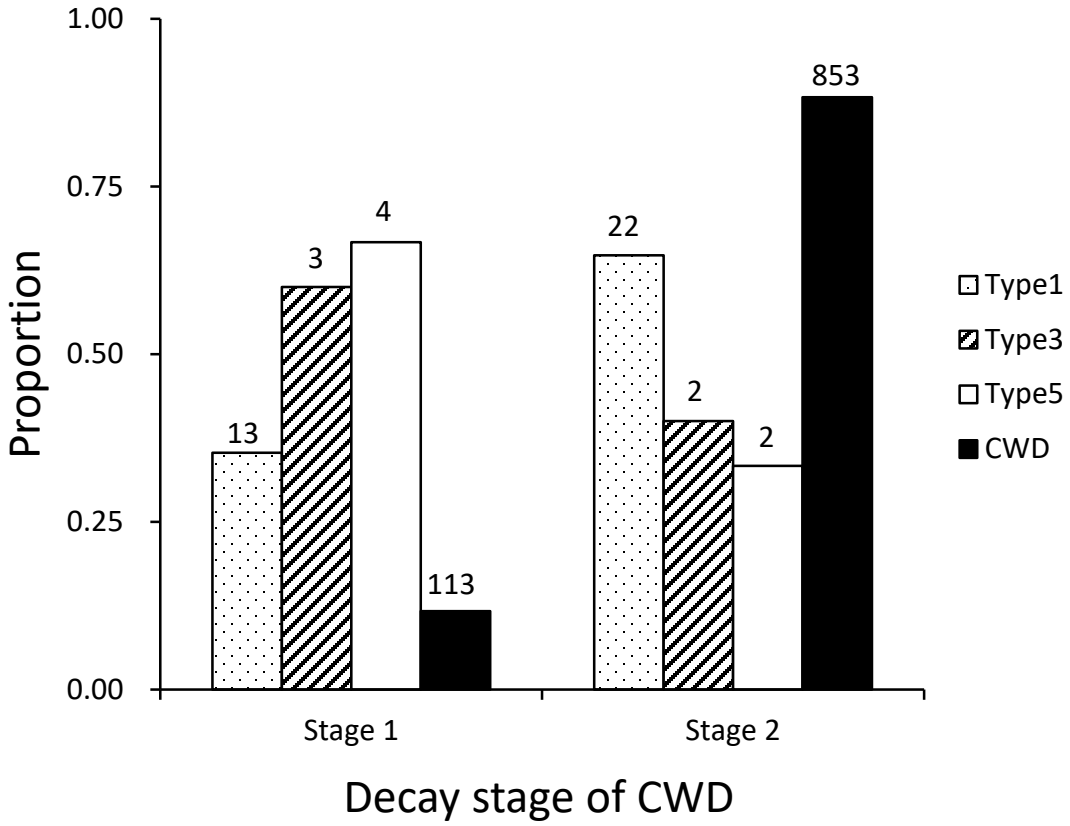
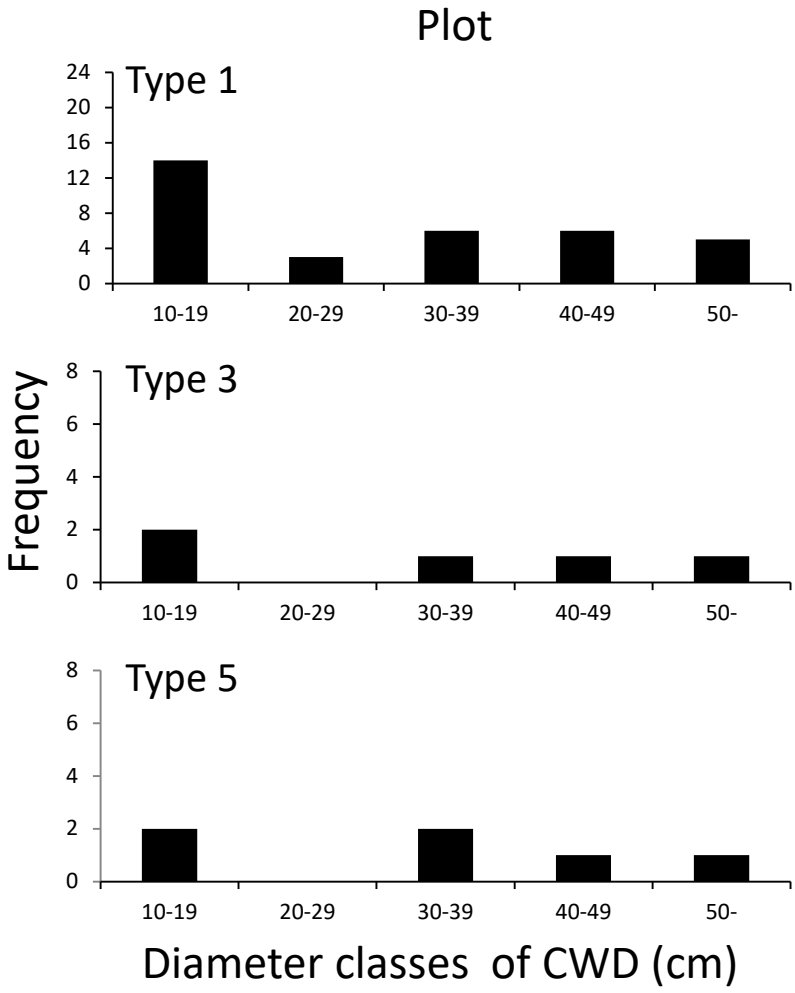

1.00
0.75
0.50
0.25
0.00
Proportion
13
3
4
113
22
2
2
853
Stage 1
Stage 2
Decay stage of CWD
Type1
Type3
Type5
CWD

Fig. 3


Plot
Type 1
24
20
16
12
8
4
0
10-19
20-29
30-39
40-49
50-
Frequency
Type 3
8
6
4
2
0
10-19
20-29
30-39
40-49
50-
Type 5
8
6
4
2
0
10-19
20-29
30-39
40-49
50-
Diameter classes of CWD (cm)

Appendix 1. List of fungal specimens deposited at the Research, Development, and Innovation Division of the Forest Department Sarawak, Kuching, Malaysia. All samples were collected by S. Yamashita.

Sample Number	Date	Site	Species	Accession No.
1-1	2009/5/31	LHNP	Ganoderma australe complex	LC084718
1-2	2009/5/31	LHNP	Ganoderma australe complex	LC084664
1-3	2009/5/31	LHNP	Ganoderma australe complex	LC084685
2-1	2009/5/31	LHNP	Ganoderma australe complex	LC084692
3-1	2009/5/31	LHNP	Ganoderma australe complex	LC084674
3-2	2009/5/31	LHNP	Ganoderma australe complex	Not determined
4-1	2009/6/1	LHNP	Ganoderma australe complex	LC084714
5-1	2009/6/1	LHNP	Ganoderma australe complex	LC084733
5-2	2009/6/1	LHNP	Ganoderma australe complex	LC084726
6-1	2009/6/1	LHNP	Ganoderma australe complex	LC084673
6-2	2009/6/1	LHNP	Ganoderma australe complex	LC084679
6-3	2009/6/1	LHNP	Ganoderma australe complex	LC084690
7-1	2009/6/2	LHNP	Ganoderma australe complex	LC084678
7-2	2009/6/2	LHNP	Ganoderma australe complex	LC084722
9-1	2009/6/3	LHNP	Ganoderma australe complex	LC084745
9-2	2009/6/3	LHNP	Ganoderma australe complex	Not determined
10-1	2009/6/3	LHNP	Ganoderma australe complex	LC084676
11-1	2009/6/3	LHNP	Ganoderma australe complex	Not determined
11-2	2009/6/3	LHNP	Ganoderma australe complex	Not determined
11-3	2009/6/3	LHNP	Ganoderma australe complex	LC084667
12-1	2009/6/3	LHNP	Ganoderma australe complex	LC084689
12-2	2009/6/3	LHNP	Ganoderma australe complex	LC084701
12-3	2009/6/3	LHNP	Ganoderma australe complex	LC084675
13-1	2009/6/3	LHNP	Ganoderma australe complex	LC084666
13-2	2009/6/3	LHNP	Ganoderma australe complex	LC084698
13-3	2009/6/3	LHNP	Ganoderma australe complex	LC084720
14-1	2009/6/4	LHNP	Ganoderma australe complex	LC084699
14-2	2009/6/4	LHNP	Ganoderma australe complex	LC084672
15-1	2009/6/4	LHNP	Ganoderma australe complex	LC084686
15-2	2009/6/4	LHNP	Ganoderma australe complex	LC084677
16-1	2009/6/4	LHNP	Ganoderma australe complex	Not determined
16-2	2009/6/4	LHNP	Ganoderma australe complex	LC084693
16-3	2009/6/4	LHNP	Ganoderma australe complex	LC084688
17-1	2009/6/4	LHNP	Ganoderma australe complex	LC084670
17-2	2009/6/4	LHNP	Ganoderma australe complex	LC084694
17-3	2009/6/4	LHNP	Ganoderma australe complex	LC084697
18-1	2009/6/4	LHNP	Ganoderma australe complex	LC084665
18-2	2009/6/4	LHNP	Ganoderma australe complex	LC084717
19-1	2009/6/4	LHNP	Ganoderma australe complex	LC084668
19-2	2009/6/4	LHNP	Ganoderma australe complex	LC084684
19-3	2009/6/4	LHNP	Ganoderma australe complex	LC084738
20-1	2009/6/4	LHNP	Ganoderma australe complex	LC084715
20-2	2009/6/4	LHNP	Ganoderma australe complex	LC084747
20-3	2009/6/4	LHNP	Ganoderma australe complex	LC084719
21-1	2009/6/5	LHNP	Ganoderma australe complex	LC084682
21-2	2009/6/5	LHNP	Ganoderma australe complex	LC084735
21-3	2009/6/5	LHNP	Ganoderma australe complex	LC084708
22-1	2009/6/5	LHNP	Ganoderma australe complex	Not determined
22-2	2009/6/5	LHNP	Ganoderma australe complex	LC084724
23-1	2009/6/5	LHNP	Ganoderma australe complex	LC084743
23-2	2009/6/5	LHNP	Ganoderma australe complex	LC084702
24-1	2009/6/5	LHNP	Ganoderma australe complex	LC084749
25-1	2009/6/5	LHNP	Ganoderma australe complex	LC084671
25-2	2009/6/5	LHNP	Ganoderma australe complex	LC084713
25-3	2009/6/5	LHNP	Ganoderma australe complex	LC084716
26-1	2009/6/5	LHNP	Ganoderma australe complex	LC084683
26-2	2009/6/5	LHNP	Ganoderma australe complex	LC084751
26-3	2009/6/5	LHNP	Ganoderma australe complex	LC084681
27-1	2009/6/8	LHNP	Ganoderma australe complex	LC084736
27-2	2009/6/8	LHNP	Ganoderma australe complex	LC084704
27-3	2009/6/8	LHNP	Ganoderma australe complex	LC084706
28-1	2009/6/8	LHNP	Ganoderma australe complex	LC084710
28-2	2009/6/8	LHNP	Ganoderma australe complex	LC084669
28-3	2009/6/8	LHNP	Ganoderma australe complex	LC084730

29-1	2009/6/8 LHNP	Ganoderma australe complex	LC084729
29-2	2009/6/8 LHNP	Ganoderma australe complex	LC084707
30-1	2009/6/8 LHNP	Ganoderma australe complex	LC084662
30-2	2009/6/8 LHNP	Ganoderma australe complex	LC084748
31-1	2009/6/8 LHNP	Ganoderma australe complex	LC084746
32-1	2009/6/8 LHNP	Ganoderma australe complex	LC084732
32-2	2009/6/8 LHNP	Ganoderma australe complex	Not determined
33-1	2009/6/8 LHNP	Ganoderma australe complex	LC084712
33-2	2009/6/8 LHNP	Ganoderma australe complex	LC084696
34-1	2009/6/8 LHNP	Ganoderma australe complex	LC084742
34-2	2009/6/8 LHNP	Ganoderma australe complex	LC084727
34-3	2009/6/8 LHNP	Ganoderma australe complex	LC084661
35-1	2009/6/10 LHNP	Ganoderma australe complex	Not determined
35-2	2009/6/10 LHNP	Ganoderma australe complex	LC084695
35-3	2009/6/10 LHNP	Ganoderma australe complex	LC084700
36-1	2009/6/10 LHNP	Ganoderma australe complex	LC084734
36-2	2009/6/10 LHNP	Ganoderma australe complex	Not determined
38-1	2009/6/10 LHNP	Ganoderma australe complex	LC084660
38-2	2009/6/10 LHNP	Ganoderma australe complex	LC084687
38-3	2009/6/10 LHNP	Ganoderma australe complex	LC084663
39-1	2009/6/10 LHNP	Ganoderma australe complex	LC084741
40-1	2009/6/10 LHNP	Ganoderma australe complex	LC084723
41-1	2009/6/10 LHNP	Ganoderma australe complex	LC084691
41-2	2009/6/10 LHNP	Ganoderma australe complex	LC084680
41-3	2009/6/10 LHNP	Ganoderma australe complex	LC084721
42-1	2009/6/12 LHNP	Ganoderma australe complex	LC084740
42-2	2009/6/12 LHNP	Ganoderma australe complex	LC084731
42-3	2009/6/12 LHNP	Ganoderma australe complex	LC084737
43-1	2009/6/12 LHNP	Ganoderma australe complex	LC084750
43-2	2009/6/12 LHNP	Ganoderma australe complex	LC084725
44-1	2009/6/12 LHNP	Ganoderma australe complex	LC084705
44-2	2009/6/12 LHNP	Ganoderma australe complex	LC084744
45-1	2009/6/12 LHNP	Ganoderma australe complex	LC084703
45-2	2009/6/12 LHNP	Ganoderma australe complex	LC084709
46-1	2009/6/12 LHNP	Ganoderma australe complex	LC084711
46-2	2009/6/12 LHNP	Ganoderma australe complex	LC084728
46-3	2009/6/12 LHNP	Ganoderma australe complex	LC084739