Comparative metabolomics implicates threitol as a fungal signal supporting colonization of *Armillaria luteobubalina* on eucalypt roots

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Abstract

Armillaria root rot is a fungal disease that affects a wide range of trees and crops around the world. Despite being a widespread disease, little is known about the plant molecular responses towards the pathogenic fungi at the early phase of their interaction. With recent research highlighting the vital roles of metabolites in plant root-microbe interactions, we sought to explore the pre-symbiotic metabolite responses of *Eucalyptus grandis* seedlings towards *Armillaria luteobuablina*, a necrotrophic pathogen native to Australia. Using a metabolite profiling approach, we have identified threitol as one of the key metabolite responses in *E. grandis* root tips specific to *A. luteobubalina* that were not induced by three other species of soil-borne microbes of different lifestyle strategies (a mutualist, a commensalist, and a hemi-biotrophic pathogen). Using isotope labeling, threitol detected in the *Armillaria*-treated root tips was found to be largely derived from the fungal pathogen. Exogenous application of D-threitol promoted microbial colonization of *E. grandis* and triggered hormonal responses in root cells. Together, our results support a role of threitol as an important metabolite signal during eucalypt-*Armillaria* interaction prior to infection thus advancing our mechanistic understanding on the earliest stage of *Armillaria* disease development.

Summary statement

Comparative metabolomics of eucalypt roots interacting with a range of fungal lifestyles identified threitol enrichment as a specific characteristic of *Armillaria* pathogenesis. Our findings suggest that threitol acts as one of the earliest fungal signals promoting *Armillaria* colonization of roots.

Keywords: plant-microbial interaction, rhizosphere, fungal tree pathogen, biomarkers, metabolomics, GC-MS, disease detection, soil microbes

Introduction

Armillaria root disease is a ubiquitous root disease threatening numerous tree species in the world including a wide range of eucalypt species. *Armillaria*-infected eucalypts usually show symptoms such as white mycelical sheets under the bark, white rot of sapwood, black rhizomorphs penetrating root surfaces and honey-coloured mushrooms clusters. Further aboveground symptoms include reduced growth of the host, distress cone crop, and crown thinning (Kile 2000). As *Armillaria* usually causes only a minor disturbance to native eucalypts forests and plantations, these fungi are often considered as an unimportant, indigenous soil-borne pathogen of eucalypts in Australia (Burgess & Wingfield 2004). However, when trees are under stress due to drought or temperature extremes, they became more prone to *Armillaria* disease (Sturrock *et al.* 2011). Therefore, in view of changing global climatic conditions, root rot attributed to *Armillaria* infection could become more prominent in the future.

Within the *Armillaria* genus, *Armillaria luteobubalina* is a particularly deadly species that can cause root rot or even mortality among eucalypts in both native forests and plantations, setting itself apart from other native *Armillaria* species in Australia (Kile 2000; Burgess & Wingfield 2004). *A. luteobubalina* has been the major causal agent of dieback and decline of eucalypts in central Victoria and south-western Australia in the last century (Kile 1981; Robinson 2003). The current diagnostic strategy for *Armillaria* disease relies heavily on visual inspection for the symptoms mentioned above, which are unfortunately similar to other root diseases and usually only appear in the later stage of the disease, making *Armillaria* disease difficult to detect (Kile 2000). Despite being a common tree disease, little is known about the molecular pathways underlying the *Armillaria* disease development in eucalypts – knowledge that could be critical to devising new methods for control of *Armillaria* root infection. Transcriptomic analysis of *Armillaria* after colonization of grand fir (Ross-Davis *et al.* 2013) and genomic and proteomic analysis of *A. mellea* (Collins *et al.* 2013) have explored the contribution of digestive enzymes and effector proteins during degradation of the plant tissues, yet the molecular mechanisms initiating the infection of *Armillaria* fungi on tree roots are largely unknown. Better knowledge concerning the onset of *Armillaria* infection in trees could aid more effective, proactive management of the disease.

Interactions between plants and soil microbes are often initiated by the exchange of metabolite signals. While the majority of metabolites used as signals between organisms in plant-microbe interactions are common to both mutualistic and pathogenic symbioses (Xu *et al.* 2015; Wong *et al.* 2019), there are also examples in the literature where either soil microbes or their plant hosts release genus- or species-specific metabolites that facilitate their interaction. For example, root exudate contents of tomato and tall fescue vary based on the type of soil-microbes with which they were interacting (Kamilova, Kravchenko, Shaposhnikov, Makarova & Lugtenberg 2006; Guo, McCulley & McNear 2015). Similarly, soil-microbes can produce specific metabolites to facilitate root colonization on host plants; the secretion of hypaphorine by the ectomycorrhizal fungus *Pisolithus tinctorius* is related to colonization (Beguiristain & Lapeyrie 1997). These studies are, therefore, a proof of concept demonstrating that a range of metabolites derived from either the plant or the interacting microbe can be selectively present during plant-microbial interaction. Further, these studies may indicate that the difference in plant metabolite responses towards different microbes could be the key to determine the interaction outcome between the two organisms. Given their key importance, these metabolite responses could also be used as 'biomarkers' to indicate the health or disease status in plants and provide further insight into the pathogenicity of the disease agent. Using gas chromatography-coupled mass spectrometry (GC-MS), metabolite biomarkers have been identified for plant diseases such as *Tomato yellow leaf curl virus* (Sade *et al.* 2014), *Ganoderma* disease in oil palm (Nusaibah, Siti Nor Akmar, Idris, Sariah & Mohamad Pauzi 2016), and *Fusarium* infection in maize (Sherif *et al.* 2016). For *Armillaria* disease, pine seedlings infected with *A. ostoyae* exhibited distinct levels of certain metabolites nine months post-inoculation despite there being no visible symptoms (Isidorov, Lech, Żółciak, Rusak & Szczepaniak 2008). To further expand our knowledge of the mechanisms regulating *Armillaria* pathogenicity, and to advance the detection strategy of *Armillaria* root rot, we need to improve our understanding of the host metabolite responses, and their underlying roles, during the early stages of the interaction.

In this study, we explore the metabolite response of *Eucalyptus grandis* roots towards *A. luteobubalina* during the earliest phases of interaction (i.e. pre-symbiosis) in an effort to advance our understanding of key metabolite signals underpinning the onset of *Armillaria* disease in eucalypts. The root metabolite responses towards *A. luteobubalina* at 24 h pre-symbiotic interaction (i.e. before the plants and fungi come into physical contact) were

93 profiled and compared to the metabolite profiles of eucalypt roots similarly exposed to three
94 other distinct groups of microbes— the mutualistic ectomycorrhizal fungus *Pisolithus*
95 *microcarpus*; the commensal fungus *Suillus granulatus* and the hemi-biotrophic oomycete
96 *Phytophthora cinnamomi*, in order to identify metabolite responses that are specific to the *E.*
97 *grandis-A. luteobubalina* interaction. We identify a number of metabolite responses specific
98 to the *Armillaria* interaction. We further characterize the role of one of these metabolites, D-
99 threitol, on *E. grandis* defence gene expression and on *Armillaria* infection efficiency.
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Materials and methods

Fungal culture condition

A total of 10 different isolates of fungi corresponding to three fungal species representing different lifestyles and one isolate of pathogenic oomycete *P. cinnamomi* were sampled from several locations in New South Wales, Australia and used in this study (Table S1). Agar plugs containing mycelium of each fungal isolates and oomycete isolate were grown on a piece of permeable, sterile cellophane membrane (Kleerview Covers by Fowlers Vacola Manufacturing Co Ltd.) in their preferred growth medium (Table S1). The fungal and oomycete cultures were allowed to grow in a dark growth cabinet controlled at 25°C for 14 d before the pre-symbiosis experiment with *E. grandis*.

Plant growth condition

To establish the experiment, *E. grandis* seeds (seedlot 20974) were obtained from the Commonwealth Scientific and Industrial Research Organisation (CSIRO, Clyton, Victoria, Australia) tree seed center. Seeds sterilization was performed by submerging the seeds in 30% (v/v) H_2O_2 for 10 min followed by washing in sterilized deionized water for 5 min five times. After sterilization, seeds were germinated in 1% water agar for three weeks before transferring into half-strength modified MMN media. The *E. grandis* seedlings were cultivated in a controlled growth chamber (22-30°C; 16 h light cycle) for 1 month prior to the pre-symbiotic interaction with microbes.

Pre-symbiotic plant-microbial interaction set-up for untargeted metabolite profiling

Both *E. grandis* seedlings, fungal cultures and oomycete cultures were allowed to acclimatize to modified half-strength MMN media without glucose for 3 d before the set-up of the pre-symbiotic interaction. At the beginning of the experiment, each cellophane membrane containing the fungal/oomycete mycelia was placed on top of the root system of a *E. grandis* seedling (2-month-old) whereby the cellophane membrane physically separated the fungal/oomycete mycelia from the *E. grandis* root system but allowed diffusion of chemical compounds between the microbe and the plant as per Wong et al. (2019). The 24 h pre-symbiotic interaction was carried out in a controlled growth chamber (22-30°C; 16 h light cycle) and root tips of *E. grandis* were sampled, subjected to snap-freezing with liquid N_2 and stored in a -80°C freezer. An untreated seedling control was also set up (*E. grandis* seedlings

covered by sterile cellophane membrane). The frozen samples were sent to Metabolomics Australia at the University of Melbourne for untargeted metabolite profiling using gas chromatograph mass spectrometer (GC-MS) as described in Roessner *et al.* (2001). Details of the sample preparation and analytical procedures are described in Supplementary Materials and Methods. While GC-MS is not able to comprehensively profile the full suite of metabolites within the root, it has the advantage of a high efficiency of peak separation and reproducible retention times that enable it to be better compared to previously performed research (Scalbert *et al.* 2009; Vinaixa *et al.* 2016). The ionization used in the method also allows for standardized spectral fingerprints that increase the possibility of positive identification against public databases. Conversely, the derivatization steps required for the analysis mean that some compounds become too unstable and are therefore missed. Other techniques could be used to generate a longer list of MFs, but as the aim of this paper was to find a method that could be used comparably between laboratories and use as simple a workflow as possible, thereby increasing the possible implementation as a potential screening tool for disease in different settings, we chose to use the GC-MS platform.

Soil-based *Armillaria*-treatment set up for untargeted metabolite profiling

Two-month-old *E. grandis* seedlings growing on half-strength MMN media were transferred individually into pots containing soil (Osmocote professional seed and cutting potting mix by Evergreen Garden Care Australia Pty Ltd.) sterilized by autoclaving two times at 121^{o}C for three hours. The seedlings were then allowed to grow in soil for another month in a growth chamber (22-30°C; 16 h light cycle). To allow soil-based interaction with *A. luteobubalina*, the three-month-old *E. grandis* seedlings were transferred into a pot with 0.5 L of soil inoculated with 25 mL of homogenized *A. luteobubalina* culture in PDA media. An uninoculated control (0.5 L soil mixed with 25 mL of sterile PDA media) was also set up. After 7 d of interaction in the abovementioned growth chamber, the soil was discarded from the pot and the root tips of the *E. grandis* seedlings were harvested and immediately frozen in liquid N_2. The frozen root tip samples were analyzed for metabolite profiles as above.

Targeted D-threitol quantification throughout *A. luteobubalina* colonization of *E. grandis* and under different nutrient regimes

In order to understand the production of threitol throughout colonization, *E. grandis* and *A. luteobubalina* were grown separately and pre-treated as above. Fungal cultures were then placed into either indirect contact with *E. grandis* roots for 24hrs, as described above, or were placed into direct physical contact. For the latter samples, at prescribed intervals (24hrs, 48hrs, 1 week, and 2 weeks) the roots and adherent fungi were separated and snap frozen in liquid nitrogen and stored at -80^{o}C until extraction and analysis. In order to understand if nutrient levels in the growth medium may serve as a signal for threitol production, we grew *A. luteobubalina* on a series of media with decreasing concentrations of potato dextrose (1x, 1/2x, 1/4x, and 1/10x) for 2 months after which fungal tissue samples were taken, snap frozen and then analyzed for threitol concentration as below.

Because of different extraction efficiencies, we used two different methods to extract threitol from roots and from fungi. For the roots, the fresh weight of the root tip samples were recorded during harvest. Approximately 20-30mg of frozen root samples per biological replicate were homogenized using a bead mill (FastPrep-24, MP Biomedicals, LLC) and then incubated with 600µl of 60% (v/v) methanol (HPLC grade) in a thermomixer (Eppendorf) set at 60°C with a mixing speed of 1,000 rpm for 30 min. The extracts were then centrifuged at 13,000 rpm for 5 min. Cleared supernatant samples were then collected and dried using a vacuum concentrator (SpeedVac, Thermo Fisher Scientific) set at ambient temperature. The dried extracts were re-suspended in 1/10 of the original volume of 60% (v/v) methanol and stored at -20°C until analysis. For the fungal samples, the fresh weight of the fungal mycelia samples were recorded during harvest. Frozen fungal samples were homogenized using a bead mill (FastPrep-24, MP Biomedicals, LLC) and then incubated with 100µl per 10mg fresh sample of pure methanol (HPLC grade) in a thermomixer (Eppendorf) set at 30°C with a mixing speed of 1,000 rpm for 15 min. The methanol extracts were then centrifuged at 13,000 rpm for 5 min. Clarified supernatant samples were then collected and set aside in a new microcentrifuge tube. 100µl per 10mg fresh samples of deionized water was added into the sample pellet, vortexed for 10 sec and incubated at ambient temperature for 5 min. The water extracts were then centrifuged at 13,000 rpm for 5 min. Clarified water extracts were collected and mixed with the aforementioned methanol extracts, and dried using a vacuum concentrator (SpeedVac, Thermo Fisher Scientific) set at ambient temperature. The dried extracts were re-suspended in 1/5 of the original volume of 50% (v/v) methanol and stored at -20°C until analysis.

Of each sample, 2µl was injected into the Agilent 1260 Infinity HPLC-system equipped with a Shodex Asahipak NH2P-50 4E column (4.6 x 250 mm, 5µm) warmed at 55°C, and a Dionex Corona charged aerosol detector (CAD). The mobile phase was optimized based on the sample types. Elution was done isocratically with 1:1 (v/v) deionized water: acetonitrile (HPLC grade) for root samples, whereas 1:4 (v/v) deionized water: acetonitrile (HPLC grade) was used for fungal samples. In both cases, the elution was done at the rate of 1.2mL/min for 10min. A set of seven D-threitol standards at concentrations ranging from 250ppm to 4,000ppm were used to identify and quantify the concentration of threitol in each sample. The resulting quantitation was normalized based on the fresh weight of each sample.

Statistical analysis of metabolite profiling data

The metabolite profiling data matrix, containing the relative response ratios of each metabolite (including both identified and unknown metabolites) in each condition, was loaded on the R platform (version 3.5.1). Data transformation (log-transformation and auto-scaling), univariate analysis and principle component analysis (PCA) were performed with MetaboAnalystR (version 1.0.1) with the metabolite profiling data matrix. Recursive partitioning and regression tree (rpart) and parallel random forest (parRF) were performed using the caret package (version 6.0-81) while sparse partial least square-discriminative analysis (sPLS-DA) was carried out with mixOmics (version 6.6.0) package on R. The workflow of this analysis can be found in Figure S1.

Threitol quantitation, ^{13}C-isotopic labelling and tracing

Prior to pre-symbiotic interaction with *E. grandis*, *A. luteobubalina* and *P. microcarpus* were labelled with ^{13}C by growing the fungi on modified half-strength MMN agar media with 1 g/L of 99% $^{13}C_6$-glucose (Cambridge Isotope Laboratories, Inc.) for one month. An unlabelled control was also prepared. The fungal cultures were then transferred to half-strength MMN media (without glucose) for 3 d, followed by pre-symbiotic interaction with *E. grandis* seedlings for 24 h as described above. Root tip samples and fungal mycelia were collected and snap-frozen in liquid N_2, and subsequently stored in -80 °C freezer until extraction and metabolite analysis by Metabolomics Australia at the University of Melbourne. Untargeted metabolite profiling, threitol ^{13}C isotope enrichment analysis, as well as targeted quantitation of threitol were performed as described in Roessner *et al.* (2001), Nanchen,

Fuhrer & Sauer (2007) and Dias *et al.* (2015) respectively. Detailed procedures can be found in Supplementary Materials and Methods.

Threitol treatment and microbial infection assay

To identify the impact of D-threitol on the rate of microbial infection, one-month-old mycelia of *A. luteobubalina,* one-week-old hyphae of *Ph. cinnamomi,* or two-week-old mycelia of *P. microcarpus* isolate SI-14 were placed directly onto *E. grandis* roots on three types of half-strength MMN agar media with different D-threitol concentrations – 0 ppm, 0.3 ppm and 12 ppm, and co-cultured for 14 d in a growth chamber set at the growth conditions described above. These D-threitol concentrations were chosen based the quantified ranges of the metabolite in the roots of *E. grandis* across all of our experiments. Sterile *E. grandis* seedlings monoculture growing on media of the same threitol concentration was set up alongside as a negative control. After 14 d, the lateral roots were observed under a stereoscope and degree of infection/colonization were counted manually for *E. grandis* seedlings. Infection for the two pathogens was classified as the percentage of root lesions caused by either *A. luteobubalina* or *Ph. cinnamomi* divided by the total number of lateral roots in contact with fungal mycelium. For the mutualistic fungus *P. microcarpus* isolate SI-14, the percentage of colonized root tips was compared between each treatment.

Electrolyte Leakage

As a secondary means to quantify damage to the roots caused by *A. luteobubalina* over time, we measured electrolyte leakage of infected roots across the timecourse of colonization (i.e. from pre-contact through 2 weeks post-contact). For these assays, 2-4 lateral roots in contact with *A. luteobubalina* were excised and placed in 3 mL of Milli-Q water and left to incubate at 25^{o}C for 1 hour. After this incubation, the conductivity of the water was measured using a conductivity meter. The samples were then boiled at 95^{o}C for one hour followed by cooling of the sample back to 25^{o}C. Following temperature equilibration, conductivity was again measured and the percentage of the first reading versus the second reading was recorded. An average of four biological replicates were performed per data point.

RNA extraction and real-time quantitative PCR (RT-qPCR) assay

E. grandis seedlings were transferred onto half-strength MMN agar media supplemented with 0 ppm or 12 ppm D-threitol. After 24 hours, the plant roots were harvested and three biological replicates from each condition were immediately frozen in liquid nitrogen. RNA was extracted from the roots with the Bioline Isolate II miRNA extraction kit. Extracted RNA was used as a template for cDNA synthesis using the Bioline SensiFAST cDNA synthesis kit. RT-qPCR analysis was conducted on a BioRad CFX96 Touch RT-PCR cycler using the Bioline SensiFAST SYBR No-ROX kit. Log_2 fold change of gene expression of 12 ppm D-threitol treated roots as compared to control roots (0 ppm D-threitol) was calculated for the closest *E. grandis* homologues to known Arabidopsis hormone responsive genes: ABI3 (*Eucgr.H00815*), PIN1 (*Eucgr.K02271*), PIN2 (*Eucgr.C00078*), PIN3 (*Eucgr.B02902*), ARR16 (*Eucgr.G03141*), ARR6 (*Eucgr.B02571*), GA3ox1 (*Eucgr.F02568*), Myc2 (*Eucgr.E00277*) and VSP2 (*Eucgr.J02927*). RT-qPCR gene expression results were normalized using *Eucgr.C00350* and *Eucgr.B03031* as control genes. Primers used in the RT-qPCR assays are listed in the Table S2. To understand if the impact of D-threitol on the transcriptomic expression of these hormone-responsive genes was specific to this compound or if it was a general response to different sugar compounds, we also exposed a second set of *E. grandis* seedlings to the sugar myo-inositol at either 0 or 25 ppm for 24 hr. RNA was then extracted from these root systems, followed by cDNA synthesis and RT-qPCR performed on the same genes as above.

Results

Metabolite responses of *E. grandis* root tips during pre-symbiosis with *A. luteobubalina*

With GC-MS based untargeted metabolite profiling, a total of 117 metabolites were detected in *E. grandis* root tips when grown axenically, including 67 identifiable metabolites and 50 unknown metabolites (Table S3). After 24 h of pre-symbiotic 'indirect' contact with *A. luteobubalina* (i.e. plant and fungus were allowed to exchange diffusible signals but were physically separated by a membrane), 13 metabolites in *E. grandis* root tips were increased in abundance by more than two-fold. Apart from the unknown metabolites, the highly repressed root metabolite responses (fold change < 0.5) mostly belong to organic acids while the majority of highly enriched metabolites (fold change >2) are either sugars, sugar alcohols, amines or amino acids (Table 1; Full list of root metabolite responses towards *A. luteobubalina* are listed in Table S4). Mannitol, trehalose and threitol exhibited the most significant enrichment in *E. grandis* roots upon interaction with *A. luteobubalina* (Figure 1).

In order to understand which of the metabolite responses by *E. grandis* might be specific to contact with *A. luteobubalina,* we compared the *E. grandis* root metabolite responses described above with root metabolite responses to three other species of soil microbes commonly found in eucalypt forests in Australia, including the pathogenic oomycete *Phytophthora cinnamomi*, the commensal fungus *Suillus granulatus*; and the mutualistic ectomycorrhizal fungus, *Pisolithus microcarpus.* Principle component analysis (PCA) could not clearly separate the metabolite profiles of *E. grandis* root tips based on the microbial treatment (Figure 2), although permutational multivariate analysis of variance (PERMANOVA) indicated that the microbial treatments have significant effect on *E. grandis* root metabolite profiles ($p < 0.001$) whereby 20.58% of the variance in the metabolite responses can be explained by the different species of interacting microbes. Our results suggest that the overall metabolite responses of *E. grandis* roots are non-random and that certain root metabolites respond selectively towards different species of microbes.

Identification of *Armillaria*-specific metabolite responses in *E. grandis* root tips

To identify potential metabolites in *E. grandis* root tips that are specific to the interaction with *A. luteobubalina,* we made use of supervised machine learning (ML) models. Three ML

models – parallel random forest (parRF), sparse partial least square discriminative analysis (sPLSDA) and recursive partitioning and regression tree (rpart) – were trained with a subset of our metabolomics datasets (n = 36) to select important metabolite responses with high discriminative power that effectively split the root metabolite profiles into three groups: *A. luteobubalina*-treated group (*Armillaria*), untreated control group (Control) or other microbial treatments (Other). The accuracy of each of the three ML models were evaluated by cross-validation and fine-tuning of parameters to optimize their performance (Table 2). Prediction performance of each model was validated externally with a subset of the data (n = 12) that was previously ommitted for testing purposes (Table 2). With the AUROC index approaching 1, the performance testing result ensured a high confidence was accrued by our ML models.

The top ten important metabolite responses with the highest discriminative capacities were selected by each of the ML models (Figure 3a). Threonic acid, shikimic acid, threitol, lactic acid and inositol were commonly selected by the three MS models as the most important features for classification between *Armillaria*, Control and Other (Figure 3b). These three classification groupings could also be effectively separated when the responses of these important metabolites (threonic acid, shikimic acid, threitol, lactic acid and inositol) were considered together (Figure 3c). Threitol was the only discriminatory metabolite induced in the *Armillaria* group but not the other groups, while the other four aforementioned metabolite responses were repressed in *Armillaria* and Other in comparison to Control (Figure 3b). In a separate, targeted threitol quantitation analysis, we found that the quantity of D-threitol in root tips treated with *A. luteobubalina* was > 20 times higher than in root tips treated with *P. microcarpus* (Table 3). Given the strong explanatory value of threitol from these results, we wished to see if it was also present in *E. grandis* root tips when they were exposed to *Armillaria* in a system that more closely resembled a natural system (i.e. a soil-based system). We found that the enrichment of threitol was also observed in *E. grandis* root tips in this soil-based setup, but only when *Armillaria* was present (Figure 4).

Threitol detected in *E. grandis* root tips is largely of fungal origin

As we identified threitol to be significantly enriched on root tips when *E. grandis* interacts with *A. luteobubalina*, we sought to ascertain the origin of the threitol—whether it was a

fungal-derived metabolite that diffused to *E. grandis* roots, or a plant-synthesized metabolite. Therefore, we used an isotope labelling experimental setup to separate fungal-derived metabolites from plant-derived metabolites. By culturing *A. luteobubalina* on $^{13}C_6$-glucose spiked media for a month, we successfully enriched the proportion of ^{13}C-labelled threitol amongst all detectable isotopomers in the fungal mycelium, especially the $^{13}C_3$-threitol (derivative m/z = 220) and $^{13}C_4$-threitol (derivative m/z = 221) isotopomers (Figure 5). In these samples, ^{13}C-labelled isotopomers made up >55% of the total threitol abundance. In comparison, threitol detected when *A. luteobubalina* was grown on a substrate without ^{13}C enrichment, had a significantly lower percentage of ^{13}C-labelled isotopomers. When *E. grandis* root tips were placed into pre-symbiotic interaction with the ^{13}C-labelled *A. luteobubalina* mycelium, >40% of the total threitol recovered in the root tips was labelled with ^{13}C. These results demonstrate that *A. luteobubalina* is able to synthesize its own threitol and suggests that the majority of threitol detected *E. grandis* root tips during pre-symbiosis originated from *A. luteobubalina.*

Threitol production occurs prior to cell damage and under nutrient limited conditions

To gain insight into the production of D-threitol in *A. luteobubalina* during colonization of *E. grandis,* and to understand the uptake of this compound in plant tissues in relation to disease progression, we quantified D-threitol in both the fungal tissues and the plant root across colonization. As shown in Figure 6a, D-threitol was found in *A. luteobubalina* tissues at very high concentrations prior to contact when grown on glucose-free medium (i.e. timepoint '0') and for the first 24hrs of interaction between the two organisms be that pre-symbiotic interaction or direct plant-fungal contact. After 24hrs, fungal production of D-threitol began to significantly decrease until it reached its lowest detected concentration at 2 weeks post-contact with the host roots. In *E. grandis,* D-threitol root concentrations prior to the interaction with *A. luteobubalina* was near the detection limit of the machine (Figure 6a). These concentrations rose steadily through 24hrs of direct physical contact between the two organisms after which root-associated D-threitol decreased slightly, but maintained a higher than control level across fungal colonization of root tissues. It was interesting to note, based on the measurement of ion leakage as a proxy for cell damage, that while D-threitol accumulation in the fungus was at its highest, plant cell damage was at its lowest (Figure 6b).

It was not until the 1 week timepoint and beyond that we observed significant increases in cell damage.

As D-threitol concentrations in fungal tissues was highest prior to extensive root damage, and because D-threitol concentration tailed off while root damage increased, this led us to question whether D-threitol production may be controlled by fungal nutrition. To test this, we grew *A. luteobubalina* on different concentrations of PDA. We found that D-threitol was accumulated at high levels in fungal hyphae when grown on medium with lower levels of nutrition than the fungus grown on 1x PDA (Figure 6c). Therefore the nutritional status of the fungal colony impacts the synthesis of D-threitol.

External treatment with threitol enhances microbial infection of *E. grandis* root tips

Given the fact that *Armillaria* produces threitol during the early stages of colonization, which coincides with the establishment phase of the fungus within the root system rather than the root damage phase (Figure 6A,B), we evaluated the effect of increased threitol levels upon the colonization ability of *A. luteobubalina* when in contact with *E. grandis* roots. Exogenous application of even very low levels of threitol enhanced root lesions caused by *A. luteobubalina;* a significant increase of ~10% and 25% by threitol treatment of 0.3 ppm and 12 ppm, respectively, was observed (Figure 7a). To understand if this phenomenon was specific to *A. luteobubalina* colonization, or if the impact were more general, we also tested the impact of exogenous D-threitol application on the colonization by either *Ph. cinnamomi* or of *P. microcarpus.* We found that lesion development of roots colonized by *Ph. cinnamomi* was increased significantly when low amounts of D-threitol were supplied, but that this effect was reduced at higher levels of D-threitol (Figure 7b). Colonization of roots by the mutualistic fungus *P. microcarpus* was significantly enhanced at both levels of D-threitol tested (Figure 7c). Therefore, this metabolite signal can improve general microbial colonization of root tissues, although not as strongly as the impact on *A. luteobubalina* disease expression.

External treatment with threitol alters transcription of hormone-responsive genes

As plant hormones are closely tied to colonization success of fungi (Chanclud & Morel 2016), we sought to examine the transcriptional changes of a selection of hormone-responsive marker genes in *E. grandis* by quantitative real-time PCR (qRT-PCR; Sarnowska *et al.* 2016). As shown in Figure 8a, threitol treatment significantly induced expression of all tested marker genes responsive to phytohormones including gibberellins (GA), jasmonic acid (JA), cytokinin (CK), auxin and abscisic acid (ABA). This was a surprising result given the fact that some of these pathways act in an antagonistic manner to each other. We, therefore, tested another one of the discriminatory metabolites from our profiling described above, myo-inositol, to determine if this response was just a stress response. We exposed the *E. grandis* root system to myo-inositol as we did for D-threitol and analysed expression of these same hormone responsive genes. In general, myo-inositol did not have any effect on the expression level of these genes with the exception of PIN2 (Figure 8b). Therefore, other metabolites found to be altered during the pre-symbiotic stage of *A. luteobubalina* disease progression have different impacts on plant signalling pathways.

Discussion

The metabolic regulation during plant-microbe interactions could be crucial in determining the outcome of the interaction ((Buee, Rossignol, Jauneau, Ranjeva & Bécard 2000; Akiyama, Matsuzaki & Hayashi 2005; Steinkellner *et al.* 2007; Stuttmann *et al.* 2011; Lahrmann *et al.* 2013; Tschaplinski *et al.* 2014). *Armillaria* root rot is not only a widespread eucalypt tree disease endemic to Australia, but also a promiscuous root disease infecting numerous species of forest trees and crops worldwide (Baumgartner, Coetzee & Hoffmeister 2011). The *Armillaria* enzymatic activities contributing to its pathogenicity, as well as the plant metabolite responses towards *Armillaria* post-infection have previously been reported (Isidorov *et al.* 2008; Ross-Davis *et al.* 2013). However, our understanding on the *in plantae* molecular pathways initiating the *Armillaria*-plant interaction is still being developed and knowledge of specific metabolite profiles characteristic of *A. luteobubalina* pathogenicity are needed. In this study, we have demonstrated metabolite responses in eucalypt root tips as early as 24 h after pre-symbiotic interaction with *A. luteobubalina*. Mannitol, threitol, and trehalose appear to be among the most significantly enriched metabolites in *A. luteobubalina*-treated roots. While the role of threitol in plant-fungal interaction has not yet been reported, both mannitol and trehalose synthesis are known biotic stress responses of plants towards fungal attack (Fernandez, Béthencourt, Quero, Sangwan & Clément 2010; Patel & Williamson 2016). Our findings suggest that these previously described metabolite responses of a plant host in response to fungal pathogens may be detectable after even very short periods of interaction with the pathogen, and that such regulation could be triggered solely by the exchange of metabolite signals without the need of physical contact.

Beyond their role in pathogenicity, metabolites have emerged as effective measures of plant performance and as biomarkers of disease during plant-microbe interactions (Sankaran, Mishra, Ehsani & Davis 2010; Fernandez *et al.* 2016). A good biomarker should achieve both high sensitivity and specificity for robust indication of the plant disease (Nagana Gowda & Raftery 2013). Studying the specificity of plant metabolite responses could thus benefit both our basic knowledge of *Armillaria* disease and also the development of biomarkers for its early detection. In this study, not only have we identified the early metabolite responses of *E. grandis* towards *A. luteobubalina* prior to infection, but these metabolite profiles were also compared with roots exposed to representatives of fungi from other lifestyles—mutualist (*P.*

microcarpus), 'commensalist' (*S. granulatus*) and hemi-biotrophic pathogen (*Ph. cinnamomi*) under the exact same conditions. Our results showed that the overall metabolite profiles of eucalypt roots after different microbial pre-symbiotic treatment was highly-overlapping, suggesting that there are common innate metabolite responses common to this very early stage of interaction regardless of the microbial species present. This observation is aligned with a study by Müller *et al.* (2013), which showed a large number of common volatile organic compounds emitted by both ectomycorrhizal fungi, pathogenic fungi and saprophytic fungi. To separate metabolite responses specific towards *A. luteobubalina* from common responses towards other microbial species, we employed an emerging tool for selection of important features in metabolomic studies –machine learning models (Poezevara *et al.* 2017; Shiokawa, Date & Kikuchi 2018). The three ML models used in this study were able to identify a panel of important features that differentiate root metabolite responses of the *Armillaria* interaction from other microbial interactions or the axenically grown control plant. We have selected threitol among the important features for further characterization as it is strongly induced in the *Armillaria* interaction. It is possible that additional untargeted metabolomic methods (e.g. LC-MS/MS) would identify further life-style or fungal-specific metabolite signals, but our work stands as a proof of concept that we can use even the simplified approach of standard GC-MS analysis for identifying specific metabolites that are linked to root colonization by a specific pathogen. Given that our comparative approach has taken the interaction of a host with microial species of other lifestyles into consideration, these current results indicate that threitol is a promising biomarker specific for *Armillaria* infection of *E. grandis* roots.

Threitol, a four-carbon sugar alcohol, has been detected in plant species such as *Nicotiana tabacum* and *Coffea arabica*, as well as in mycelia of *Armillaria* fungal species (Birkinshaw, Stickings & Tessier 1948; Martins, Araújo, Tohge, Fernie & DaMatta 2014; Hacham, Matityahu & Amir 2017). Hence, it was unclear whether the threitol detected in the *E. grandis* roots with the current study was derived from the fungal pathogen or the *E. grandis* itself. By determining the isotopic composition of threitol in *E. grandis* root tissue after interaction with ^{13}C-labelled *A. luteobubalina*, we identified that threitol detected in root tissues were ^{13}C-enriched—meaning that it is chiefly secreted by *A. luteobubalina* and translocated to *E. grandis* root tissues. This conclusion was further reinforced when comparing the relative concentration differences of D-threitol in between *A. luteobubalina*

and *E. grandis* across all of the colonization timecourse (Figure 6). Specifically, D-threitol levels in the roots followed fungal production levels, albeit at a lower concentration than in fungal tissues. It is also interesting to note that fungal production of D-threitol may be nutritionally regulated. In both culturing conditions, and during the stage when *A. luteobubalina* would be recovering nutrients from its host (i.e. >48hrs when ion leakage increases) we observe that D-threitol production decreases. Therefore, this is not only a signal produced by *A. luteobubalina*, but it is perhaps also related to enhancing nutrient acquisition by the fungus.

The function and metabolic pathway of threitol in either plants or fungi remain obscure despite being a natural product of both. Therefore, it is currently impossible to follow the transcriptomic expression patterns of threitol-related biosynthetic genes nor to make fungal mutants that produce less threitol. Threitol was found to be a derivative of sorbose in plants (McComb & Rendig 1963), a stereoisomer of erythritol in *Armillaria mellea* (Birkinshaw *et al.* 1948), and a precursor of erythrulose and erythrose in bacteria *Mycobacterium smegmatis* (Huang *et al.* 2015). The effect of fungal-derived threitol on plant roots has hitherto been undescribed. We have tested the effect of threitol on hormonal responses and microbial colonization in *E. grandis*. Our findings indicate induced expression of hormone-responsive genes in roots towards gibberellins, jasmonic acid, cytokinin, auxin and abscisic acid upon threitol treatment, an effect that was not observed when myo-inositol, one of the other *Armillaria*-specific metabolites was also exposed to *E. grandis* roots. In spite of its large impact of a wide range of hormonal pathways in the plant, colonization of *A. luteobubalina* appears to be favored by exogenous threitol treatment. This colonization promotion was also observed to a lesser extent when *E. grandis* was placed into contact with either *Ph. cinnamomi* or *P. microcarpus.* These results suggest that while threitol may be produced by *A. luteobubalina* to foster colonization, this metabolite may alter plant immunity in general way that can benefit more than just *Armillaria* colonization. More research on the specific mechanism of threitol's action during plant-microbe interactions will be necessary in future.

Our study has advanced our understanding of the pre-symbiotic metabolite regulation in *E. grandis* prior to infection by *A. luteobubalina*. We identified threitol enrichment as an important early stage metabolite in the *Armillaria*-induced response and highlighted the

519 potential of threitol as a biomarker for *Armillaria* disease detection. In addition, our study
520 provides insight into the promotional effect of threitol on root colonization by varying
521 microbes in *E. grandis*. Given that *Armillaria* species are found in major forest ecosystems
522 globally, further investigation should follow to better our understanding of the role of their
523 metabolites in pathogenicity and soil ecology.

524

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Conflict of interest

The authors declare that they have no conflict of interest.

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667 **Tables:**

668 Table 1- The highly-regulated metabolite responses in *E. grandis* root tips after 24 h pre-
669 symbiotic interaction with *A. luteobubalina*

Metabolite	Metabolite class	Mean fold change[†]	p-value
Induced by *A. luteobubalina*			
Threitol	sugars and sugar alcohols	18.80	0.01*
Tartaric acid	organic acids	13.29	0.09
Trehalose	sugars and sugar alcohols	11.29	0.02*
Mannitol	sugars and sugar alcohols	8.26	0.02*
Unknown_37 (mz = 231, rt = 20.0801)	unclassified	5.55	0.01*
Unknown_50 (mz = 357, rt = 25.0806)	unclassified	2.96	0.12
Unknown_34 (mz = 246, rt = 19.6291)	unclassified	2.29	0.30
Ethanolamine	amino acids and amines	2.27	0.09
Proline	amino acids and amines	2.22	0.16
Unknown_28 (mz = 129, rt = 18.3399)	unclassified	2.22	0.08
Phosphoric acid	other	2.13	0.37
Unknown_52 (mz =333, rt = 25.2714)	unclassified	2.11	0.05
Unknown_48 (mz = 333, rt = 24.8404)	unclassified	2.08	0.04*
Repressed by *A. luteobubalina*			
Glyceric acid	organic acids	0.41	0.00*
Unknown_49 (mz = 366, rt = 24.9799)	unclassified	0.41	0.12
Gulonic acid	organic acids	0.41	0.03*
Malic acid	organic acids	0.41	0.04*
Unknown_65 (mz = 446, rt = 28.4172)	unclassified	0.37	0.02*
Unknown_13 (mz = 173, rt = 12.4636)	unclassified	0.37	0.01*
Unknown_35 (mz = 333, rt = 19.7161)	unclassified	0.35	0.01*
Oxalic acid	organic acids	0.32	0.00*
Unknown_26 (mz = 275, rt = 18.1341)	unclassified	0.29	0.08
Shikimic acid	organic acids	0.28	0.00*
Unknown_20 (mz = 159, rt = 16.6234)	unclassified	0.26	0.05*
Pyroglutamic acid	amino acids and amines	0.20	0.00*
Lactic acid	organic acids	0.14	0.08
Threonic acid	organic acids	0.12	0.00*

670 [†] Fold change is calculated in relation to un-inoculated control *E. grandis* root tips.

671 * p-value < 0.05

672

673 Table 2- Performance index of the machine learning models used to select potential

674 biomarkers for *Armillaria* infection in *E. grandis*

Machine learning model	**Optimized parameters**	**Performance index**			**Prediction performance index**
		RMSE†	R^2	Q^2	AUROC‡
RF	mtry = 44	0.1965	0.9605	n.a.	1
rpart	cp = 0.1974	0.1373	0.9445	n.a.	0.9815
sPLSDA	keepX = 4, 4, 5; ncomp = 3	n.a.	0.9064	0.5493	0.8333

675

676 †RMSE = Root Mean Square Error

677 ‡AUROC = Area Under ROC (Receiver operating characteristic)

678 n.a. = not applicable

679 Table 3- Unlabelled D-threitol quantitated with triple quadrupole GC-MS

Sample	**Unlabelled D-threitol measured quantity (pmole/mg; mean ± SD)**
Root tips after 24 h pre-contact with *A. luteobubalina* growing in $^{12}C_6$-glucose media	126.3 ± 14.9
Root tips after 24 h pre-contact with *A. luteobubalina* growing in $^{13}C_6$-glucose media	43.4 ± 12.6
Root tips after 24 h pre-contact with *Pisolithus microcarpus* growing in $^{13}C_6$-glucose media	2.4 ± 2.8 †

680 † D-threitol was measured to be below range for quantitation but within detection limit

Figure legends:

Figure 1: Volcano plot shows differential metabolite responses of *E. grandis* root tips towards *A. luteobubalina* pre-symbiotic interaction (n = 8) in comparison to untreated control root tips (n = 4). The x-axis and y-axis explain the $\log_2$-transformed fold change and the significance of the fold change in form of $-\log_{10}$ p-value, respectively. Each point represents a type of metabolite detected by GC-MS untargeted metabolite profiling, with the colour of the points represent the classification of the metabolites. Significantly differential metabolite responses ($|\log_2\text{fold change}| > 2$ and p-value < 0.05) are labelled in the plot.

Figure 2: Scatter plot matrix demonstrates the dispersion of overall metabolite profiles for *E. grandis* root tips under pre-symbiotic interaction with five distinct microbial species. The plot describes the correlation of the first four principle components (PCs) of the PCA. Each point represents the metabolite profile of a *E. grandis* root tips sample, with the color representing a different microbial treatment.

Figure 3: (a) The variable importance of the top-ten metabolite responses selected by three MS models. The variable importance is an indicator of the predictive power of the metabolite responses in discriminating between the three classifiers: *A. luteobubalina*-treated roots (Armi), untreated control roots (Ctrl) and roots treated with other microbial species (Other). (b-c) The boxplot and scatter matrix plot showing the normalized metabolite responses of threonic acid, lactic acid, threitol, shikimic acid and inositol across three classification groups. These five metabolite responses were commonly selected by all three MS models with the best predictive powers.

Figure 4: The threitol response of root tips towards *Armillaria* in pot soil-based sample in comparison to mock-inoculated control condition. The threitol response is normalized by dividing the detected peak corresponding to threitol by the weight of root tip samples, followed by log-transformation and auto-scaling. The difference in threitol response is significant with p-value = 0.031.

Figure 5: Distribution of different isotopomers of threitol detected across a set of *A. luteobubalina* fungal mycelium samples (FM) and the interacting root tip samples (RT) in labelled and unlabeled control condition. The proportion of each isotopomer of threitol is calculated by dividing the detected intensity with the combined intensities of all detectable isotopomers. The shade of grey represent different isotopomers of derivatized threitol with distinct m/z values : unlabeled threitol (m/z = 217), $^{13}C_1$-threitol (m/z = 218), $^{13}C_2$-threitol (m/z = 219), $^{13}C_3$-threitol (m/z = 220) and $^{13}C_4$-threitol (m/z = 221).

Figure 6: Quantification of threitol level (a) and cell damages as represented in form of electrolytes leakage (b) in *E. grandis* root tissues (black line) and in *A. luteobubalina* fungal mycelia tissues (grey line) over the timecourse of interaction. Threitol levels (ppm) are expressed as means ± standard error (SE). Different letters indicate significant differences (p-value < 0.05) among different time points. (c) Quantification of threitol level in *A. luteobubalina* fungal mycelia grown in PDA media of different strength. Asterisks indicate statistically significant differences (*p*-value < 0.001, one-way ANOVA).

Figure 7: Effect of threitol enrichment at 0.3ppm and 12ppm levels on the interaction of *E. grandis* with different microbes. The bar-graphs depicts the percentage of root lesion caused by *A. luteobubalina* (a) and *Ph.* cinnamomi (b), as well as the percentage of root colonization by *P. microcarpus* (c). Data points are means ± SE. Different letters indicate significant differences (p-value < 0.05) among different threitol levels.

Figure 8: Fold change corresponding to the expression of nine marker genes responsive towards different hormones (shown in bracket) in *E. grandis* roots after 1 d exposure to threitol (a) and to inositol (b). Fold changes of these genes are $\log_2$-transformed and shown in comparison to 0ppm control condition. Data points are means ± SE. Asterisk (*) above the bars indicate the significance of the gene expression changes in relation to the 0 ppm control condition (*p-value < 0.05, **p-value < 0.01, ***p-value < 0.001).

Additional Files:

Supplementary Materials and Methods: This document details the analytical procedures for Untargeted metabolite profiling, ^{13}C enrichment analysis as well as targeted quantitation of threitol in samples used in this study.

Figure S1: Schematic diagram of the workflow for the machine learning models used in this study for selecting the important and specific metabolite responses for *A. luteobubalina* in *E. grandis* roots during pre-symbiotic interaction. parRF = parallel random forest; rpart = recursive partitioning; sPLSDA = sparse partial least square discriminative analysis.

Table S1: Isolates of fungi and oomycete, and their respective growth medium used in this study.

Table S2: Primer sequences used in the RT-qPCR assay.

Table S3: Metabolite profiling data matrix containing the relative metabolite responses of *E. grandis* roots after pre-symbiotic interaction with different species of microbes.

Table S4: Root metabolite responses after 24 h pre-symbiotic interaction with *A. luteobubalina.* The fold-change and the *p*-value of each metabolite response, as well as their metabolite classes are provided in the table.