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A fungal symbiont converts provisioned cellulose into edible yield for its leafcutter ant farmers

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While ants are dominant consumers in terrestrial habitats, only the leafcutters practice herbivory. Leafcutters do this by provisioning a fungal cultivar (Leucoagaricus gongylophorus) with freshly cut plant fragments and harnessing its metabolic machinery to convert plant mulch into edible fungal tissue (hyphae and swollen hyphal cells called gongylidia). The cultivar is known to degrade cellulose, but whether it assimilates this ubiquitous but recalcitrant molecule into its nutritional reward structures is unknown. We use in vitro experiments with isotopically labelled cellulose to show that fungal cultures from an Atta colombica leafcutter colony convert cellulose-derived carbon into gongylidia, even when potential bacterial symbionts are excluded. A laboratory feeding experiment showed that cellulose assimilation also occurs in vivo in A. colombica colonies. Analyses of publicly available transcriptomic data further identified a complete, constitutively expressed, cellulose-degradation pathway in the fungal cultivar. Confirming leafcutters use cellulose as a food source sheds light on the eco-evolutionary success of these important herbivores.

1. Introduction

Cellulose is a major constituent of plant cell walls and the most abundant organic compound on earth, with enormous potential as an energy source in terrestrial ecosystems [1,2]. However, cellulose is also a recalcitrant molecule that is metabolically inaccessible to most animals without help from bacterial or fungal symbionts [2,3]. While leafcutter ants are the only ants to forage fresh vegetation, they cannot directly consume this cellulose-rich material. Instead, the ants use it to provision an obligate fungal symbiont, Leucoagaricus gongylophorus (Basidiomycota, Agaricaceae). The fungus converts plant material into structural hyphae and swollen hyphal cells called gongylidia (growing in bundles called staphylae) that are the main food source for the ants [4–6]. Leafcutter farming systems can be massive. Colonies in the genus Atta (Hymenoptera, Formicidae) can contain millions of ant workers and are dominant herbivores in neotropical ecosystems [7]. Despite their large-scale herbivory, it remains uncertain whether these farming systems can use recalcitrant plant polymers, like cellulose, as a source of nutrition [8,9] (electronic supplementary material, table S1).
Recent studies have shown the presence of cellulose degradation and cellulose-degrading enzymes in leafcutter fungus gardens [10–17]. However, it remains unclear if these enzymes serve primarily to degrade the cell wall and thus provide access to more readily metabolized nutrients inside, or if the fungus is also capable of assimilating cellulose-derived carbon (C) into edible nutritional rewards (i.e. gongylidia). Cellulose digestion may also be context specific, with the cultivar prioritizing more accessible carbon sources whenever possible [13], as is also reported from other fungal lineages [18]. Alternatively, cellulose degradation has been attributed to bacterial symbionts within the fungus garden rather than the fungus itself [11,16,17], but see [19]. We review the literature on cellulose degradation in the leafcutter symbiosis in electronic supplementary material, table S1.

We tested the links between cellulose provisioning, cellulose metabolism and the cultivar’s production of nutritional rewards in three steps. First, an in vitro experiment with 13C-labelled cellulose measured the uptake of cellulose-derived carbon into hyphae and staphylae. The inclusion of dextrose as a more accessible carbon source in the media provided a secondary test of whether the fungus uses cellulose as an energy source even when simpler sugars are available. Second, an in vivo laboratory feeding experiment tested if the in vitro results could be replicated in a colony of the Panamanian leafcutter ant Attta colombica. Foragers collected agar-based substrate containing 13C-labelled cellulose which gardeners used to provision their fungus garden, containing a natural assemblage of ants and microbes. Third, we tested if the fungal cultivar can directly metabolize cellulose in two steps. In silico analysis of previously published transcriptomic data assessed if the cultivar constitutively expresses a complete metabolic pathway for cellulose degradation, even when this compound is not expected to be present in the provisioned substrate. An in vitro experiment with media containing 13C-labelled cellulose and antibiotics assessed cellulose metabolism following targeted bacterial exclusion.

2. Methods

(a) In vitro assays

Fresh fungal cultures of L. gongylphorus were isolated from a Panamanian A. colombica colony (Ac-2012-1) onto potato-dextrose agar (PDA) [20]. Isotopically enriched media were prepared by adding 0.1 g l−1 of 13C-enriched glucose (β-glucose-1,2,3,4,5-13C, Sigma-Aldrich, USA) or 0.1 g l−1 of 13C-enriched cellulose (U-13C Cellulose, U-10508, IsoLifeg; The Netherlands) to PDA. Media were autoclaved and 10 ml aliquots were transferred into 60 mm Petri dishes (n = 30 per treatment). The 13C-enriched glucose treatment represented a positive control as its metabolism and assimilation have previously been confirmed [21]. PDA without enriched compounds was the negative control. Inoculation of the fungus followed established protocols with incubation at 23.5°C [20]. Polycarbonate track-etched (PCTE) membrane discs (diameter 47 mm, PCTE 0.1 µm; GVS, USA) were placed in Petri dishes to facilitate collection of fungal tissues for subsequent analyses after 79 days.

A second experiment repeated this approach but added antibiotics (ampicillin, chloramphenicol and streptomycin) (for concentrations, see [22]) to each treatment (n = 15 per treatment) and was performed over 52 days. We confirmed that bacteria were excluded from antibiotic-treated plates by collecting fungal mycelia from the antibiotic-treated and control plates and extracting DNA using a Chelex® (Sigma-Aldrich, USA) protocol [23,24]. DNA for positive controls was extracted, using the same method, from pure colonies of bacteria: Streptomyces sp. (Gram-positive) and Stenotrophomonas sp. (Gram-negative). DNA extracts were diluted to 10% of the original concentration using ddH2O before analyses. Bacterial load was quantified using ddPCR with eubacterial primers (63F and 355R) following established protocols (Bio-Rad, USA) [25,26]. Based on values for the negative controls, a detection threshold of 10 000 was used (electronic supplementary material, figure S2 and table S2).

(b) In vivo assay

Baseline samples of hyphae and staphylae (n = 4 per tissue type) were collected from the middle layer of the fungus garden of Ac-2012-1, maintained in the laboratory at 23.5°C [27]. The colony was provided with a 13C-cellulose-enriched diet (see in vitro assays), which was completely consumed by the ants within 24 h. Hyphae and staphylae were sampled from the middle layer of the garden after 2 days (n = 4 per tissue type), the time when peak 13C enrichment levels were previously detected [21].

(c) Testing for 13C assimilation

We collected 0.05–0.1 mg (dry mass) of hyphae and staphylae from each in vitro plate and each in vivo fungal sample. In addition, remaining media from the initial in vitro experiment were collected (electronic supplementary material, figure S1). Samples were prepared following established protocols [21] and then analysed by isotope ratio mass spectrometry (IRMS) for 13C/12C concentrations (13C enrichment). The system used a Eurovector CN analyser (Pavia, Italy) coupled with an Isoprime mass spectrometer (Cheadle Hulme, UK). We used the results to calculate 13C enrichment (13Cµg g−1) in the excess of natural abundance. Each cellulose molecule ([13C6H10O5]n) had a sixfold higher 13C enrichment than each glucose molecule ([13C6-C3H2O6]), so we corrected for this by dividing 13Cµg g−1 values in the cellulose treatment by 6 before further analyses. We used Z-scores to normalize enrichment values relative to baseline abundances for each tissue type, allowing for direct statistical comparisons between tissues and carbon sources (electronic supplementary material, table S3).

(d) Data analysis

All data were analysed in R (v. 4.0.2 [28]). The homogeneity of variance was tested using Levene’s test (car v. 3.1–10 [29]) and normality was tested using a Shapiro–Wilks test. Based on these results, in vitro IRMS data were analysed non-parametrically using permutational analysis of variance (Adonis with Euclidean distances and 9999 permutations; vegan version: 2.5–7 [30]). In vivo IRMS and ddPCR data were analysed using linear model with emmeans (v. 1.7.2 [31]) used to test for between-tissue differences on Day 2 of the in vitro experiment. We performed three separate analyses (two in vitro, one in vivo experiment), using Z-scores, calculated relative to the control for that tissue type, as the dependent variable unless otherwise specified. The independent variables were as follows: EnrichedCarbonSource (enriched cellulose, enriched glucose, none control), Tissue (hyphae, staphylae) and AntiBioticTreatment (±antibiotics). For the first in vitro experiment, we tested EnrichedCarbonSource + Tissue, and for the second in vitro experiment we tested AntiBioticTreatment*EnrichedCarbonSource + Tissue. 13C enrichment in the media after the experimental period was tested using 13Cµg g−1 EnrichedCarbonSource (electronic supplementary material, figure S1). For the in vivo experiment, we tested Tissue*EnrichedCarbonSource to compare enrichment in staphylae and hyphae to the baseline natural.
abundance. To test for bacterial DNA in the second in vitro experiment, we tested log10(165 copies) against AntibioticTreatment + CarbonSource. When main effects were significant, we used pairwi-
seAdonis (v: 0.0.1 [32]) to perform pairwise post hoc tests with adjusted p-values calculated using false-discovery rate with a sig-
nificance threshold of p_{adj} = 0.05.

(e) In silico analysis of capacity for cellulose metabolism
Transcriptome assemblies [33] were downloaded from the NCBI TSA database, translated using translog (EMBOSS v: 6.6.0 [34]) and carbohydrate-active enzymes (CAZymes) annotated using peptide pattern recognition (PPR) (HotPep v: 1.0 [35]). While previous studies have identified CAZY families expressed in the fungus garden and in vitro cultures [13,14,33], PPR predicted enzyme commission (EC) numbers, enabling us to identify the specific reactions catalysed [35]. Predicted EC numbers were compared to the BRENDA [36] cellulose-degradation pathway. We identified all enzymes in the BRENDA pathway.

3. Results
(a) In vitro cellulose assimilation by the cultivar
Fungal tissue was significantly enriched for 13C in both the
13C-cellulose and 13C-glucose treatments relative to the con-
control (F_{1,152} = 18.487, p < 0.001, figure 1a). The cultivar
responded similarly for both treatments with overall enrich-
ment levels that did not differ statistically, and with
staphylae being more enriched than hyphae (F_{1,152} = 24.168,
p < 0.001; figure 1a; electronic supplementary material, figure S1).

(b) In vivo cellulose assimilation by an intact fungus
garden
The fungus garden assimilated 13C-cellulose from the sub-
strate collected by foragers and provisioned by gardeners
inside the nest, as both hyphae and staphylae sampled from the middle layer of the fungus garden had significantly
elevated 13C-content (F_{1,12} = 14.405, p = 0.003) relative to base-
line natural abundances (figure 1b). Enrichment in staphylae and hyphae did not differ significantly from each other
(overall: F_{1,12} = 0.162, p = 0.694; Day 2: F_{1,12} = −0.569, p = 0.580).

(c) Cultivar mediated cellulose metabolism
High-resolution in silico analysis of transcriptomic data [33]
confirmed that L. gongylophorus expresses all enzymes
required for cellulose degradation and that these genes are
expressed in a PDA medium lacking cellulose (figure 2a),
potentially indicating constitutive expression of these bio-
degrative pathways. In total, we identified three cellulase
genes (EC:3.2.1.4), four lytic cellulose monoxygenases
(EC:1.14.99.54), one lytic cellulose monoxygenase
(EC:4.2.1.176), and two β-glucosidases (EC:3.2.1.21) (figure 2b).

The antibiotic assay excluded the possibility that bacterial
symbionts were necessary for cellulose metabolism, as the
cultivar was significantly enriched for 13C in both the 13C-cell-
ulose and 13C-glucose treatments, relative to samples from
control PDA plates (F_{1,171} = 130.114, p < 0.001, figure 2b).

Pairwise tests showed higher 13C enrichment in the glucose
treatment relative to the cellulose treatment, even as both
were still significantly enriched relative to the control (figure 2b). Despite evidence for 13C enrichment when bact-
eria were excluded, overall 13C enrichment was lower on
plates with antibiotics relative to the respective control
plates with only 13C-cellulose or 13C-glucose (F_{1,171} = 48.295,
p < 0.001, figure 2b). However, a significant interaction
between carbon source and antibiotic treatment (F_{2,171} =
47.314, p < 0.001), and subsequent pairwise tests, indicated
the main effect was driven by reductions in 13C enrichment
in the glucose treatment and with no significant effect of
the antibiotic treatment on the cellulose medium (figure 2b).
Staphylae were significantly enriched relative to hyphae
(F_{1,171} = 58.084, p < 0.001, figure 2b).

4. Discussion
While L. gongylophorus is known to degrade cellulose [10,12,
14,19] (electronic supplementary material, table S1), our iso-
topic enrichment experiments provide the first empirical
confirmation of the prediction that it also metabolizes and
assimilates cellulose-derived carbon into nutritional reward
structures for ant farmers. The fungal cultivar further
expresses its own complete enzymatic pathway for the degra-
dation of cellulose to glucose and can metabolically
transform cellulose following the targeted in vitro removal
of bacteria (and ant farmers). The cultivar’s metabolic conver-
sion of cellulose to glucose and packaging in edible
nutritional rewards may have contributed to the dietary
niche expansion that has made leafcutter ants dominant
herbivores across neotropical ecosystems.

Like free-living fungi [18], L. gongylophorus has been pre-
predicted to preferentially metabolize simple sugars over
recalcitrant plant compounds like cellulose [9,10,12,13], with
some further predicting that cellulase expression serves to
degrade the plant cell wall rather than releasing usable
carbon for the fungus [9,10,12,13]. However, the cultivar in
this study metabolized cellulose despite having access to
the simple sugar dextrose, at a concentration approximately
200 times higher than cellulose in the PDA medium. Tran-
scriptomic analysis further identified expressed cellulase
genes despite being collected from cultivars grown on cellu-
lose-free PDA [33]. The ubiquity of cellulose in plant tissues
may have favoured the evolution of a constitutive cellulose
metabolism even when the individual fragments foraged
contain this molecule at low concentrations, with cellulase
production having been shown to increase in the presence
of fresh plant material [13]. It will be interesting to perform
differential-expression analyses testing whether cellulose
gradients in provisioned substrates directly mediate cellulase
gene expression levels and ultimately govern behavioural
decisions in the colony about sending foraged leaf material
directly to waste piles.

These results shed light on cellulose processing within
L. gongylophorus fungus gardens. Fungal cellulase expression
appears highest in the top and bottom layers of the garden
[9,10,12], and the cultivar is assumed to only prioritize cellu-
lose digestion once highly degraded plant material reaches
the bottom layer [10,12,13]. Our in vivo results indicate that
freshly foraged cellulose can be rapidly (within 2 days) con-
verted into edible gongylidia in the middle layer, perhaps
assisted by the constitutive expression of cellulase. Although we do not observe differential enrichment between staphylae and the surrounding mycelium in the \textit{in vivo} experiment, our sampling point was based on rapidly assimilated glucose, with more complex substrates like cellulose potentially taking longer. Our results are based on a single attine cultivar, but we predict that this process of cellulose assimilation will hold across cultivars of other leafcutter colonies, species and genera, as their cultivars exhibit high degrees of relatedness [37]. Moreover, results of the present study add to an expanding catalogue of adaptions [6,27,33] enabling the domesticated fungal cultivar to extract nutrition from taxonomically and biochemically diverse plant fragments [20].

\textbf{Figure 1.} Isotopic evidence that the fungal cultivar assimilates carbon (C) from cellulose molecules. (a) An \textit{in vitro} experiment detected significant overall $^{13}$C enrichment in fungal hyphae and staphylae on $^{13}$C-enriched media compared to the control. Levels of $^{13}$C enrichment for staphylae and hyphae did not differ between isotopic enrichment treatments but staphylae were more enriched than hyphae. Letters show groupings based on pairwise tests ($p_{adj} < 0.05$). (b) An \textit{in vivo} experiment showed that staphylae and hyphae were significantly $^{13}$C-enriched after 2 days compared to baseline natural abundance with no significant differences between fungal tissues. Z-scores relative to control/baseline, diamonds indicate means.

\textbf{Figure 2.} The fungal cultivar can directly metabolise and assimilate cellulose. (a) A complete cellulose-degradation pathway was identified from transcriptomic data. (b) The \textit{in vitro} cultivar remained significantly $^{13}$C-enriched relative to the baseline natural abundance (control) when bacteria were specifically excluded using antibiotics. Z-scores relative to control, diamonds indicate means, letters show groupings based on pairwise tests ($p_{adj} < 0.05$).


