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1	Chytrid rhizoid mo	orphogenesis is adaptive and resembles hyphal development
2	'higher' fungi.	
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4	Davis Laundon ^{1,2} , N	lathan Chrismas ^{1,3} , Glen Wheeler ¹ & Michael Cunliffe ^{1,4}
5		
6	¹ Marine Biological Association of the UK, The Laboratory, Citadel Hill, Plymouth, UK	
7	² School of Environmental Sciences, University of East Anglia, Norwich, UK	
8	³ School of Geographical Sciences, University of Bristol, Bristol, UK	
9	⁴ School of Biologica	I and Marine Sciences, University of Plymouth, Plymouth, UK
10		
11	Correspondence:	Michael Cunliffe
12		Marine Biological Association of the United Kingdom,
13		The Laboratory, Citadel Hill, Plymouth, PL1 2PB, UK.
14		E: micnli@mba.ac.uk
15		T: +44 (0)1752 426328
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23 Abstract

24 Fungi are major components of the Earth's biosphere [1], sustaining many critical ecosystem 25 processes [2, 3]. Key to fungal prominence is their characteristic cell biology, our 26 understanding of which has been principally based on 'higher' dikaryan hyphal and yeast 27 forms [4-6]. The early-diverging Chytridiomycota (chytrids) are ecologically important [2, 7, 8] 28 and a significant component of fungal diversity [9-11], yet their cell biology remains poorly 29 understood. Unlike dikaryan hyphae, chytrids typically attach to substrates and feed 30 osmotrophically via anucleate rhizoids [12]. The evolution of fungal hyphae appears to have 31 occurred from lineages exhibiting rhizoidal growth [13] and it has been hypothesised that a 32 rhizoid-like structure was the precursor to multicellular hyphae and mycelial feeding in fungi 33 [14]. Here we show in a unicellular chytrid, *Rhizoclosmatium globosum*, that rhizoid 34 development has equivalent features to dikarvan hyphae and is adaptive to resource 35 availability. Rhizoid morphogenesis exhibits analogous properties with growth in hyphal 36 forms, including tip production, branching and decreasing fractal geometry towards the 37 growing edge, and is controlled by β -glucan-dependent cell wall synthesis and actin 38 polymerisation. Chytrid rhizoids from individual cells also demonstrate adaptive 39 morphological plasticity in response to substrate availability, developing a searching 40 phenotype when carbon starved and exhibiting spatial differentiation when interacting with 41 particulate substrates. Our results show striking similarities between unicellular early-42 diverging and dikaryan fungi, providing insights into chytrid cell biology, ecological 43 prevalence and fungal evolution. We demonstrate that the sophisticated cell biology and 44 developmental plasticity previously considered characteristic of hyphal fungi are shared 45 more widely across the Kingdom Fungi and therefore could be conserved from their most 46 recent common ancestor.

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48

49 Introduction

50 The phylum Chytridiomycota (chytrids) diverged approximately 750 million years ago and, 51 with the Blastocladiomycota, formed a critical evolutionary transition in the Kingdom Fungi 52 dedicated to osmotrophy and the establishment of the chitin-containing cell wall [10]. 407-53 million-year-old chytrid fossils from the Devonian Rhynie Chert deposit show chytrids 54 physically interacting with substrates via rhizoids in a comparative way to extant taxa [15]. 55 Rhizoids play key roles in chytrid ecological function, in terms of both attachment to 56 substrates and osmotrophic feeding [10, 12]. Yet surprisingly, given the importance of 57 rhizoids in chytrid ecology, there remains a lack of understanding of chytrid rhizoid biology. 58 including potential similarities with the functionally analogous hyphae in other fungi. 59 While both rhizoids and hyphae are polar, elongated and bifurcating structures, 60 rhizoid feeding structures are a basal condition within the true fungi (Eumycota), and the 61 dikaryan mycelium composed of multicellular septate hyphae is highly derived (Figure 1A 62 and B). Hyphal cell types are observed outside of the Eumycota, such as within the 63 Oomycota, however the origin of fungal hyphae within the Eumycota was independent [13, 64 16] and has not been reported in their closest relatives the Holozoans (animals, 65 choanoflagellates and their kin). Comparative genomics has indicated that hyphae originated 66 within the Chytridiomycota-Blastocladiomycota-Zoopagomycota nodes of the fungal tree 67 [16], and is supported by fossil Blastocladiomycota and extant Monoblepharidomycetes 68 having hyphae [13, 17]. However, even though rhizoids have been considered precursory to 69 hyphae [14], comparisons between rhizoid and hyphal developmental biology have not yet 70 been made. 71 R. globosum JEL800 is a monocentric eucarpic chytrid, with extensive anucleate thin 72 rhizoids (230.51 ± 62.40 nm in width; Supplementary Figures 1 and 2) and an archetypal 73 chytrid lifecycle (Figure 1C). With an available sequenced genome [18], easy laboratory 74 culture and amenability to live cell imaging (this study), R. globosum represents a promising

new model organism to investigate the cell biology of rhizoid-bearing, early-diverging fungi.

76 To study the developing rhizoid system for morphometric analyses, we established a live cell

3D/4D confocal microscopy approach in combination with neuron tracing software to 3D
reconstruct developing cells (Figure 1D; Supplementary Figures 3 and 4). From these
reconstructions, we were able to generate a series of cell morphometrics adapted from
neuronal biology to describe and quantify rhizoid development (Supplementary Figure 5).

81

82 Results and Discussion

83 Chytrid rhizoid morphogenesis fundamentally resembles mycelial development

- 84 During rhizoid development we observed a continuous increase in rhizoid length (110.8 ±
- 85 24.4 μ m h⁻¹) ($n = 5, \pm$ SD) and the number of rhizoid tips (4.6 \pm 1.2 tips h⁻¹) (Figure 1E;
- 86 Supplementary Table 1; Supplementary Movies 1-5), with a continuous increase in the
- thallus surface area (21.1 \pm 5.2 μ m² h⁻¹), rhizoid bifurcations (4.2 \pm 1.0 bifurcations h⁻¹),

88 cover area $(2,235 \pm 170.8 \ \mu\text{m}^2 \ h^{-1})$ and maximum Euclidean distance $(5.4 \pm 0.1 \ \mu\text{m} \ h^{-1})$

89 (Supplementary Figure 6). The rhizoidal growth unit (RGU) (i.e. the distance between two

90 rhizoid compartments) increased continuously during the first 6 h of the development period

91 (i.e. cells became relatively less branched) before stabilising during the later phase of growth

92 (Figure 1E).

93 The RGU patterns that we report here for a unicellular non-hyphal fungus are 94 comparable to the hyphal growth units (HGU) recorded in multicellular hyphal fungi 95 (Supplementary Figure 7) [19]. Trinci (1974) assessed hyphal development in three major 96 fungal lineages (Ascomycota, Basidiomycota, Mucoromycota) and observed that the growth 97 patterns of major morphometric traits (HGU, total length and number of tips) were similar 98 across the studied taxa. When the data from our study are directly compared to that of Trinci 99 (1974), we see that the hyphal growth pattern is also analogous to the rhizoids of the early-100 diverging unicellular Chytridiomycota (Supplementary Figure 7).

In *R. globosum*, the local rhizoid bifurcation angle remained consistent at 81.4° ± 6.3
 after ~2 h (Supplementary Figure 6), suggesting the presence of a currently unknown control
 mechanism regulating rhizoid branching in chytrids. During rhizoid development, lateral
 branching was more frequent than apical branching (Figure 1F and G), as observed in

105 dikaryan hyphae [20]. Fractal analysis (fractal dimension = Db) of 24 h chytrid cells revealed 106 that rhizoids approximate a 2D biological fractal (Mean $Db = 1.51 \pm 0.24$), with rhizoids 107 relatively more fractal at the centre of the cell (Max Db = 1.69-2.19) and less fractal towards 108 the growing periphery (Min Db = 0.69-1.49) (Supplementary Figure 8). Similar patterns of 109 fractal organisation are also observed in hyphae-based mycelial colonies [21]. Together 110 these findings suggest that a form of apical dominance at the growing edge rhizoid tips may 111 suppress apical branching to maintain rhizoid network integrity as in dikaryan hyphae [22, 112 23]. 113 114 Cell wall and actin dynamics govern branching in chytrid rhizoids

115 Given the apparent hyphal-like properties of the chytrid cell, we sought a greater 116 understanding of the potential subcellular machinery underpinning rhizoid morphogenesis. 117 Chemical characterisation of the R. globosum rhizoid showed that the chitin-containing cell 118 wall and actin patches were located throughout the rhizoid (Figure 2A). As the cell wall and 119 actin control hyphal morphogenesis in dikaryan fungi [4-6], they were selected as targets for 120 chemical inhibition in the chytrid. Inhibition of cell wall β -1,3-glucan synthesis and actin 121 proliferation with caspofungin and cytochalasin B respectively induced a concentration-122 dependent decrease in the RGU and the development of atypical cells with hyperbranched 123 rhizoids (Figures 2B-D; Supplementary Table 2; Supplementary Movies 6-7). These effects 124 in *R. globosum* are similar to disruption of normal hyphal branching reported in *Aspergillus* 125 fumigatus (Ascomycota) in the presence of caspofungin [24], and in Neurospora crassa 126 (Ascomycota) in the presence of cytochalasins [25], suggesting that β -1,3-glucan-dependent 127 cell wall synthesis and actin dynamics also govern branching in chytrid rhizoids by 128 comparable processes.

In silico studies of fungal genomes have proposed that the Chytridiomycota
(represented by *Batrachochytrium dendrobatidis*) lack β-1,3-glucan synthase FSK1 gene
homologs [26-28], which is the target for caspofungin. Despite the absence of FKS1
homologues in chytrid genomes, guantification of glucans in *R. globosum* showed that they

are present (Figure 2E), with 58.3 \pm 7.6 % β -glucans and 41.6 \pm 7.6 % α -glucans of total glucans.

135 To identify putative β -glucan synthesis genes, we surveyed the *R. globosum* JEL800 136 genome and focused on glycosyltransferase family 2 (GT2) encoding genes, which include 137 typical glucan synthases in fungi. A total of 28 GT2 domains were found within 27 genes 138 (Figure 2F). Of these genes, 20 contained putative chitin synthase domains and many 139 contained additional domains involved in transcriptional regulation. Nine encode chitin 140 synthase 2 family proteins and 11 encode chitin synthase 1 family proteins (with two GT2 141 domains in ORY48846). No obvious genes for β -1,3-glucan or β -1,6-glucan synthese were 142 found within the genome, consistent with previous *B. dendrobatidis* studies [27, 28]. 143 However, the chitin synthase 2 gene ORY39038 included a putative SKN1 domain (Figure 144 2F), which has been implicated in β -1,6-glucan synthesis in the ascomycete yeasts 145 Saccharomyces cerevisiae [29] and Candida albicans [30]. These results indicate a yet 146 uncharacterised β-glucan-dependent cell wall production process in chytrids (also targeted 147 by caspofungin) that is not currently apparent using gene/genome level assessment and 148 warrants further study.

149

150 Chytrid rhizoids undergo adaptive development in response to carbon starvation

151 To examine whether chytrids are capable of modifying rhizoid development in response to 152 changes in resource availability, we exposed R. globosum to carbon starvation (i.e. 153 development in the absence of exogenous carbon). When provided with 10 mM N-acetyl-D-154 glucosamine (NAG) as an exogenous carbon source, the entire life cycle from zoospore to 155 sporulation was completed (Supplementary Movie 8). Carbon-starved cells did not produce 156 zoospores and cell growth stopped after 14-16 h (Supplementary Movie 9). However, using 157 only endogenous carbon (i.e. zoospore storage lipids) carbon starved cells underwent 158 substantially differential rhizoid development compared to cells from the exogenous carbon 159 replete conditions that we interpret to be an adaptive searching phenotype (Figure 3A and B; 160 Supplementary Table 4; Supplementary Movie 10). Under carbon starvation, R. globosum

161 cells invested less in thallus growth than in carbon replete conditions, with the development 162 of longer rhizoids with a greater maximum Euclidean distance (Figure 3C). Carbon starved 163 cells were also less branched, had wider bifurcation angles and subsequently covered a 164 larger surface area. These morphological changes in response to exogenous carbon 165 starvation (summarised in Figure 3B) suggest that individual chytrid cells are capable of 166 controlled reallocation of resources away from reproduction (i.e. the production of the 167 zoosporangium) and towards an extended modified rhizoidal structure indicative of a 168 resource searching phenotype. Exogenous carbon starvation has also been shown to be 169 associated with a decrease in branching in the multicellular dikarvan fungus Aspergillus 170 oryzae (Ascomycota) [31]. Branching zones in dikaryan mycelia are known to improve 171 colonisation of trophic substrates and feeding, while more linear 'exploring' zones search for 172 new resources [32].

173

174 Chytrids exhibit spatially differentiated rhizoids in response to patchy environments 175 In the natural environment, chytrids inhabit structurally complex niches made up of 176 heterologous substrates, such as algal cells [33], amphibian epidermises [34] and 177 recalcitrant particulate organic carbon [35]. R. globosum is a freshwater saprotrophic chytrid 178 that is typically associated with chitin-rich insect exuviae [36]. We therefore quantified rhizoid 179 growth of single cells growing on chitin microbeads as an experimental particulate substrate 180 (Figure 4A and B; Supplementary Movie 11). Initially, rhizoids grew along the outer surface 181 of the bead and were probably used primarily for anchorage to the substrate. Scanning 182 electron microscopy (SEM) showed that the rhizoids growing externally on the chitin particle 183 formed grooves on the bead parallel to the rhizoid axis (Supplementary Figure 1F and G). 184 suggesting extracellular enzymatic chitin degradation by the rhizoid on the outer surface. 185 Penetration of the bead occurred during the later stages of particle colonisation (Figure 4A; 186 Supplementary Movie 12). Branching inside the bead emanated from 'pioneer' rhizoids that 187 penetrated into the particle (Figure 4C).

188 Given the previous results of the searching rhizoid development in response to 189 carbon starvation, we created a patchy resource environment using the chitin microbeads 190 randomly distributed around individual developing cells in otherwise carbon-free media to 191 investigate how encountering a carbon source affected rhizoid morphology (Figure 4D; 192 Supplementary Movies 13-15). Particle-associated rhizoids were shorter than rhizoids not in 193 particle contact, were more branched (i.e. lower RGU), had a shorter maximum Euclidean 194 distance and covered a smaller area (Figure 4E). These simultaneous feeding and searching 195 modifications in individual cells linked to particle-associated and non-associated rhizoids 196 respectively are similar to the rhizoid morphometrics of the cells grown under carbon replete 197 and carbon deplete conditions previously discussed (Figure 4F and Figure 3B). The 198 simultaneous display of both rhizoid types in the same cell suggests a controlled spatial 199 regulation of branching and differentiation of labour within the individual anucleate rhizoidal 200 network. Functional division of labour is seen in multicellular mycelia fungi [32, 37], including 201 developing specialised branching structures for increased surface area and nutrient uptake 202 as in the plant symbiont mycorrhiza (Glomeromycota) [38]. Our observation of similar 203 complex development in a unicellular chytrid suggests that multicellularity is not a 204 prerequisite for adaptive spatial differentiation in fungi.

205

206 Conclusions

207 Appreciation for the ecological significance of chytrids as saprotrophs, parasites and 208 pathogens is greatly expanding. For example, chytrids are well-established plankton 209 parasites [8], responsible for the global-scale amphibian pandemic [7] and have recently 210 emerged as important components of the marine mycobiome [2]. The improved 211 understanding of chytrid rhizoid biology related to substrate attachment and feeding we 212 present here opens the door to a greater insight into the functional ecology of chytrids and 213 their ecological potency. From an evolutionary perspective, the early-diverging fungi are a 214 critical component of the eukaryotic tree of life [9, 39], including an origin of multicellularity 215 and the establishment of the archetypal fungal hyphal form, which is responsible in part, for

216 the subsequent colonisation of land by fungi, diversity expansion and interaction with plants 217 [10]. Our cell biology focused approach advances this developing paradigm by showing that 218 a representative monocentric, rhizoid-bearing (i.e. non-hyphal) chytrid displays hyphal-like 219 morphogenesis, with evidence that the cell structuring mechanisms underpinning chytrid 220 rhizoid development are equivalent to reciprocal mechanisms in dikaryan fungi. Perhaps our 221 key discovery is that the anucleate chytrid rhizoid shows considerable developmental 222 plasticity. R. alobosum is able to control rhizoid morphogenesis to produce a searching form 223 in response to carbon starvation and, from an individual cell, is capable of spatial 224 differentiation in adaptation to patchy substrate availability indicating functional division of 225 labour. The potential for convergent evolution aside, we conclude by parsimony from the 226 presence of analogous complex cell developmental features in an extant representative 227 chytrid and dikaryan fungi that adaptive rhizoids, or rhizoid-like structures, are precursory to 228 hyphae, and are a shared feature of their most recent common ancestor.

229

230 Methods

231 Culture and maintenance. For routine maintenance, Rhizoclosmatium globosum JEL800 232 was grown on PmTG agar [40]. Agar plugs were excised from established cultures using a 233 sterile scalpel, inverted onto new agar plates and incubated at 22 °C in the dark for 48 h. 234 Developed zoosporangia were sporulated by covering each plug with 100 µl dH₂O and 235 incubating at room temperature for 30 min. The released zoospores were distributed across 236 the agar surface by tilting, dried for 10 min in a laminar flow hood and incubated as above. 237 To harvest zoospores for experiments, plates were flooded with 1 ml dH₂O and the zoospore 238 suspension passed through a 10 µm cell strainer (pluriSelect) to remove mature thalli. 239 Zoospore density was quantified using a Sedgewick Raft Counter (Pyser SCGI) and a Leica 240 DM1000 (10 x objective) with cells fixed in 2% formaldehyde at a dilution of 1:1,000. 241 Zoospores were diluted to a working density of 6.6 x 10³ ml⁻¹ for all experiments. Because 242 PmTG is a complex medium, all experiments detailed below were conducted in Bold's Basal

Medium (BBM) supplemented with 1.89 mM ammonium sulfate and 500 μl.l⁻¹ F/2 vitamin
solution [41].

245

246 General cell imaging. To visualise the rhizoids, cell plasma membranes were labelled with 247 8.18 µM FM® 1-43 and imaged using a Zeiss LSM 510 Meta confocal laser scanning 248 microscope (CLSM) (Carl Zeiss) under a 40 x oil-immersion objective lens, with excitation by 249 a 488 nm Ar laser and emission at 500-530 nm. Z-stacks were acquired at 1 µm intervals. 250 For Scanning Electron Microscopy (SEM) of rhizoids growing along a 2D surface, culture 251 dishes were lined with EtOH-sterilised Aclar® disks and filled with 3 ml of BBM with 10 mM 252 NAG, before inoculation with zoospores and incubation for 24 h at 22 °C. For SEM of cells 253 growing on chitin beads, dishes were prepared as described below and were also inoculated 254 and incubated for 24 h. Following incubation, cells were fixed overnight in 2.5% 255 glutaraldehyde and then rinsed twice in 0.1 M cacodylate buffer (pH 7.2). Fixed samples 256 were dehydrated in a graded alcohol series (30%, 50%, 70%, 90%, 100%) with a 15 min 257 incubation period between each step. Cells were then dried in a Critical Point Drier (K850, 258 Quorum) and attached to SEM sample stubs using carbon infiltrated tabs prior to Cr sputter-259 coating using a sputter coating unit (Q150T, Quorum). Samples were imaged with a Field 260 Emission Gun Scanning Electron Microscope (JSM-7001F, JEOL) operating at 10 kV. For 261 Transmission Electron Microscopy (TEM), 24 h cells grown in suspension were fixed as 262 previously described. The samples were secondarily fixed with osmium tetroxide (1%, in 263 buffer pH 7.2, 0.1M) for 1 h, rinsed, and alcohol dehydrated as above. The alcohol was 264 replaced with agar low viscosity resin through a graded resin series (30%, 50%, 70%, 100%, 265 100%) with 12 h intervals between each step. Samples were transferred to beem capsules 266 and placed in an embedding oven at 60 °C overnight to enable resin polymerisation. The 267 resulting blocks were sectioned at 50 nm intervals with an ultramicrotome (Ultracut E, Leica) 268 using a diatome diamond knife. The sections were stained using a saturated solution of 269 uranyl acetate (for 15 min) and Reynold's lead citrate (15 min) before being examined using 270 a transmission electron microscope (JEM-1400, JEOL).

271

272 **4D rhizoid development.** Glass bottom dishes (n = 5) containing 3 ml BBM with 10 mM 273 NAG as the available carbon source were inoculated with 500 µl zoospore suspension. 274 Zoospores settled for 1h prior to imaging before z-stacks to 50 µm depth were acquired at 275 30 min time intervals for 10 h at 22 °C. Throughout the imaging duration, an optically clear 276 film permitting gas exchange covered the dish. Branching was counted manually from 277 maximum intensity projected z-stacks. To quantify rhizoid fractal dimensions, cells were 278 grown on glass bottom dishes for 24 h. Due to the large size of the 24 h cells, z-stacks were 279 stitched together in Fiji [42] from four individual stacks. Stitched stacks (n = 5) were 280 converted to maximum intensity projections, processed into binary masks by default 281 thresholding and denoised. Local Connected Fractal Dimension (LCFD) analysis was 282 conducted using default parameters on binary masks with the Fiji plugin FracLac [43]. 283

284 Rhizoid tracing and reconstruction. Z-stacks of rhizoids were imported into the neuron 285 reconstruction software NeuronStudio [44, 45] and adjusted for brightness and contrast. 286 Rhizoids were semi-automatically traced with the 'Build Neurite' function using the basal 287 point of the sporangium as the rhizoidal origin. Tracing used fixed intensity thresholds input 288 optimally for each image and rhizoids were manually curated and corrected by removing 289 tracing artefacts (e.g. correcting for loop-splitting). Cells were discarded during quality 290 control if the tracing was substandard, accounting for the occasional variation in sample size. 291 Cells grown for 24 h in BBM 10 mM NAG or on chitin beads were too dense to be manually 292 curated and therefore were automatically traced using dynamic thresholding with a minimum 293 neurite length of 2 µm, although due to their high-density tracings should be considered 294 imperfect. For 4D image stacks, the rhizoid was reconstructed in 3D at each 30 min interval. 295 For particle associated and non-associated rhizoids, traced rhizoid systems from individual 296 cells were manually split into their respective categories.

297 Rhizoids were exported as SWC file extensions [46] and morphometrically quantified 298 using the btmorph2 library [47] run with Python 3.6.5 implemented in Jupyter Notebook

299 4.4.0. Reconstructed rhizoids were visualised by converting the SWC files first to VTK files 300 using the swc2vtk Python script (Daisuke Miyamoto: github.com/ DaisukeMiyamoto 301 /swc2vtk/) and then to OBJ files using the 'Extract Surface' filter in ParaView [48]. OBJ files 302 were then imported into Blender (2.79), smoothed using automatic default parameters and 303 rendered for display. OBJ meshes were used for final display only and not analysis. To 304 visualise chitin beads, z-stacks were imported into the Fiji plugin TrakEM2 [49]. Chitin beads 305 were manually segmented, and 3D reconstructed by automatically merging traced features 306 along the z-axis. Meshes were then preliminarily smoothed in TrakEM2 and exported as 307 OBJ files into Blender for visualisation.

308

309 **Chemical characterisation of the rhizoid.** To label the cell wall and F-actin throughout the 310 rhizoid system, cells were grown for 24 h in 3 ml BBM with 10 mM NAG on glass bottom 311 dishes. The culture medium was aspirated from the cells, which were then washed three 312 times in 500 µl 1 x PBS (phosphate buffered saline). Cells were subsequently fixed for 1 h in 313 4% formaldehyde in 1 x PBS and then washed three times in 1 x PBS and once in PEM (100 314 mM PIPES (piperazine-N,N'-bis(2-ethanesulfonic acid)) buffer at pH 6.9, 1 mM EGTA 315 (ethylene glycol tetraacetic acid), and 0.1 mM MgSO₄). Fixed cells were stained with 1:50 316 rhodamine phalloidin in PEM for 30 min, washed three times in PEM, and finally stained with 317 5 µg/ml Texas Red-conjugated wheat germ agglutinin (WGA) in PEM for 30 min. Stained 318 cells were further washed three times in PEM and mounted under a glass coverslip with one 319 drop of ProLong[™] Gold Antifade Mountant (ThermoFisher). Cells were imaged using the same CLSM as described above with a 63 x oil immersion objective lens. F-Actin was 320 321 imaged by excitation with a 543 nm HeNe laser and emission at 535-590 nm, and the cell 322 wall by excitation with a 633 nm HeNe laser and emission at 650-710 nm. No dye controls 323 were run for each excitation/emission channel.

324

325 **Chemical inhibition of rhizoid growth.** Autoclaved glass coverslips (VWR) were placed in 326 a culture dish and submerged in 3 ml BBM with 10 mM NAG. Following 1 h of incubation to

327 allow normal zoospore settlement and germination, 1 ml of growth medium was removed 328 from the dish and 1 ml of poison-containing media was introduced. Caspofungin diacetate 329 (working concentration 1-50 μ M) was used to inhibit cell wall β -glucan synthesis and 330 cytochalasin B (working concentration 0.1-10 µM) was used to inhibit actin filament 331 formation. Cells were further incubated for 6 h, which was found to be sufficient to observe 332 phenotypic variation before being removed from the incubator and held at 4 °C prior to 333 imaging. Coverslips were removed from the dishes using EtOH-cleaned forceps and placed 334 cell-side down into a glass bottom dish containing 100 µl of membrane dye. 3D, as opposed 335 to 4D imaging, was chosen to allow more replication for statistical analysis. Three plates 336 were imaged in triplicate (n = 9) for each poison treatment and for solvent-only (i.e. no 337 poison) controls.

338

β-glucan quantification. *R. globosum* was grown to 250 ml in BBM with 10 mM NAG (n =5) for 7 d before harvesting by centrifugation at 4,700 rpm for 10 min in 50 ml aliquots and washed in 50 ml MilliQ H₂O. The cell pellet from each flask was processed for β-glucans in duplicate using a commercial β-Glucan assay (Yeast & Mushroom) (K-YBGL, Megazyme) following the manufacturer's protocol. A sample of shop-bought baker's yeast was used as a control. Glucans were quantified spectrophotometrically using a CLARIOstar® Plus microplate reader (BMG Labtech).

346

Identification of putative glucan synthases genes. All glycosyl transferase group 2 (GT2)
domain-containing proteins within the *R. globosum* genome were identified using the JGI
MycoCosm online portal. GT2 functional domains were identified using DELTA-BLAST [50]
and aligned with MAFFT [51]. Maximum Likelihood phylogenies were calculated with RAxML
[52] using the BLOSUM62 matrix and 100 bootstrap replicates and viewed in FigTree
(Andrew Rambaut: github.com/rambaut/figtree/). Overall protein architecture was displayed
using genoplotR [53].

354

355 **Carbon starvation and growth on chitin beads.** To guantify differential rhizoidal growth 356 under carbon replete and carbon deplete conditions, coverslips were placed in a culture dish 357 and submerged in 3 ml growth medium (either carbon-free BBM or BBM with 10 mM NAG). 358 Dishes were then inoculated with zoospores and incubated for either 1, 4, 7 or 24 h, with the 359 24 h cell z-stacks stitched as described in the fractal analysis. Three plates were also 360 imaged in triplicate for each treatment at each time point (n = 9). For both sets of 361 experiments, cells were imaged as per the chemical inhibition experiments above. 362 Chitin beads (New England Biolabs) were washed three times in carbon-free BBM 363 using a magnetic Eppendorf rack and suspended in carbon-free BBM at a working 364 concentration of 1:1,000 stock concentration. Glass bottom dishes containing 3 ml of the 365 diluted beads were inoculated with zoospores and incubated for either 1, 4, 7 or 24 h prior to 366 imaging. For imaging, the culture medium was appirated off and beads were submerged in 367 100 μ I FM® 1-43. Three plates were imaged in triplicate for each time point (n = 9). To 368 understand rhizoid development in a starved cell that had encountered a chitin bead, we 369 imaged cells that contacted a chitin bead following development along the glass bottom of 370 the dish.

371

372 **Statistical Analysis.** Rhizoid width was measured from TEM images (n = 25). The 373 comparison between apical and lateral branching was conducted using a Wilcoxon Rank 374 Sum test. Univariate differences in rhizoid morphometrics between experimental treatments 375 were evaluated using Welch's t-tests unless stated otherwise. Shapiro-Wilk and Levene's 376 tests were used to assess normality and homogeneity of variance respectively. If these 377 assumptions could not be met, then Wilcoxon Rank Sum was used as a nonparametric 378 alternative. Univariate morphometric differences between particle-associated and non-379 associated rhizoids were evaluated using a paired t-test. All data were analysed in RStudio 380 v1.1.456. [54]

381

382 Data availability

383 All data that support the findings of this study are freely available via the corresponding

- 384 author.
- 385

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399 Author Contributions

- 400 D.L. and M.C. conceived the study. D.L. conducted the laboratory work and data analysis.
- 401 N.C. analysed the *R. globosum* JEL800 genome. G.W. provided support with microscopy.
- 402 M.C. secured the funding. D.L. and M.C. critically assessed and interpreted the findings. D.L.
- 403 and M.C. wrote the manuscript, with the help of N.C. and G.W.
- 404

405 **Competing Interests**

406 The authors declare no competing interests

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540 **Figure Legends**

541 Figure 1 - Rhizoids are the basal feeding condition within the fungal kingdom and 542 their morphogenesis is similar to hyphal development. (A-B) Correlating the major 543 feeding types in fungi (A) to phylogeny (B) shows rhizoids to be the basal feeding condition 544 in the true fungi (Eumycota). Tree adapted from [11]. (C) R. globosum exhibits an archetypal 545 chytrid lifecycle. (D) Chytrid rhizoids were reconstructed using the neuron tracing workflow 546 outlined in Supplementary Figure 3. Example of a 3D reconstructed *R. globosum* rhizoid 547 system taken from a 10 h time series. Scale bar = 20 μ m. (E) Rhizoid growth trajectories for 548 4D confocal time series (n = 5, mean \pm S.E.M.) of rhizoidal growth unit, total length and 549 number of tips. (F) Apical and lateral branches occur in chytrid rhizoids. Apical branching 550 occurs when a branch is formed at the rhizoid tip parallel to the established rhizoidal axis. 551 Lateral branching occurs when a branch is formed distally to the rhizoidal tip, establishing a 552 new rhizoidal axis. (G) 4D confocal imaging (n = 5, mean \pm S.E.M.) revealed that lateral 553 branching dominates over apical branching *p < 0.05.

554

555 Figure 2 - Cell wall synthesis and actin dynamics govern rhizoid branching. (A)

556 Fluorescent labelling of cell wall and actin structures in 24 h R. globosum cells. The cell wall 557 and actin patches were found throughout the rhizoid. WGA = conjugated Wheat Germ 558 Agglutinin. Scale bar = $10 \,\mu m$. (B) Representative 3D reconstructions of 7 h R. *globosum* 559 cells following treatment with caspofungin diacetate and cytochalasin B at stated 560 concentrations to inhibit cell wall and actin filament biosynthesis respectively, relative to 561 solvent only controls. Scale bar = 20 µm (C) Application of caspofungin diacetate and 562 cytochalasin B resulted in a concentration-dependent decrease in the rhizoidal growth unit, 563 resulting in atypical hyperbranched rhizoids ($n \sim 9$, mean ± S.E.M.). n.s p > 0.05 (not 564 significant), p < 0.05, p < 0.01, p < 0.01, p < 0.01. This differential growth is diagrammatically 565 summarised in (D). (E) β -glucan concentration of R. globosum (n = 10) relative to a baker's 566 yeast control (n = 2). (F) Maximum likelihood phylogeny of GT2 domains (BcsA and WcaA 567 domains) within the *R. globosum* genome (midpoint rooting). Full architecture of each protein

is shown. Asterisk indicates the putative glucan synthesis protein ORY39038 containing aputative SKN1 domain.

570

571 Figure 3 - Chytrids are capable of adaptive rhizoid development under carbon

572 **starvation.** (A) Representative 3D reconstructions of *R. globosum* cells grown under carbon

573 replete or carbon deplete conditions at different timepoints. Scale bar = 20 μm. When

574 exposed to carbon starvation, chytrids are capable of differential adaptive growth to produce

575 a searching phenotype. This differential growth is summarised in (B). (C) Differential growth

576 trajectories of major morphometric traits between *R. globosum* cells ($n \sim 9$, mean \pm S.E.M.)

577 grown under carbon replete and carbon deplete conditions over time. n.s p > 0.05 (not

578 significant), **p* < 0.05, ***p* < 0.01, ****p* < 0.001

579

580 Figure 4 - Rhizoids associated with heterogenous particulate carbon exhibit spatial

581 differentiation (A) Representative 3D reconstructions of *R. globosum* cells (blue) growing 582 on chitin beads (beige) at different timepoints. Scale bar = $20 \,\mu m$. (B) Growth trajectories for 583 total rhizoid length and thallus surface area for *R. globosum* cells growing on chitin beads (*n* 584 \sim 9, mean ± S.E.M.). (C) Diagrammatic summary of *R. globosum* rhizoid development on 585 chitin beads. (D) Representative 3D reconstruction of a 24 h searching R. globosum cell 586 (blue) that has encountered a chitin bead (beige). The colour coded panel shows parts of the 587 rhizoid system in contact (green) and not in contact (blue) with the bead. Scale bar = $20 \,\mu m$. 588 (E) Comparison of rhizoids in contact or not in contact with the chitin bead (n = 8, mean ± 589 S.E.M.). (F) Diagrammatic summary of spatial differentiation in a starved, searching rhizoid 590 that has encountered a particulate carbon patch.

591

592 Supplementary Figure 1 - Scanning Electron Microscopy (SEM) images of *R*.

593 globosum rhizoids. (A-D) R. globosum cells grown on a 2D, inert surface (Aclar®) in NAG

594 supplemented media. (A) Shown are multiple thalli anchored to the surface by threadlike

rhizoids. (B) The spherical thallus of *R. globosum* is connected to the rhizoid system via an

apophysis (subsporangial swelling). (C) High-magnification image of the apophysis. (D) Rhizoids are branched and bifurcating structures that frequently overlap. The fusion of rhizoids (anastomoses) was never observed from SEM images. (E-G) Chytrid cells growing on chitin beads. (F-G) External rhizoids growing along the surface of the particle formed superficial lacerations (indicated by asterisks). a, apophysis; b, bifurcation; t, thallus. Scale bar (A,E) = 10 μ m. Scale bar (B-D, F-G) = 1 μ m.

602

Supplementary Figure 2 - Transmission Electron Microscopy (TEM) images of *R*. *globosum* rhizoids. (A-C) TEM images of the apophysis. The apophysis is not septated from the thallus and the two are connected by continuous cytoplasm (A-B), as are the apophysis and the rhizoid (C). (D-F) TEM images of the apophysis. The rhizoid is always

607 enveloped by a cell wall and no structure was observed to demarcate rhizoid branches at

bifurcation nodes (D). Although no formal subcellular organelles could be identified within the

609 rhizoid, a dense and complex endomembrane system permeated the entire system (E-F).

610 This suggested that the rhizoid is a dynamic organelle governed by high levels of trafficking

and endomembrane reorganisation. a, apohpysis; b, bifurcations; e, endomembrane; r,

612 rhizoid; w, cell wall. Asterisks mark the connection between the apophysis and the thallus.

613 Scale bar (A) = 2 μ m. Scale bar (B-F) = 200 nm.

614

615 **Supplementary Figure 3 - Neuron tracing was used to reconstruct and quantify chytrid**

616 **rhizoid development.** Flow-diagram protocol for the acquisition, reconstruction, analysis

617 and visualisation of *R. globosum* rhizoids based on neuron tracing.

618

619 Supplementary Figure 4 - 3D reconstructions of developing *R. globosum* rhizoids.

620 Total series of 3D reconstructed *R. globosum* rhizoids taken from 4D development

621 experiments. Scale bar = $20 \mu m$.

622

623	Supplementary Figure 5	- Chytrid rhizoids were	quantified using	g morphometric
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624 parameters adapted from neurobiology. Diagrammatic glossary of neuronal morphometric

- 625 parameters used to describe 3D reconstructed chytrid rhizoids from growth experiments.
- 626 Chytrids are represented by an aerial 2D diagram, as if from a z-stack maximum intensity
- 627 projection.
- 628

629 Supplementary Figure 6 - Development trajectories of major morphometric traits in *R*.

630 *globosum* rhizoids. Growth patterns of morphometric features for developing *R. globosum*

631 rhizoids taken from 4D microscopy experiments. Plateau in the z-axis depth occurs due

for growth outside of the designated experimental imaging field. Scale bar = $20 \,\mu m$.

633

634 **Supplementary Figure 7 - Development of chytrid rhizoids fundamentally resembles**

635 mycelial development in hyphal fungi. Comparison of the growth trajectories of the growth

636 unit, total length and number of tips of the rhizoids or hyphae in fungi from the Ascomycota,

637 Basidiomycota, Mucoromycota and Chytridiomycota. Data for Ascomycota, Basidiomycota

and Mucoromycota fungi are not from this study and are reproduced as new figures directlyfrom (Trinci, 1974).

Υ.

640

641 Supplementary Figure 8 - Fractal organisation of the chytrid rhizoid resembles that of

642 mycelial colonies. Processing and fractal analysis workflow for 24 h R. globosum cells.

643 Chytrid rhizoid systems become decreasingly fractal towards the growing edge. Final column644 images are pseudo-coloured by fractal dimension.

645

Supplementary Table 1 – Morphometric features of developing *R. globosum* rhizoids
 associated with Figure 1 E-G.

648

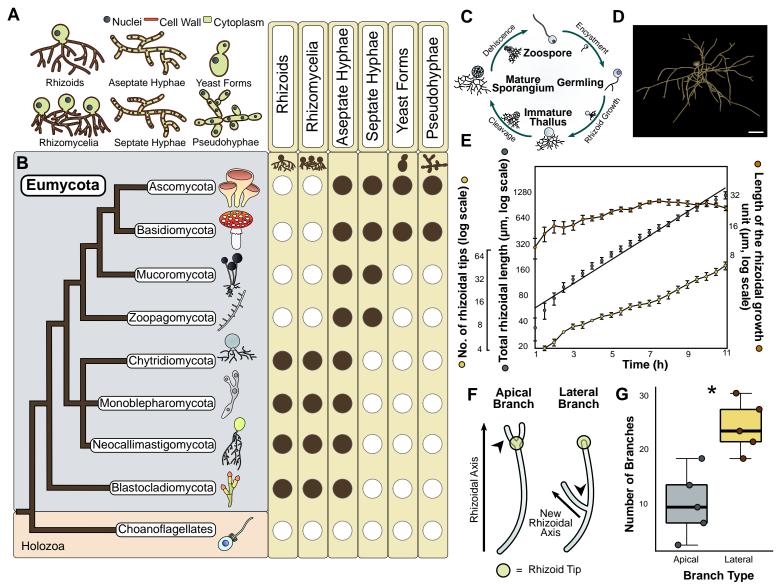
649 Supplementary Table 2 – Morphometric features and statistical comparisons of

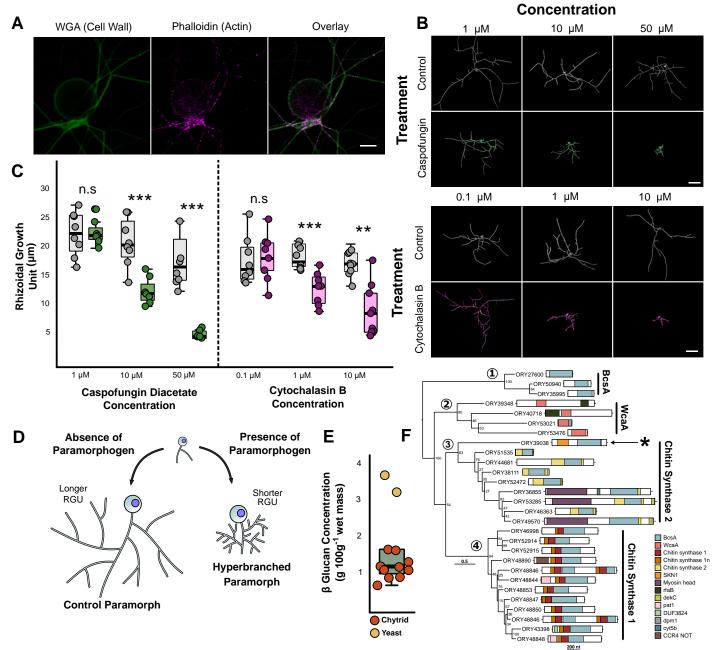
650 chemically inhibited *R. globosum* rhizoids, associated with Figure 2 B-C.

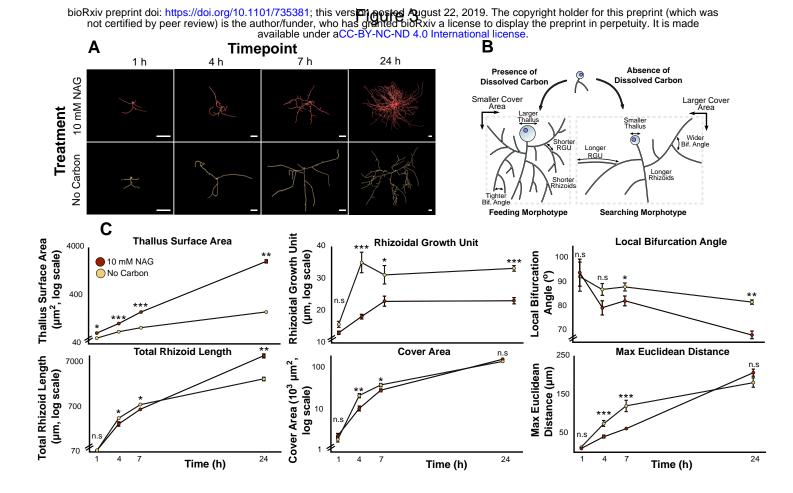
651	
652	Supplementary Table 3 – Morphometric features and statistical comparisons of <i>R</i> .
653	globosum rhizoids growing in carbon replete or deplete media, associated with Figure
654	3 A-C.
655	
656	Supplementary Table 4 – Morphometric features of <i>R. globosum</i> rhizoids growing on
657	chitin beads, associated with Figure 4 A-B.
658	
659	Supplementary Table 5 – Morphometric features and statistical comparisons of
660	searching <i>R. globosum</i> rhizoids encountering chitin beads, associated with Figure 4
661	D-E.
662	
663	Supplementary Movie 1 – 4D imaging of developing <i>R. globosum</i> rhizoids used for
664	quantifying morphometric growth trajectories (Replicate 1). Time in HH:MM
665	
666	Supplementary Movie 2 – 4D imaging of developing <i>R. globosum</i> rhizoids used for
667	quantifying morphometric growth trajectories (Replicate 2). Time in HH:MM
668	
669	Supplementary Movie 3 – 4D imaging of developing <i>R. globosum</i> rhizoids used for
670	quantifying morphometric growth trajectories (Replicate 3). Time in HH:MM
671	
672	Supplementary Movie 4 – 4D imaging of developing <i>R. globosum</i> rhizoids used for
673	quantifying morphometric growth trajectories (Replicate 4). Time in HH:MM
674	
675	Supplementary Movie 5 – 4D imaging of developing <i>R. globosum</i> rhizoids used for
676	quantifying morphometric growth trajectories (Replicate 5). Time in HH:MM
677	

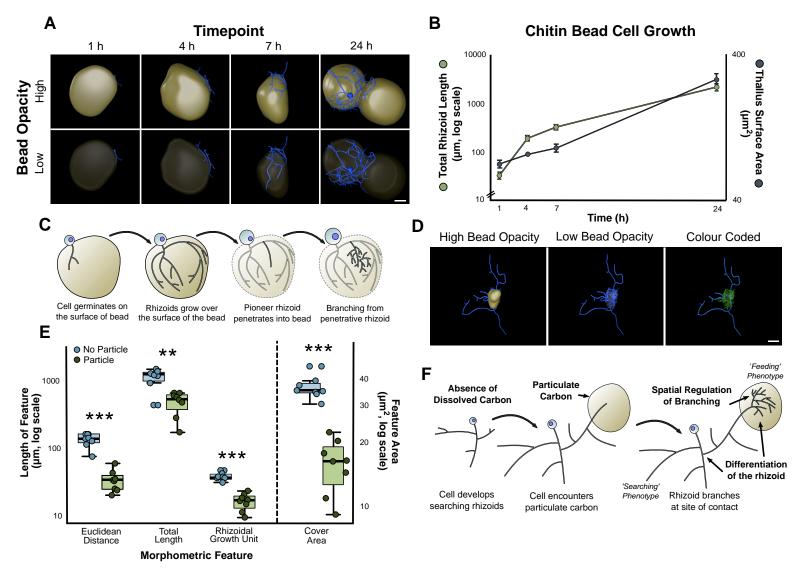
678	Supplementary Movie 6 – Representative 3D reconstructions of 7 h R. globosum
679	rhizoids from caspofungin treated and control cells. Cell wall inhibited rhizoids display
680	atypical hyperbranching.
681	
682	Supplementary Movie 7 – Representative 3D reconstructions of 7 h R. globosum
683	rhizoids from cytochalasin B treated and control cells. Actin inhibited rhizoids display
684	atypical hyperbranching.
685	
686	Supplementary Movie 8 – 4D imaging of the entire <i>R. globosum</i> life cycle growing on
687	10 mM NAG. Cell completes its entire lifecycle and sporulates. Time in HH:MM
688	
689	Supplementary Movie 9 – 4D imaging of <i>R. globosum</i> growing in carbon deplete
690	media. Cell does not complete lifecycle and ceases growth after 14-16 h. Time in HH:MM
691	
692	Supplementary Movie 10 – Representative 3D reconstructions of <i>R. globosum</i>
693	rhizoids from carbon replete and carbon deplete cells. Cells in the carbon deplete
694	condition display the differential searching phenotype. Reconstructions are scaled relative to
695	timepoint.
696	
697	Supplementary Movie 11 – Representative 3D reconstructions of <i>R. globosum</i>
698	rhizoids from cells growing on chitin beads. Reconstructions are scaled relative to
699	timepoint.
700	
701	Supplementary Movie 12 – 4D imaging of <i>R. globosum</i> growing on a chitin microbead.
702	Note that branching within the bead emanates from 'pioneer' penetrative rhizoids. Time in
703	HH:MM
704	

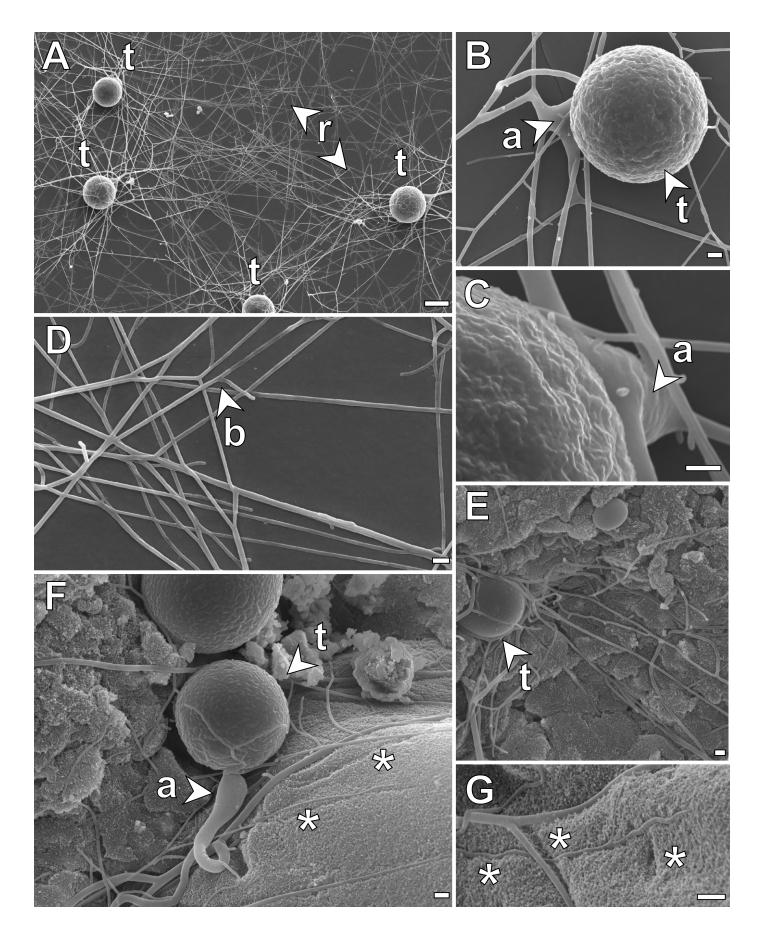
705	Supplementary Movie 13 – 4D imaging of searching <i>R. globosum</i> rhizoids
706	encountering a chitin bead (XY). Note how rhizoids not in contact with the particle continue
707	to grow in a searching pattern. Time in HH:MM
708	
709	Supplementary Movie 14 – 4D imaging of searching <i>R. globosum</i> rhizoids
710	encountering a chitin bead (YZ). Note how branching is most profuse in rhizoids in contact
711	with the particle. Time in HH:MM
712	
713	Supplementary Movie 15 – Representative 3D reconstruction of <i>R. globosum</i> rhizoids
714	from a searching cell in carbon deplete media that has encountered a chitin
715	microbead. The rhizoid is spatially differentiated and coloured whether in contact (green) or
716	not in contact with (blue) the chitin bead.
716 717	not in contact with (blue) the chitin bead.
	not in contact with (blue) the chitin bead. Supplementary File 1 – Total raw data used for analysis in this study
717	



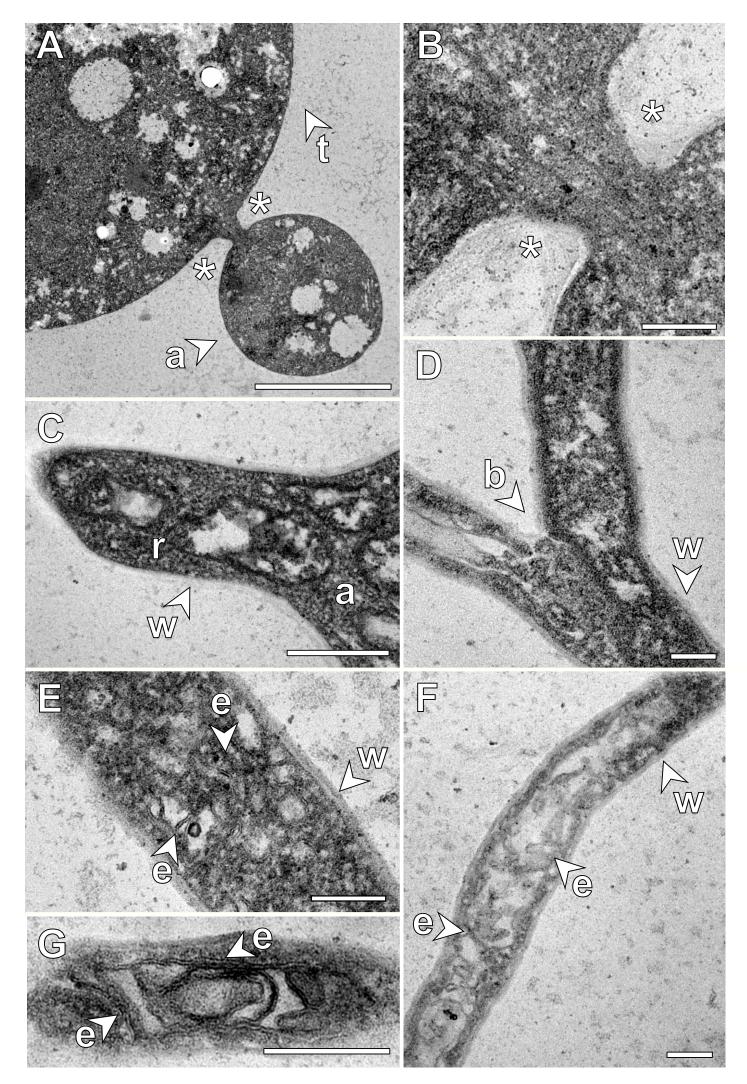


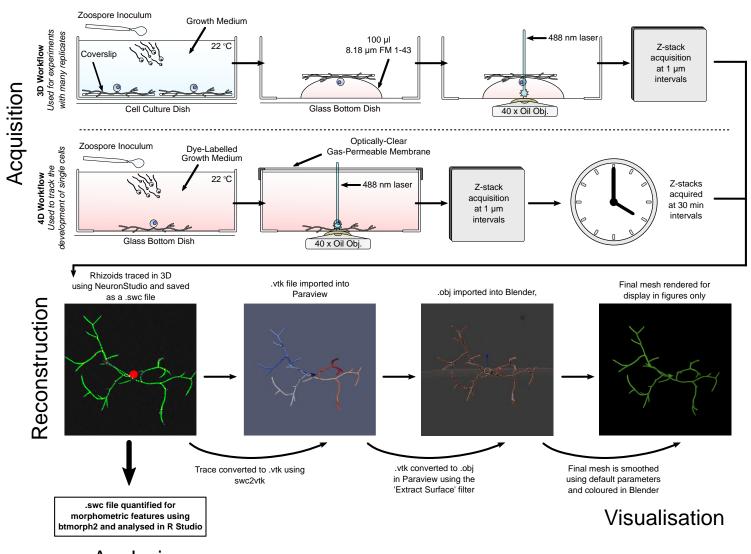




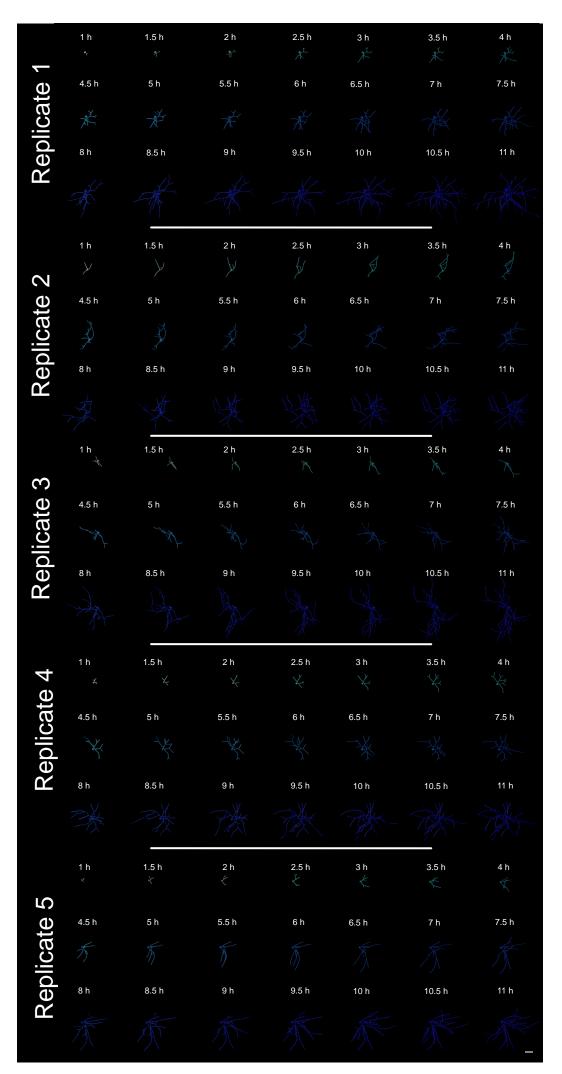


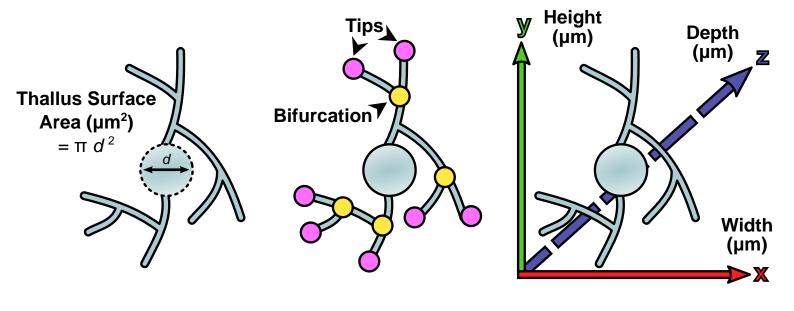
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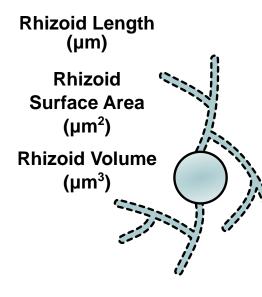
Analysis

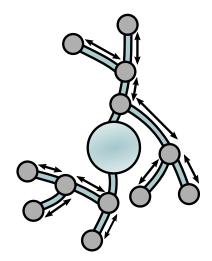


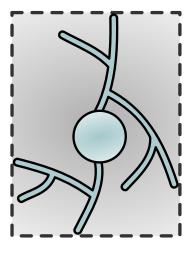


Rhizoidal Growth Unit (µm) (Total Length / No. of Tips) *Mean length between branches*

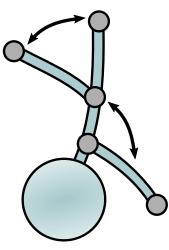
Cover Area (µm²) (Width x Height)



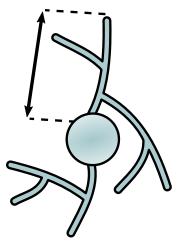




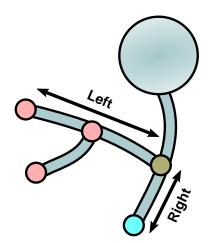
Bifurcation Angle (°)

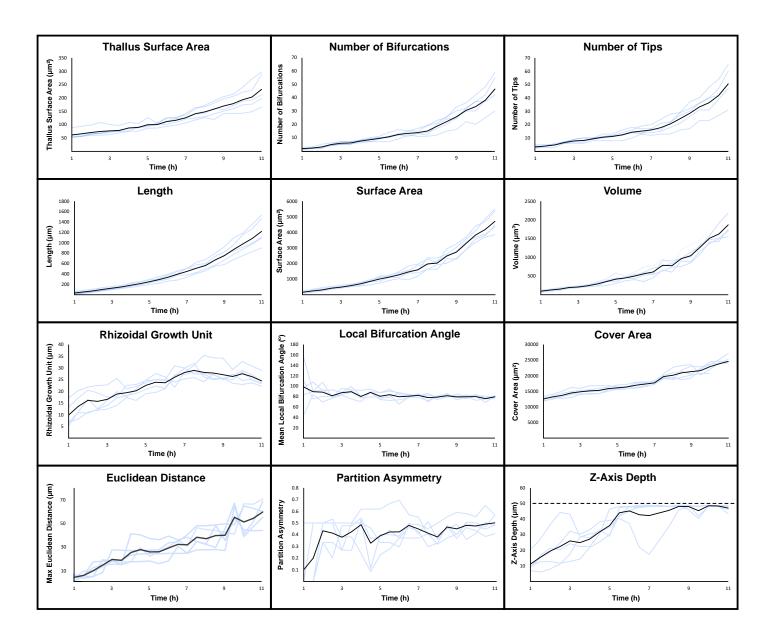


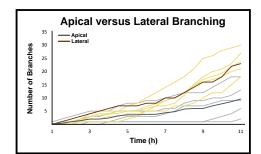
Euclidean Distance (µm) (with respect to thallus)



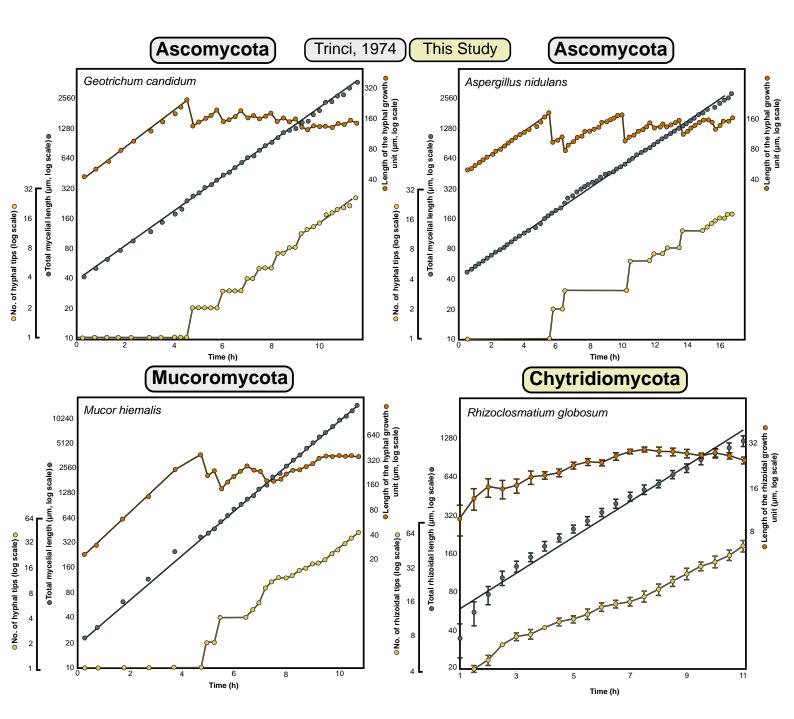
Partition Asymmetry (n1 - n2) / (n1 + n2 - 2)where n1 = left tips n2 = right tips

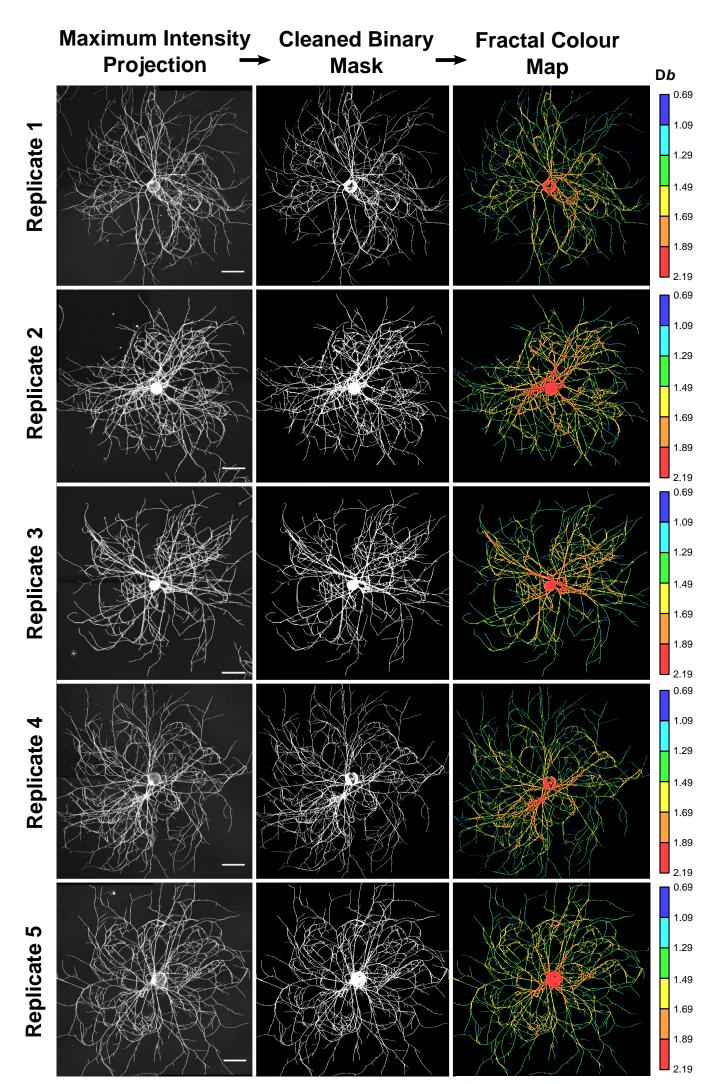






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4D Development	(1 h)	± Stondord	(1 E b)	± Stopdard	(2 h)	± Standard
Morphometric Feature	(1 h) (Mean)	Standard Deviation	(1.5 h) (Mean)	Standard Deviation	(2 h) (Mean)	Deviation
Thallus Diameter (µm ²)	61.73	15.55	65.73	15.90	70.65	15.91
Number of Bifurcations	1.80	0.84	2.20	0.45	3.00	1.22
Number of Tips	3.40	1.14	4.00	0.71	4.80	1.10
Width (µm)	115.28	2.31	118.40	0.76	120.92	1.52
Height (µm)	108.89	4.02	111.68	5.43	113.31	7.81
Depth (µm)	11.13	5.23	15.48	7.68	19.48	10.83
Total Length (μm)	34.96	23.27	55.49	26.18	76.24	27.57
Surface Area (µm ²)	160.28	67.69	242.43	86.65	309.83	95.17
Volume (µm³)	95.35	24.87	126.35	24.33	150.28	27.20
Rhizoidal Growth Unit (µm)	9.87	5.15	13.57	5.02	16.16	5.17
Cover Area (µm ²)	12558.93	680.10	13222.81	663.30	13701.19	945.32
Mean Bifurcation Angle (°)	98.56	41.45	89.28	11.85	88.46	14.35
Partition Asymmetry	0.10	0.22	0.20	0.27	0.43	0.09
Max Euclidean Distance (µm)	4.59	2.06	6.24	2.21	10.10	5.36
Max Path Distance (µm)	4.92	2.43	7.21	2.93	11.50	5.88
Number of Apical Branches	0.20	0.45	0.40	0.89	1.00	1.22
Number of Lateral Branches	0.00	0.00	0.40	0.55	0.80	0.84
	(2.5 h) (Mean)	± Standard Deviation	(3 h) (Mean)	± Standard Deviation	(3.5 h) (Mean)	± Standard Deviation
Thallus Diameter (µm ²)	74.64	19.18	80.28	13.97	78.74	10.72

Number of Bifurcations	4.80	0.84	6.00	1.10	6.00	1.00
Number of Tips	6.60	0.55	8.17	1.30	8.20	1.79
Width (µm)	124.56	1.06	126.69	2.62	127.67	2.68
Height (µm)	116.33	9.44	117.53	8.31	118.83	10.80
Depth (µm)	22.43	13.50	24.05	12.05	24.90	6.66
Total Length (µm)	103.01	29.69	129.64	28.92	150.42	26.09
Surface Area (µm ²)	419.67	78.87	498.16	80.13	579.40	69.78
Volume (µm ³)	191.82	25.09	216.88	19.13	239.34	23.15
Rhizoidal Growth Unit (µm)	15.72	4.89	16.14	3.97	18.85	4.29
Cover Area (µm ²)	14489.81	1178.25	14876.19	798.19	15148.16	1056.39
Mean Bifurcation Angle (°)	81.51	6.51	85.40	5.20	89.34	8.82
Partition Asymmetry	0.41	0.14	0.39	0.11	0.42	0.10
Max Euclidean Distance (µm)	14.85	4.23	19.28	4.71	18.90	4.97
Max Path Distance (µm)	18.14	5.13	23.20	5.13	23.75	5.18
Number of Apical Branches	1.40	1.67	2.50	2.00	2.00	2.00
Number of Lateral Branches	1.80	0.84	3.00	1.30	3.40	1.82
	(4 h) (Mean)	± Standard Deviation	(4.5 h) (Mean)	± Standard Deviation	(5 h) (Mean)	± Standard Deviation
Thallus Diameter (µm ²)	87.55	13.18	89.84	10.18	99.90	15.33
Number of Bifurcations	7.40	0.89	8.40	1.34	9.40	1.52
Number of Tips	9.40	0.89	10.60	1.82	11.20	1.92
Width (µm)	128.49	4.98	130.81	6.80	133.09	8.08
Height (µm)	119.48	13.29	121.85	11.97	121.57	10.10
Depth (µm)	27.16	5.01	31.81	4.67	35.82	7.13
Total Length (µm)	183.21	34.22	212.60	35.17	250.30	39.92

Surface Area (µm ²)	697.97	112.24	856.05	134.33	1004.34	184.45
Volume (µm ³)	286.28	51.44	351.77	63.07	416.94	108.92
Rhizoidal Growth Unit (µm)	19.40	2.28	20.23	2.71	22.54	2.55
Cover Area (µm ²)	15298.59	1096.41	15874.79	707.32	16119.89	603.53
Mean Bifurcation Angle (°)	80.11	7.99	87.90	5.39	80.59	6.54
Partition Asymmetry	0.49	0.14	0.33	0.23	0.39	0.14
Max Euclidean Distance (µm)	25.42	9.73	27.94	8.30	26.01	7.13
Max Path Distance (µm)	30.92	11.74	35.03	10.52	34.40	11.86
Number of Apical Branches	2.40	1.95	3.20	2.68	3.60	2.97
Number of Lateral Branches	3.80	1.92	4.20	2.28	5.00	2.12
	(5 5 1)	±	(01)	±	(0 5 1)	±
	(5.5 h) (Mean)	Standard Deviation	(6 h) (Mean)	Standard Deviation	(6.5 h) (Mean)	Standard Deviation
Thallus Diameter (µm ²)	100.34	7.52	111.63	13.83	116.66	12.51
Number of Bifurcations	10.60	2.51	12.40	2.51	13.20	1.79
Number of Tips	12.40	2.97	14.40	2.97	15.20	2.68
Width (µm)	134.75	8.19	137.86	8.19	141.14	9.67
Height (µm)	122.19	8.54	123.33	8.78	123.15	8.15
Depth (µm)	44.05	3.44	45.24	4.66	42.83	11.70
Total Length (µm)	290.01	48.65	336.86	55.51	394.34	70.39
Surface Area (µm ²)	1131.95	138.18	1268.24	186.91	1460.13	325.84
Volume (µm ³)	448.43	45.57	497.52	79.06	560.30	140.57
Rhizoidal Growth Unit (µm)	23.87	3.07	23.65	2.33	26.07	3.45
Cover Area (µm ²)	16414.85	525.82	16960.99	817.17	17329.43	639.39
Mean Bifurcation Angle (°)	83.58	8.62	79.63	9.66	80.75	2.71
Partition Asymmetry	0.42	0.15	0.42	0.16	0.48	0.07

Max Euclidean Distance (µm)	26.12	7.24	29.34	8.08	32.36	4.80
Max Path Distance (µm)	35.29	10.43	39.00	12.77	44.57	8.77
Number of Apical Branches	3.60	2.97	3.80	3.35	3.80	3.35
Number of Lateral Branches	5.40	2.07	6.80	2.17	7.80	2.59
	(7 h) (Mean)	± Standard Deviation	(7.5 h) (Mean)	± Standard Deviation	(8 h) (Mean)	± Standard Deviation
Thallus Diameter (µm ²)	125.80	13.55	140.79	20.30	153.26	21.19
Number of Bifurcations	13.80	2.28	15.00	3.81	19.83	4.28
Number of Tips	16.00	3.08	17.80	4.55	22.00	5.55
Width (µm)	144.14	10.96	149.97	9.68	150.13	11.91
Height (µm)	123.26	6.90	131.91	7.67	136.32	9.30
Depth (µm)	42.26	13.92	43.90	9.92	46.12	5.77
Total Length (µm)	447.68	83.46	507.96	93.67	590.88	85.01
Surface Area (µm ²)	1602.52	321.61	1977.68	343.82	2181.31	275.48
Volume (µm ³)	609.97	132.73	786.87	146.15	847.84	112.19
Rhizoidal Growth Unit (µm)	28.05	1.97	28.96	2.52	27.66	4.29
Cover Area (µm ²)	17710.48	522.73	19733.66	687.82	20439.86	1649.74
Mean Bifurcation Angle (°)	82.27	2.76	77.85	6.87	78.96	2.85
Partition Asymmetry	0.45	0.07	0.41	0.08	0.40	0.07
Max Euclidean Distance (µm)	31.95	7.37	38.37	8.62	38.31	8.82
Max Path Distance (µm)	44.88	11.89	53.08	14.99	55.74	13.07
Number of Apical Branches	4.40	3.78	4.80	4.15	6.83	4.76
Number of Lateral Branches	9.00	3.39	10.20	3.49	12.50	3.94

		±		±		±
	(8.5 h) (Mean)	Standard Deviation	(9 h) (Mean)	Standard Deviation	(9.5 h) (Mean)	Standard Deviation
Thallus Diameter (µm ²)	158.24	28.84	169.98	28.77	178.45	30.65
Number of Bifurcations	22.00	4.53	25.60	6.50	30.40	5.18
Number of Tips	24.40	5.73	28.40	7.50	33.20	6.53
Width (µm)	153.49	15.50	154.51	15.11	157.71	17.56
Height (µm)	136.95	9.97	138.78	14.09	137.92	9.11
Depth (µm)	48.11	1.32	48.03	1.18	45.40	3.89
Total Length (µm)	664.75	106.31	749.34	131.57	869.09	162.80
Surface Area (µm ²)	2484.50	341.81	2736.00	427.52	3290.47	372.99
Volume (µm³)	963.75	163.46	1043.59	195.90	1269.05	150.26
Rhizoidal Growth Unit (µm)	27.84	3.78	27.12	3.95	26.35	2.25
Cover Area (µm ²)	20955.39	1838.27	21331.96	1840.64	21626.97	1102.86
Mean Bifurcation Angle (°)	81.69	3.23	79.24	4.05	79.52	2.78
Partition Asymmetry	0.47	0.06	0.45	0.09	0.48	0.08
Max Euclidean Distance (µm)	39.80	10.19	40.08	8.86	55.31	10.81
Max Path Distance (µm)	55.92	12.69	57.55	16.95	74.23	12.13
Number of Apical Branches	6.00	4.90	6.00	4.90	7.00	5.48
Number of Lateral Branches	14.60	4.62	17.00	5.39	18.20	5.22
	(10 h) (Mean)	± Standard Deviation	(10.5 h) (Mean)	± Standard Deviation	(11 h) (Mean)	± Standard Deviation
Thallus Diameter (µm ²)	193.39	38.51	203.54	47.69	232.18	57.64
Number of Bifurcations	33.20	8.53	38.00	8.46	46.40	11.41
Number of Tips	36.40	9.61	41.80	10.03	50.60	13.16

Width (µm)	166.25	21.27	168.86	22.61	170.74	25.31
Height (µm)	138.76	12.08	142.45	15.78	145.67	16.12
Depth (µm)	48.55	0.42	48.39	0.30	47.04	2.34
Total Length (µm)	977.64	186.20	1084.53	220.20	1219.15	268.22
Surface Area (µm ²)	3836.65	422.94	4187.25	549.42	4707.64	704.53
Volume (µm ³)	1510.22	145.44	1623.77	209.37	1868.34	280.25
Rhizoidal Growth Unit (µm)	27.51	3.84	26.30	2.78	24.48	2.67
Cover Area (µm ²)	22884.73	1500.84	23811.10	1536.94	24595.64	1879.28
Mean Bifurcation Angle (°)	79.91	4.24	75.90	4.53	79.41	2.45
Partition Asymmetry	0.47	0.06	0.49	0.10	0.50	0.07
Max Euclidean Distance (µm)	51.27	13.40	54.37	9.71	59.69	10.78
Max Path Distance (µm)	72.72	13.07	78.64	11.26	86.12	12.58
Number of Apical Branches	7.80	5.97	8.60	6.58	9.60	6.19
Number of Lateral Branches	19.40	5.81	21.80	5.07	23.80	4.76

Poisoned 1 µM Caspofungin Control ± + Standard Diacetate Cells Standard Cells t-test p-**Morphometric Feature** Deviation Deviation value (Mean) (Mean) Thallus Diameter (µm²) 156.35 33.59 149.01 12.84 p > 0.05Number of Bifurcations 22.25 5.26 20.75 3.73 p > 0.05Number of Tips 25.63 6.16 23.38 3.29 p > 0.05Width (µm) 171.95 23.36 183.52 20.38 p > 0.05166.01 Height (µm) 149.81 16.35 12.42 p < 0.05Depth (µm) 14.84 12.85 5.98 2.09 p > 0.05Total Length (µm) 558.41 113.78 511.62 117.53 p > 0.05Surface Area (µm²) 2188.88 922.56 2019.66 312.08 p > 0.05Volume (µm³) 927.54 561.11 841.85 139.38 p > 0.05Rhizoidal Growth Unit (µm) 22.08 2.13 21.88 3.83 p > 0.05Cover Area (µm²) 25841.89 4907.30 30447.12 4005.04 p > 0.05Mean Bifurcation Angle (°) 83.87 7.23 77.41 4.13 p > 0.05Partition Asymmetry 0.06 0.61 0.08 p > 0.050.65 Max Euclidean Distance (µm) 58.60 12.95 60.06 13.31 p > 0.05Max Path Distance (µm) 89.46 27.71 69.70 15.94 p > 0.0510 µM Caspofungin Poisoned Control ± ± Diacetate Cells Standard Cells Standard t-test p-**Morphometric Feature** (Mean) Deviation (Mean) Deviation value Thallus Diameter (µm²) 116.66 10.21 146.81 8.06 *p* < 0.001 Number of Bifurcations 16.38 4.21 22.75 4.50 p < 0.05Number of Tips 20.00 4.72 25.50 3.93 p < 0.05Width (µm) 147.69 18.06 178.64 28.42 p < 0.05Height (µm) 117.83 21.04 158.94 27.44 p < 0.01Depth (µm) 9.73 2.93 12.66 p > 0.052.56 Total Length (µm) 236.11 56.46 507.82 60.22 *p* < 0.001 Surface Area (µm²) 778.83 168.46 1938.29 176.30 *p* < 0.001 Volume (µm³) 335.65 62.71 780.04 56.72 *p* < 0.001 Rhizoidal Growth Unit (µm) 11.91 20.41 p < 0.0012.20 4.22 Cover Area (µm²) 17415.38 4017.82 28280.04 6059.43 p < 0.01Mean Bifurcation Angle (°) 82.95 7.60 83.81 5.53 p > 0.05Partition Asymmetry 0.43 0.20 0.69 0.07 p < 0.01Max Euclidean Distance (µm) 59.78 27.08 5.83 8.10 p < 0.001Max Path Distance (µm) 35.56 7.84 67.72 7.82 p < 0.001

50 μM Caspofungin Diacetate Morphometric Feature	Poisoned Cells (Mean)	± Standard Deviation	Control Cells (Mean)	± Standard Deviation	<i>t-</i> test <i>p</i> - value
Thallus Diameter (µm ²)	102.66	4.58	138.43	21.87	<i>p</i> < 0.01
Number of Bifurcations	12.63	3.38	20.50	8.28	<i>p</i> < 0.05
Number of Tips	15.13	3.36	23.38	8.21	<i>p</i> < 0.05
Width (µm)	144.14	5.03	207.57	82.07	<i>p</i> < 0.05
Height (µm)	116.13	24.38	166.90	81.07	<i>p</i> < 0.001
Depth (µm)	7.41	3.17	11.87	2.89	<i>p</i> < 0.05
Total Length (µm)	68.02	16.73	409.88	102.22	<i>p</i> < 0.001
Surface Area (µm ²)	268.76	58.11	1523.21	576.05	<i>p</i> < 0.001
Volume (µm ³)	182.96	20.38	664.00	386.28	<i>p</i> < 0.001
Rhizoidal Growth Unit (µm)	4.52	0.64	20.67	13.09	<i>p</i> < 0.001
Cover Area (µm ²)	16742.96	3613.72	40161.41	43389.89	<i>p</i> < 0.01
Mean Bifurcation Angle (°)	87.60	9.17	86.20	11.15	<i>p</i> > 0.05
Partition Asymmetry	0.53	0.16	0.60	0.12	<i>p</i> > 0.05
Max Euclidean Distance (µm)	14.68	3.36	43.64	13.05	<i>p</i> < 0.001
Max Path Distance (µm)	18.54	4.36	57.03	10.59	<i>p</i> < 0.001
0.1 µM Cytochalasin B	Poisoned Cells	± Standard	Control Cells	± Standard	<i>t</i> -test <i>p</i> -
Morphometric Feature	(Mean)	Deviation	(Mean)	Deviation	value
Thallus Diameter (µm ²)	145.42	16.91	152.08	16.20	<i>p</i> > 0.05
Number of Bifurcations	21.00	3.64	23.13	4.09	<i>p</i> > 0.05
Number of Tips	24.11	3.95	26.63	4.00	<i>p</i> > 0.05
Width (µm)	163.22	22.88	165.33	12.90	<i>p</i> > 0.05
Height (µm)	166.00	21.01	157.67	41.68	<i>p</i> > 0.05
Depth (µm)	7.68	1.63	11.22	2.83	<i>p</i> < 0.01
Total Length (µm)	423.42	83.00	449.15	72.78	<i>p</i> > 0.05
Surface Area (µm ²)	1631.14	359.82	1653.61	228.71	<i>p</i> > 0.05
Volume (µm ³)	684.48	158.14	693.87	128.98	<i>p</i> > 0.05
Rhizoidal Growth Unit (µm)	17.87	3.85	17.24	4.13	<i>p</i> > 0.05
Cover Area (µm ²)	27253.95	5988.26	26356.21	8234.10	<i>p</i> > 0.05
Mean Bifurcation Angle (°)	85.37	8.44	82.42	5.49	<i>p</i> > 0.05
Partition Asymmetry	0.65	0.13	0.68	0.09	<i>p</i> > 0.05
Max Euclidean Distance (µm)	47.01	11.52	55.56	13.49	<i>p</i> > 0.05
Max Path Distance (µm)	59.53	11.47	67.04	16.50	<i>p</i> > 0.05
1 µM Cytochalasin B	Poisoned	± Standard	Control Cells	± Standard	<i>t-</i> test <i>p</i> -
Morphometric Feature	Cells (Mean)	Deviation	(Mean)	Deviation	value

Number of Bifurcations	22.63	11.75	22.13	4.70	<i>p</i> > 0.05
Number of Tips	27.38	12.58	25.38	5.07	<i>p</i> > 0.05
Width (µm)	155.00	28.00	189.01	16.61	<i>p</i> < 0.01
Height (µm)	125.73	33.95	144.44	21.41	<i>p</i> > 0.05
Depth (µm)	18.21	5.57	13.09	4.95	<i>p</i> > 0.05
Total Length (µm)	355.41	222.00	459.83	72.31	<i>p</i> > 0.05
Surface Area (µm ²)	1422.36	1066.42	1994.94	353.44	<i>p</i> > 0.05
Volume (µm ³)	663.73	513.32	873.25	178.13	<i>p</i> > 0.05
Rhizoidal Growth Unit (µm)	12.41	2.78	18.35	2.05	<i>p</i> < 0.001
Cover Area (µm ²)	20192.72	7376.37	27145.56	3479.91	<i>p</i> < 0.05
Mean Bifurcation Angle (°)	82.90	3.27	81.86	6.59	<i>p</i> > 0.05
Partition Asymmetry	0.56	0.06	0.64	0.07	<i>p</i> < 0.05
Max Euclidean Distance (µm)	33.95	16.23	48.33	9.11	<i>p</i> > 0.05
Max Path Distance (µm)	44.62	17.45	64.48	11.60	<i>p</i> < 0.05
10 µM Cytochalasin B	Poisoned	±	Control	±	
Morphometric Feature	Cells (Mean)	Standard Deviation	Cells (Mean)	Standard Deviation	<i>t-</i> test <i>p</i> - value
-			• •		<i>p</i> < 0.05
Thallus Diameter (µm²)	104.17	23.54	124.72	13.06	D < U U D
Number of Differentians			40.00		•
Number of Bifurcations	10.78	1.79	16.33	3.43	<i>p</i> < 0.01
Number of Tips	10.78 14.00	1.79 2.40	19.22	3.43 2.44	<i>p</i> < 0.01 <i>p</i> < 0.001
Number of Tips Width (µm)	10.78 14.00 145.38	1.79 2.40 12.72	19.22 179.84	3.43 2.44 22.04	<i>p</i> < 0.01 <i>p</i> < 0.001 <i>p</i> < 0.01
Number of Tips Width (µm) Height (µm)	10.78 14.00 145.38 103.63	1.79 2.40 12.72 28.11	19.22 179.84 139.30	3.43 2.44 22.04 16.38	p < 0.01 p < 0.001 p < 0.01 p < 0.01
Number of Tips Width (µm) Height (µm) Depth (µm)	10.78 14.00 145.38 103.63 8.70	1.79 2.40 12.72 28.11 2.56	19.22 179.84 139.30 8.92	3.43 2.44 22.04 16.38 2.64	p < 0.01 p < 0.001 p < 0.01 p < 0.01 p > 0.05
Number of Tips Width (µm) Height (µm) Depth (µm) Total Length (µm)	10.78 14.00 145.38 103.63	1.79 2.40 12.72 28.11	19.22 179.84 139.30 8.92 319.61	3.43 2.44 22.04 16.38 2.64 57.12	p < 0.01 p < 0.001 p < 0.01 p < 0.01
Number of Tips Width (µm) Height (µm) Depth (µm) Total Length (µm) Surface Area (µm²)	10.78 14.00 145.38 103.63 8.70	1.79 2.40 12.72 28.11 2.56	19.22 179.84 139.30 8.92	3.43 2.44 22.04 16.38 2.64	p < 0.01 p < 0.001 p < 0.01 p < 0.01 p > 0.05
Number of Tips Width (µm) Height (µm) Depth (µm) Total Length (µm)	10.78 14.00 145.38 103.63 8.70 119.58	1.79 2.40 12.72 28.11 2.56 61.95	19.22 179.84 139.30 8.92 319.61	3.43 2.44 22.04 16.38 2.64 57.12	p < 0.01
Number of Tips Width (µm) Height (µm) Depth (µm) Total Length (µm) Surface Area (µm²)	10.78 14.00 145.38 103.63 8.70 119.58 489.73	1.79 2.40 12.72 28.11 2.56 61.95 237.80	19.22 179.84 139.30 8.92 319.61 1099.97	3.43 2.44 22.04 16.38 2.64 57.12 250.29	p < 0.01
Number of Tips Width (µm) Height (µm) Depth (µm) Total Length (µm) Surface Area (µm²) Volume (µm³)	10.78 14.00 145.38 103.63 8.70 119.58 489.73 259.75	1.79 2.40 12.72 28.11 2.56 61.95 237.80 97.96	19.22 179.84 139.30 8.92 319.61 1099.97 449.04	3.43 2.44 22.04 16.38 2.64 57.12 250.29 115.66	p < 0.01
Number of Tips Width (µm) Height (µm) Depth (µm) Total Length (µm) Surface Area (µm²) Volume (µm³) Rhizoidal Growth Unit (µm)	10.78 14.00 145.38 103.63 8.70 119.58 489.73 259.75 8.68	1.79 2.40 12.72 28.11 2.56 61.95 237.80 97.96 4.52	19.22 179.84 139.30 8.92 319.61 1099.97 449.04 16.62	3.43 2.44 22.04 16.38 2.64 57.12 250.29 115.66 2.06	p < 0.01
Number of Tips Width (µm) Height (µm) Depth (µm) Total Length (µm) Surface Area (µm²) Volume (µm³) Rhizoidal Growth Unit (µm) Cover Area (µm²)	10.78 14.00 145.38 103.63 8.70 119.58 489.73 259.75 8.68 15140.54	1.79 2.40 12.72 28.11 2.56 61.95 237.80 97.96 4.52 4661.50	19.22 179.84 139.30 8.92 319.61 1099.97 449.04 16.62 25114.02	3.43 2.44 22.04 16.38 2.64 57.12 250.29 115.66 2.06 4842.67	p < 0.01
Number of Tips Width (µm) Height (µm) Depth (µm) Total Length (µm) Surface Area (µm²) Volume (µm³) Rhizoidal Growth Unit (µm) Cover Area (µm²) Mean Bifurcation Angle (°)	10.78 14.00 145.38 103.63 8.70 119.58 489.73 259.75 8.68 15140.54 90.58	1.79 2.40 12.72 28.11 2.56 61.95 237.80 97.96 4.52 4661.50 5.79	19.22 179.84 139.30 8.92 319.61 1099.97 449.04 16.62 25114.02 90.28	3.43 2.44 22.04 16.38 2.64 57.12 250.29 115.66 2.06 4842.67 7.59	p < 0.01

(1 h) Morphometric Feature	Carbon Replete (Mean)	± Standard Deviation	Carbon Deplete (Mean)	± Standard Deviation	<i>t-</i> test <i>p</i> - value
Thallus Diameter (µm ²)	65.33	10.96	51.85	11.85	<i>p</i> < 0.01
Number of Bifurcations	4.33	1.58	3.63	2.70	<i>p</i> > 0.05
Number of Tips	5.78	1.30	4.75	2.60	<i>p</i> > 0.05
Width (µm)	47.59	7.42	42.38	22.60	<i>p</i> > 0.05
Height (µm)	49.04	12.71	45.21	20.65	<i>p</i> > 0.05
Depth (µm)	7.58	2.60	6.74	1.68	<i>p</i> > 0.05
Total Length (µm)	75.54	16.57	74.47	55.59	<i>p</i> > 0.05
Surface Area (µm ²)	207.65	36.34	173.69	205.38	<i>p</i> > 0.05
Volume (µm ³)	98.70	22.65	70.36	70.72	<i>p</i> < 0.001
Rhizoidal Growth Unit (µm)	13.19	1.53	15.82	2.75	<i>p</i> > 0.05
Cover Area (µm ²)	2400.60	934.82	1959.75	2892.47	<i>p</i> > 0.05
Mean Bifurcation Angle (°)	93.94	16.81	92.24	16.11	<i>p</i> > 0.05
Partition Asymmetry	0.50	0.13	0.54	0.17	<i>p</i> > 0.05
Max Euclidean Distance (µm)	11.26	4.81	13.08	11.37	<i>p</i> > 0.05
Max Path Distance (µm)	13.67	5.78	16.05	12.60	<i>p</i> > 0.05
(4 h) Morphometric Feature	Carbon Replete (Mean)	± Standard Deviation	Carbon Deplete (Mean)	± Standard Deviation	<i>t-</i> test <i>p</i> - value
Thallus Diameter (µm ²)	103.87	16.89	70.28	10.53	<i>p</i> < 0.001
Number of Bifurcations	14.38	4.47	10.44	2.88	<i>p</i> > 0.05
Number of Tips	16.25	4.33	12.00	2.74	<i>p</i> < 0.05
Width (µm)	102.31	17.57	142.60	20.37	<i>p</i> < 0.001
Height (µm)	103.86	22.07	152.28	40.59	<i>p</i> < 0.01
Depth (µm)	9.35	1.63	7.23	1.68	<i>p</i> < 0.05
Total Length (µm)	297.44	91.96	400.84	41.77	<i>p</i> < 0.05
Surface Area (µm ²)	1052.25	355.81	1353.25	399.14	<i>p</i> > 0.05
Volume (µm ³)	413.31	174.59	440.55	231.56	<i>p</i> > 0.05
Rhizoidal Growth Unit (µm)	18.23	2.12	35.06	9.50	<i>p</i> < 0.001
Cover Area (µm ²)	10840.47	3982.10	22043.11	7629.16	<i>p</i> < 0.01
Mean Bifurcation Angle (°)	79.35	8.36	86.91	7.40	<i>p</i> > 0.05
Partition Asymmetry	0.60	0.11	0.58	0.09	<i>p</i> > 0.05
Max Euclidean Distance (µm)	41.41	10.76	75.16	22.69	<i>p</i> < 0.01
Max Path Distance (µm)	47.53	10.83	91.44	23.97	<i>p</i> < 0.001
(7 h) Morphometric Feature	Carbon Replete (Mean)	± Standard Deviation	Carbon Deplete (Mean)	± Standard Deviation	<i>t-</i> test <i>p</i> - value

Thallus Diameter (µm ²)	179.38	28.07	85.36	85.36	<i>p</i> < 0.001
Number of Bifurcations	25.67	6.08	25.56	25.56	<i>p</i> > 0.05
Number of Tips	28.11	6.33	26.89	26.89	<i>p</i> > 0.05
Width (µm)	173.98	19.14	185.34	185.34	<i>p</i> > 0.05
Height (µm)	166.68	26.11	215.32	215.32	<i>p</i> < 0.05
Depth (µm)	10.88	3.14	10.85	10.85	<i>p</i> > 0.05
Total Length (µm)	635.08	135.09	800.14	800.14	<i>p</i> < 0.05
Surface Area (µm ²)	2394.43	484.77	2914.51	2914.51	<i>p</i> > 0.05
Volume (µm ³)	982.62	190.12	946.72	946.72	<i>p</i> > 0.05
Rhizoidal Growth Unit (µm)	23.00	4.75	31.23	31.23	p < 0.05
Cover Area (µm ²)	29227.45	6934.82	39176.52	39176.52	p < 0.05
Mean Bifurcation Angle (°)	82.19	6.23	88.03	88.03	p < 0.05
Partition Asymmetry	0.63	0.07	0.65	0.65	<i>p</i> > 0.05
Max Euclidean Distance (µm)	62.15	7.66	120.92	120.92	<i>p</i> < 0.01
Max Path Distance (µm)	75.05	5.18	156.50	156.50	<i>p</i> < 0.001
(24 h)	Carbon	±	Carbon	±	
Morphometric Feature	Replete (Mean)	Standard Deviation	Deplete (Mean)	Standard Deviation	<i>t-</i> test <i>p</i> - value
Morphometric Feature Thallus Diameter (µm ²)	· ·		•		-
-	(Mean)	Deviation	(Mean)	Deviation	value
Thallus Diameter (µm ²)	(Mean) 2038.41	Deviation 336.41	(Mean) 180.49	Deviation 24.79	value <i>p</i> < 0.01
Thallus Diameter (µm ²) Number of Bifurcations	(Mean) 2038.41 365.75	Deviation 336.41 80.22	(Mean) 180.49 88.00	Deviation 24.79 24.42	value <i>p</i> < 0.01 <i>p</i> < 0.01
Thallus Diameter (µm ²) Number of Bifurcations Number of Tips	(Mean) 2038.41 365.75 433.25	Deviation 336.41 80.22 106.58	(Mean) 180.49 88.00 90.63	Deviation 24.79 24.42 23.74	value p < 0.01
Thallus Diameter (µm ²) Number of Bifurcations Number of Tips Width (µm)	(Mean) 2038.41 365.75 433.25 402.03	Deviation 336.41 80.22 106.58 28.77	(Mean) 180.49 88.00 90.63 364.64	Deviation 24.79 24.42 23.74 48.94	value p < 0.01
Thallus Diameter (µm²) Number of Bifurcations Number of Tips Width (µm) Height (µm)	(Mean) 2038.41 365.75 433.25 402.03 401.90	Deviation 336.41 80.22 106.58 28.77 15.90	(Mean) 180.49 88.00 90.63 364.64 393.74	Deviation 24.79 24.42 23.74 48.94 19.71	value p < 0.01
Thallus Diameter (µm²) Number of Bifurcations Number of Tips Width (µm) Height (µm) Depth (µm)	(Mean) 2038.41 365.75 433.25 402.03 401.90 25.14	Deviation 336.41 80.22 106.58 28.77 15.90 5.19	(Mean) 180.49 88.00 90.63 364.64 393.74 9.69	Deviation 24.79 24.42 23.74 48.94 19.71 2.75	value p < 0.01
Thallus Diameter (µm²) Number of Bifurcations Number of Tips Width (µm) Height (µm) Depth (µm) Total Length (µm)	(Mean) 2038.41 365.75 433.25 402.03 401.90 25.14 9918.81	Deviation 336.41 80.22 106.58 28.77 15.90 5.19 2094.98	(Mean) 180.49 88.00 90.63 364.64 393.74 9.69 3015.64	Deviation 24.79 24.42 23.74 48.94 19.71 2.75 815.10	value p < 0.01
Thallus Diameter (µm²) Number of Bifurcations Number of Tips Width (µm) Height (µm) Depth (µm) Total Length (µm) Surface Area (µm²)	(Mean) 2038.41 365.75 433.25 402.03 401.90 25.14 9918.81 43028.44	Deviation 336.41 80.22 106.58 28.77 15.90 5.19 2094.98 9579.73	(Mean) 180.49 88.00 90.63 364.64 393.74 9.69 3015.64 12093.19	Deviation 24.79 24.42 23.74 48.94 19.71 2.75 815.10 3594.02	value p < 0.01
Thallus Diameter (µm²) Number of Bifurcations Number of Tips Width (µm) Height (µm) Depth (µm) Total Length (µm) Surface Area (µm²) Volume (µm³)	(Mean) 2038.41 365.75 433.25 402.03 401.90 25.14 9918.81 43028.44 28425.62	Deviation 336.41 80.22 106.58 28.77 15.90 5.19 2094.98 9579.73 4653.46	(Mean) 180.49 88.00 90.63 364.64 393.74 9.69 3015.64 12093.19 4245.75	Deviation 24.79 24.42 23.74 48.94 19.71 2.75 815.10 3594.02 1349.18	value p < 0.01
Thallus Diameter (µm²) Number of Bifurcations Number of Tips Width (µm) Height (µm) Depth (µm) Total Length (µm) Surface Area (µm²) Volume (µm³) Rhizoidal Growth Unit (µm)	(Mean) 2038.41 365.75 433.25 402.03 401.90 25.14 9918.81 43028.44 28425.62 23.16	Deviation 336.41 80.22 106.58 28.77 15.90 5.19 2094.98 9579.73 4653.46 1.92	(Mean) 180.49 88.00 90.63 364.64 393.74 9.69 3015.64 12093.19 4245.75 33.23	Deviation 24.79 24.42 23.74 48.94 19.71 2.75 815.10 3594.02 1349.18 2.53	value p < 0.01
Thallus Diameter (µm²) Number of Bifurcations Number of Tips Width (µm) Height (µm) Depth (µm) Total Length (µm) Surface Area (µm²) Volume (µm³) Rhizoidal Growth Unit (µm) Cover Area (µm²)	(Mean) 2038.41 365.75 433.25 402.03 401.90 25.14 9918.81 43028.44 28425.62 23.16 161828.23	Deviation 336.41 80.22 106.58 28.77 15.90 5.19 2094.98 9579.73 4653.46 1.92 16638.78	(Mean) 180.49 88.00 90.63 364.64 393.74 9.69 3015.64 12093.19 4245.75 33.23 143817.79	Deviation 24.79 24.42 23.74 48.94 19.71 2.75 815.10 3594.02 1349.18 2.53 22032.07	value p < 0.01
Thallus Diameter (µm²) Number of Bifurcations Number of Tips Width (µm) Height (µm) Depth (µm) Total Length (µm) Surface Area (µm²) Volume (µm³) Rhizoidal Growth Unit (µm) Cover Area (µm²) Mean Bifurcation Angle (°)	(Mean) 2038.41 365.75 433.25 402.03 401.90 25.14 9918.81 43028.44 28425.62 23.16 161828.23 68.06	Deviation 336.41 80.22 106.58 28.77 15.90 5.19 2094.98 9579.73 4653.46 1.92 16638.78 3.21	(Mean) 180.49 88.00 90.63 364.64 393.74 9.69 3015.64 12093.19 4245.75 33.23 143817.79 81.69	Deviation 24.79 24.42 23.74 48.94 19.71 2.75 815.10 3594.02 1349.18 2.53 22032.07 2.63	value p < 0.01

Particulate Carbon	(4.1.)	±	(41)	±	(71)	±	(041)	±
Morphometric Feature	(1 h) (Mean)	Standard Deviation	(4 h) (Mean)	Standard Deviation	(7 h) (Mean)	Standard Deviation	(24 h) (Mean)	Standard Deviation
Thallus Diameter (µm ²)	71.38	12.81	83.29	9.78	91.89	16.18	269.71	55.76
Number of Bifurcations	2.22	1.30	8.89	4.70	10.75	4.83	112.75	62.47
Number of Tips	3.22	1.30	10.89	5.49	13.50	6.07	143.50	91.81
Width (µm)	131.18	14.57	152.85	30.43	153.14	17.21	171.85	15.96
Height (µm)	97.68	23.73	105.45	22.29	121.57	33.43	145.96	28.79
Depth (µm)	6.92	2.26	32.81	15.63	42.38	9.70	58.99	10.02
Total Length (µm)	32.95	16.05	191.55	73.31	324.11	108.77	2160.80	722.46
Surface Area (µm ²)	151.11	48.92	715.97	237.15	1164.11	457.21	7260.26	3195.89
Volume (µm ³)	104.61	26.55	291.69	96.99	422.49	177.54	2740.66	1364.26
Rhizoidal Growth Unit (µm)	10.50	4.15	18.97	5.76	25.68	6.64	17.54	5.72
Cover Area (µm ²)	12718.87	2934.84	15959.67	4130.87	18483.84	4996.53	24937.91	4319.79
Mean Bifurcation Angle (°)	94.20	18.51	81.76	12.22	92.12	9.37	82.45	1.73
Partition Asymmetry	0.37	0.28	0.40	0.19	0.56	0.07	0.58	0.12
Max Euclidean Distance (µm)	10.43	5.91	52.95	31.98	43.05	17.77	41.48	15.56
Max Path Distance (µm)	12.63	7.17	88.61	61.80	66.92	21.46	63.91	15.28

Rhizoid Differentiation Morphometric Feature	Particle Associated (Mean)	± Standard Deviation	Not Particle Associated (Mean)	± Standard Deviation	<i>t-</i> test <i>p</i> - value
Number of Bifurcations	24.63	11.33	28.50	8.65	<i>p</i> > 0.05
Number of Tips	30.50	12.75	30.25	8.43	<i>p</i> > 0.05
Width (µm)	150.84	22.60	217.94	10.43	<i>p</i> < 0.001
Height (µm)	146.25	31.11	201.50	29.49	<i>p</i> < 0.001
Depth (µm)	33.32	6.52	9.49	5.17	<i>p</i> < 0.001
Total Length (µm)	465.18	167.59	1090.68	310.27	<i>p</i> < 0.01
Surface Area (µm ²)	1415.67	623.56	3913.74	1420.74	<i>p</i> < 0.01
Volume (µm ³)	406.93	236.86	1291.92	595.80	<i>p</i> < 0.001
Rhizoidal Growth Unit (µm)	15.88	4.42	36.16	4.44	<i>p</i> < 0.001
Cover Area (µm ²)	22093.22	6323.01	43929.59	6729.19	<i>p</i> < 0.001
Mean Bifurcation Angle (°)	85.71	9.99	92.76	7.28	<i>p</i> < 0.001
Partition Asymmetry	0.54	0.11	0.53	0.15	<i>p</i> > 0.05
Max Euclidean Distance (µm)	32.80	11.82	127.76	27.94	<i>p</i> < 0.001
Max Path Distance (µm)	85.76	41.84	171.28	57.36	<i>p</i> < 0.05