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Alkane-grown *Beauveria bassiana* produce mycelial pellets displaying peroxisome proliferation, oxidative stress, and cell surface alterations

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- 2 Alkane-grown Beauveria bassiana produce mycelial pellets displaying peroxisome
- 3 proliferation, oxidative stress, and cell surface alterations

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#### Abstract

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The entomopathogenic fungus Beauveria bassiana is able to grow on insect cuticle hydrocarbons as the sole carbon source, inducing several enzymes involved in alkane assimilation and concomitantly increasing virulence against insect hosts. In this study, we describe some physiological and molecular processes implicated in growth, nutritional stress response, and cellular alterations found in alkane-grown fungi. The fungal cytology was investigated using light and transmission electron microscopy (TEM) while the surface topography was examined using atomic force microscopy (AFM). Fungal hydrophobicity was also measured on the cell surface. Additionally, the expression pattern of several genes associated with oxidative stress, peroxisome biogenesis, and hydrophobicity were analysed by qPCR. We found a novel type of growth in alkane-cultured B. bassiana similar to mycelial pellets described in other alkane-free fungi, which were able to germinate and produce viable conidia in media without a carbon source and to be pathogenic against larvae of the beetles Tenebrio molitor and Tribolium castaneum. Optical microscopy and TEM showed that pellets were formed by hyphae cumulates with high peroxidase activity, exhibiting peroxisome proliferation and an apparent surface thickening. Alkane-grown conidia appeared to be more hydrophobic and cell surfaces displayed different topography than glucose-grown cells, as it was observed by AFM. We also found a significant induction in several genes encoding for peroxins, catalases, superoxide dismutases, and hydrophobins. These results show that both morphological and metabolic changes are triggered in mycelial pellets derived from alkane-grown B. bassiana.

37 **Keywords:** entomopathogenic fungi, hydrocarbon degradation, hydrophobicity, peroxins.

#### Introduction

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Entomopathogenic fungi do not require any specialized mode of entry to invade their insect hosts; they usually start the infection cycle by penetrating through the insect epicuticle. This outermost cuticle layer is composed by lipids, mostly aliphatic hydrocarbons or alkanes with both straight-chain and methyl-branched, usually between 20 to more than 40 carbons (Pedrini et al., 2007). The ability of entomopathogenic fungi to degrade insect hydrocarbons and utilize them for energy production and for the biosynthesis of cellular components was first shown in Beauveria bassiana and Metarhizium anisopliae (Napolitano and Juárez, 1997). In addition, alkane-grown B. bassiana was more virulent than glucose-grown fungi by producing either higher insect mortality or lesser mean lethal time against different hosts (Crespo et al. 2002; Pedrini et al. 2009). Thus, alkane degradation by B. bassiana represents a key metabolic pathway related to the insect pathogenic nature of the fungus. However, growth on alkanes causes major changes in fungal metabolism (Crespo et al., 2000) and a scenario of oxidative stress is caused by the accumulation of reactive oxygen species, which is successfully overcome by the induction of antioxidant genes and enzymes (Huarte-Bonnet et al., 2015). Moreover, the spore yields in alkane-grown fungi are usually lower than those obtained in fungi grown in rich media (Napolitano and Juárez, 1997), impairing the achievement for acceptable mass production in industrial resources.

Filamentous fungi often grow in liquid cultures exhibiting a plethora of morphological structures, e.g. three-dimensional aggregates ranging from loose clumps of mycelia to dense pellets. Pellet growth seems favorable for the production of several biotechnological products, and the optimizations of pellets formation are constantly revised

(Wucherpfenning et al., 2010). In this regard, cell aggregation is dependent on several cultivation conditions like the initial particle concentration, the hydrodynamic conditions, and the pH value, among other factors (Grimm et al., 2005a). As far as we know, there are no reports about pellet formation in alkane-grown fungi. The aim of the current study was to characterise a novel type of cellular growth produced in alkane-cultured *B. bassiana*, similar to mycelial pellets described in other filamentous fungi. We described an oxidative stress scenario associated with peroxidase activity and peroxisome proliferation, the same as cell surface alterations in alkane-grown *B. bassiana*.

#### Materials and methods

#### 71 Cultivation of fungi

# 72 Fungal cultivation and inoculants preparation

Beauveria bassiana strain GHA was routinely cultured and maintained on potato dextrose agar (PDA) (BD Difco, Sparks, USA). Conidia harvested from this medium were suspended in 0.01% Tween 80 in sterile distilled water, vortexed for approximately 3 min, and filtered through a 75 μm sieve to remove debris. These conidial suspensions were adjusted in a Neubauer chamber to 1 × 10<sup>7</sup> conidia ml<sup>-1</sup>, and were used to inoculate complete liquid medium (CM) flasks and incubated at 26°C for 2 days with aeration (180 rpm). CM is composed by 0.4 g KH<sub>2</sub>PO<sub>4</sub>, 1.4 g Na<sub>2</sub>HPO<sub>4</sub>, 0.6 g MgSO<sub>4</sub>.7H<sub>2</sub>O, 1.0 g KCl, 0.7 g NH<sub>4</sub>NO<sub>3</sub>.7H<sub>2</sub>O, 10 g glucose, and 5 g yeast extract in 1,000 ml of distilled water. Fungi were harvested by centrifugation for 20 min at 7200×g, washed with sterile water, weighted and used as initial inoculums to grow under the same conditions for additional 3,

5 and 7 days in both CM and minimal liquid medium (MM) supplemented with *n*-hexadecane (MM-C16). MM is composed of CM without the glucose and yeast extract, and MM-C16 is MM supplemented with *n*-hexadecane (Sigma-Aldrich, USA) (C16, 1% final concentration) as previously described (Pedrini et al., 2010).

Conidia suspensions were inoculated in CM flasks and incubated at 26°C for 2 days with aeration (180 rpm). Fungi were harvested and grown under the same conditions for additional 3 and 7 days in CM and MM C16. Mycelia and conidia (referred from now on as biomass) were obtained by pellet centrifugation for 20 min at 7200×g. The remaining fungal cells that were found in close contact with the alkane interface in the supernatant were isolated from the media culture by filtration and are referred from now on as mycelial pellets. All cell samples were washed with sterile water. At each time period, pH was measured on the remaining media, and humid biomass was weighted. Humid biomass ratio was calculated as humid final biomass/initial inoculum mass.

#### Microbial adhesion to hydrocarbons (MATH) assay

Cell surface hydrophobicity was determined as Holder et al. (2007). Briefly, conidia obtained in CM and MM-C16 after 3, 5, and 7 days were washed in PUM buffer (per litre: 22.2 g K<sub>2</sub>HPO<sub>4</sub>, 7.26 g KH<sub>2</sub>PO<sub>4</sub>, 1.8 g urea, 0.2 g MgSO<sub>4</sub>. 7H<sub>2</sub>O, final pH 7.1). Fungal cell suspensions were adjusted to OD<sub>470</sub> 0.4 and dispensed into acid-washed glass tubes. Hexadecane was then added to each tube and samples were vortexed three times for 30 s each. The tubes were then incubated at 4°C for 10 min and after removal of the *n*-hexadecane solid phase the density of the resultant cell suspension determined in a spectrophotometer at 470nm. The hydrophobic index was calculated using the following

equation:  $(A_{470, \text{ control}}-A_{470, \text{ hexadecane treated}})/(A_{470, \text{ control}})$ . Four biological replicates with five repetitions each were measured.

#### Microscopy images

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For optical and transmission electron microscopy (TEM) images, seven day cultures from CM, MM-C16, and mycelial pellets were used. Fresh samples were observed with a Nikon eclipse e200 optical microscope (Nikon Corp., Japan). For TEM, samples were washed and fixed in glutaraldehyde 2% for 2 h with soft vacuum, then washed three times with phosphate buffer (pH 7.2-7.4). Postfixation was performed with 1% osmium tetroxide at 4°C for 1 h, followed by dehydration with a series of alcohols in a vacuum chamber. Samples were finally infiltrated with epoxy resin and thin sections of approximately 70 nm were cut. TEM observation was made in a JEM 1200 EX II (JEOL Ltd., Japan). For 3,3diaminobenzidine (DAB) (Sigma-Aldrich, USA) staining, an additional staining overnight with DAB was included in both fresh and fixated samples with glutaraldehyde 2%. In order to characterise the cell topography of fungi grown on CM and MM-C16, atomic force microscopy (AFM) images from 5 d conidia were obtained in air, using a MultiMode Scanning Probe Microscope (Veeco, USA) equipped with a Nanoscope V controller (Veeco). All measurements were obtained with Tapping® mode, using probes doped with silicon nitride (RTESP, Veeco with tip nominal radius of 8-12 nm, 271-311 kHz, force constant 20-80 N/m). Typical rate scanners were 1Hz. Fungal cells were placed on 0.22 μm pore-size Millipore filters and air-dried before examination.

#### Mycelial pellets viability and pathogenicity

Sporulation and viability of 7 d mycelial pellets were assessed as follows: fungal propagules were placed in Petri plates and held for 5 d at 4°C in a desiccator with activated silica gel until moisture content was reduced to  $\leq$  5% (w/w). Then, 30 mg of dried pellets were cultured in agar-agar media with ampicillin for 14 d at 26°C, growth was monitored daily and conidia produced were harvested with sterile water. Conidial production from the suspension was determined with a Neubauer chamber, calculated as total conidia/ initial dried pellet mass. To establish conidial viability, the suspension was also used to inoculate CM-agar plates and germination was monitored and calculated after 24 h at 26°C. For each replicate, 300 conidia were studied, and germination was calculated as 100 × germinated conidia/total conidia. For these tests, five replicates were done.

For pathogenicity assays, three groups of 10 larvae of each *T. castaneum* and *T. molitor* were placed in sterile plates containing a mixture of fresh 7 d mycelial pellets and humid vermiculite, prepared as follows: 0.325 g of mycelial pellets were placed in a sterile plate with 1.5 ml of sterile water, then 1.75 g of sterile vermiculite was added and mixed gently with a sterile spatula. Control plates were similarly prepared without the mycelial pellets. Beetles were maintained at 26°C and 70% RH. Mortality was checked every three days and all dead larvae were removed after each count. Afterward, dead beetles were washed in 70% ethanol for 30 s, rinsed in sterile distilled water for 2 min, allowed to dry, and then placed in individual humid chambers at 25°C to confirm fungal infection. The experiment was repeated two more times. Mortality data were corrected for control mortality using the Abbott's equation (Abbott, 1925).

# Gene expression analysis

148	Total RNA was extracted employing the RNAeasy Plant Mini kit (Qiagen,
149	Germany), including an on-column DNA digestion step (Qiagen). RNA samples were
150	quantified with a Nanodrop spectrophotometer (Thermo, USA), and the integrity was
151	assessed on a 1% (w/v) agarose gel. Two-step real-time polymerase chain reaction (RT-
152	PCR) was carried out with iScript cDNA Synthesis Kit and iQ SYBR Green Supermix
153	(Bio-Rad, USA). Amplification was performed in an StepOne Plus equipment (Applied
154	Biosystems, USA) employing 20 ng reverse transcribed total RNA for each sample.
155	Primers corresponding to oxidative stress markers Bbsod1, Bbsod2, Bbsod3, BbcatA,
156	BbcatB, BbcatC, BbcatD, BbcatP, Bbgpx and Bbgst, peroxisome biogenesis genes Bbpex5,
157	Bbpex7, Bbpex14/17 and Bbpex19, and hydrophobicity related genes Bbhyd1 and Bbhyd2
158	were designed using Gene Runner program. In order to confirm that only single products
159	were amplified, a temperature-melting step was then performed. The calibration curve
160	method was used for the analysis of data obtained from the RT-PCR system, with gamma
161	actin (Bbact) as the housekeeping gene. This gene was selected after a validation test with
162	geNorm algorithm for several commonly used housekeeping genes; i.e., Bb28, BbcypA,
163	Bbtub, BbCrza, Bbact and Bbgpd using Qbaseplus software (https://www.qbaseplus.com).
164	Four independent biological replicates were tested, with technical duplicates for each
165	sample. The relative expression ratio of each target gene was calculated with $\Delta\Delta Ct$
166	approach in MM-C16 cells and mycelial pellets, using CM cells as control. Primers used,
167	PCR efficiencies, and putative functions of the proteins encoded are listed in Table 1.

# Statistical analysis

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Differences among means were determined by two-way analysis of variance
(ANOVA) followed by the Tukey posttest, using GraphPad Prism (GraphPad Software
Inc., San Diego, CA).

#### Results

#### Fungal growth on hydrocarbons

After three days of culture with vigorous agitation, several macroscopic, spherical, non-uniform size aggregates appeared in C16-added MM (Fig. 1A). These aggregates were found in close contact with the hydrocarbon phase (they could not be isolated from the aqueous phase by centrifugation) but were not found in CM in the same growing conditions. Humid biomass (fungal cells excluding the mycelial pellets) and pH of the media were monitored and results are shown in Table 2. In all cases, biomass ratio (calculated as humid final mass/initial inoculum mass) was significantly lower (p < 0.05) in MM-C16 than in CM. pH behavior appeared to be inverted for minimal and complete cultures; cell-free MM-C16 had a decreased but not significant tendency in pH over days, whereas cell-free CM increased pH significantly (p < 0.01).

## Microbial adhesion to hydrocarbons (MATH) assay

Conidia from CM and MM-C16 cultures were isolated after 3, 5, and 7 days. The hydrophobic index (HI) for all samples is shown in Fig. 2. The HI from CM conidia decreased from 0.62 (day 3) to 0.25 (day 7) (p < 0.001). On day 3, the HI was significantly

higher (p < 0.05) in CM conidia than in MM-C16 conidia. On the contrary, on day 5 the HI was significantly higher (p < 0.01) in MM-C16 conidia than in CM conidia.

#### Microscopy images

After observation by optical microscopy, the spherical aggregates showed to be formed by hyphae cumulate. Optical microscopy showed that the spherical aggregates are formed by hyphal cumulates (Fig. 1B). Visible *n*-hexadecane droplets were found surrounding the pellet surface (Fig. 1C). Alkane-grown mycelial pellets were also stained with DAB, a chemical used for determining peroxidase activity, which is usually employed as peroxisome marker (Fahimi, 2017). The hyphal cumulates appeared strongly stained, different from hyphae close to the aggregate borders, which showed lower staining reaction. (Figs. 1D, E).

Alkane-grown mycelial pellets were also processed and observed by TEM, the same as fungal conidia and mycelia. The preparative section cuts from mycelial pellets were previously analysed by optical microscopy (Fig. 3A), where spheres looked like low dense clusters of fungal cells that might contain other compounds, like hydrocarbons, immersed in their structure. In the fungal cells forming the hyphal aggregates, TEM images showed surfaces with an irregular comb-like form facing the cytoplasm and small vesicles (Fig. 3B), the same as an apparent surface thickening  $(0.36 \,\mu\text{m})$  compared to MM-C16  $(0.15 \,\mu\text{m})$  (Fig. 3C) and CM cells  $(0.11 \,\mu\text{m})$  (Fig. 3D). Images from DAB stained mycelial pellets revealed higher peroxidase activity, visualized as small black dots due to DAB reaction with  $H_2O_2$ , inside the cells and also in cellular interconnections; several peroxisomes and clear hairpin-like structures in the cell surface were also observed (Figs.

211	3E, F). On the contrary, DAB staining CM cells revealed lower peroxidase activity, mainly
212	found in vacuoles, fewer or not clear mature peroxisomes and smooth cell surfaces (Figs.
213	3G, H).

AFM images were obtained for CM and MM-C16 conidia from 5-day cultures, showing distinctive differences on cell surfaces. CM conidia displayed irregular forms and different and variable diameters (between 1.5 and 5.4 μm) (Figs. 4A, C). On the contrary, MM-C16 conidia looked like a spherical form, smaller, and homogeneous (between 0.9 and 2.5 μm) (Figs. 4B, D). Also, CM conidia showed distinctive topographical characteristics with deep and rough edges, whereas MM conidia showed a more uniform structure (Figs. 4E, F).

# Mycelial pellets viability and pathogenicity

Dried mycelial pellets were cultured in agar-agar plates. Hyphal growth was visible after two days and sporulation started on day 6. At day 14, conidia were harvested and counted. Conidial production varied from  $1 \times 10^9$  to  $5 \times 10^9$  conidia per gram of dried pellet and germination in CM plates was 99.7%. Pathogenicity bioassays were done with fresh 7 d mycelial pellets and results are shown in Table 3. At day 8, *T. castaneum* mortality was  $67.3 \pm 13.1$  % mortality in all replicates, whereas *T. molitor* reached  $96.7 \pm 1.9$  % at day 8. These results showed that mycelial pellets are formed by active fungal cells, pathogenic against beetle larvae, which can grow without an external carbon source producing viable conidia.

#### Gene expression analysis

Antioxidant stress-marker genes displayed different expression patterns in alkane-
grown mycelial pellets (Fig. 5A). For the superoxide dismutase family, Bbsod1 was
induced on day 3 (6.1-fold induction), but not as significantly as on day 7. In contrast,
Bbsod3 was induced on day 3 and day 7 (1.7- and 4.9-fold induction, respectively).
However, Bbsod2 was not induced in the conditions tested. For the glutathione system,
Bbgst showed little induction (3.4- and 1.8-fold on day 3 and day 7, respectively), and
Bbgpx expression was reduced on day 3 (0.7-fold) and induced at day 7 (2.5-fold). For the
catalase family, Bbcatb (4.9-fold expression at day 3), Bbcatc (4.2- and 4.7-fold on day 3
and day 7, respectively) and Bbcatp (14.8-fold and 4.3-fold on day 3 and day 7,
respectively) were induced in alkane cultures. Moreover, the peroxisomal-protein encoding
gene <i>Bbcatp</i> was significantly induced ( $p < 0.01$ ) on day 3 compared with day 7.

In order to study the expression pattern of genes involved in the peroxisomes biosynthesis pathway, several genes encoding for PEX proteins were also measured by qPCR (Fig. 5B). Some *pex* genes were induced in mycelial pellets, as follows: *Bbpex7* (2.5-fold expression on day 3), *Bbpex14/17* (1.9-fold and 4.5-fold on day 3 and 7, respectively) and *Bbpex19* (2.8-fold and 3.9-fold on day 3 and 7, respectively). In contrast, *Bbpex7* and *Bbpex5* were not induced on day 7, and at both time periods, respectively.

To study candidate genes involved in cell surface hydrophobicity, hydrophobin genes were measured in mycelial pellets and MM-C16 biomass, using CM biomass as control (Fig. 5C). Although *Bbhyd1* and *Bbhyd2* genes were not induced in mycelial pellets, both genes were strongly induced on day 3 and day 7 in MM-C16 biomass. The transcripts levels of *Bbhyd1* were 22.8-fold induction and 5.8-fold induction on day 3 and day 7, respectively. For *Bbhyd2*, the expression level was 74.1-fold induction on day 3, and 13.9-

fold induction on day 7. Thus, gene expression for *Bbhyd2* at day 3 was significantly higher (p<0.001) than on day 7.

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#### Discussion

A novel type of growth was described in B. bassiana cultured in hexadecanesupplemented liquid minimal media, consisting in hyphal aggregates similar to mycelial pellets found in other filamentous fungi (Grimm et al., 2005a; Metz and Kossen, 1977). However, B. bassiana pellets were found only in alkane-grown fungi but not in glucosegrown cells. These complex structures resulted to be stable, spherical aggregates, formed by branched and partially intertwined hyphae networks that were able to germinate and produce viable conidia without an external carbon source. Preliminary pathogenity assays showed that after one week, these propagules caused the death of mealworms and red flour beetle larvae. Apart from the mycelial pellets development, no significant increment was recorded in MM-C16 biomass during the entire incubation period; in contrast to CM cultures, where biomass was more than 4 times higher than the initial inoculums. It has been already reported that B. bassiana is capable of growing on media supplemented with hydrocarbons; moreover, it was established that n-hexadecane was the preferred substrate among several hydrocarbons tested (Huarte-Bonnet et al., 2017; Pedrini et al., 2010). Thus, these results indicate that alkane-grown B. bassiana is actually under active division and growth, but these new cells are forming mycelial pellets in the alkane interface and are not part of the initial biomass.

Differences in both hydrophobic cell surface indexes and pH pattern were found in conidial cells isolated from CM and MM-C16 biomass. AFM images also showed topographical differences between CM and MM-C16 conidia. It is clear that the presence of *n*-hexadecane is triggering different cell responses in order to uptake this hydrophobic substrate. Although it is well established how *B. bassiana* degrade cuticular hydrocarbons (Pedrini et al., 2007; 2010; 2013), little is known about the mechanisms involved in the uptake of alkanes by entomopathogenic fungi. It is believed that different compounds are secreted or anchored to the fungal cell surface to internalize those carbon sources, as shown by TEM images in both conidia (Pedrini et al., 2007) and mycelial pellets (this study).

The present study also showed different pH patterns between CM and MM-C16 remaining liquid media. In this regard, secretion of acid compounds could be responsible for the acidification of the media observed in MM-C16 cultures. Oxalic acid was reported to be secreted by *B. bassiana* as a virulence factor against ticks, and its secretion was dependent on the media used (Kirkland et al., 2005). Also, alkane-assimilating microorganisms are known to secrete acid biosurfactants to facilitate hydrocarbon uptake; e.g., acidic sophorolipids, free fatty acids, among others (Kitamoto et al., 2002). Thus, it could be expected that similar compounds might be found in the remaining media of alkane-grown *B. bassiana*. Differential pH in the remaining media and cell surface hydrophobicity might indirectly shed light to possible mechanisms of secretion and cell surface adaptation to hydrocarbon growth that is still to be discovered. It was also previously shown that *B. bassiana*, neither *M. anisopliae* nor *Aspergillus niger*, strongly acidified the liquid minimal media supplemented with alkanes (Huarte-Bonnet et al., 2017). As pellet formation is highly regulated by pH in other filamentous fungi (Dynesen and

Nielsen, 2003; Glazebrook et al., 1992; Grimm et al., 2005b; Ryoo and Choi, 1999), pH values might be either the cause or the consequence to pellet formation in alkane-grown *B. bassiana*. Also, hydrophobins might play a role in hydrocarbons uptake. In this regard, we found that though no induction was observed for *hyd* genes in mycelial pellets, MM-C16 biomass showed high expression of both *Bbhyd1* and *Bbhyd2*. However, hydrophobins play a key role in pellet formation in *A. niger*, and hydrophobic interactions in the cell surface were reported to favor the formation and stability of these aggregates (Dynesen and Nielsen, 2003). These results suggest that although *hyd* genes are highly induced in *B. bassiana* biomass immediately after contact with hydrocarbons, the mycelial pellets derived from those cells did not express these genes since they might already have these proteins in their surfaces. However, further assays to specifically detect hydrophobins in both fungal cells are required to confirm this hypothesis.

An antistress response was triggered in mycelial pellets during growth on alkanes, in coincidence with previous results obtained for MM-C16 biomass grown in similar culture conditions (Huarte-Bonnet et al., 2015). In mycelial pellets, at least one gene of each antistress response family was up-regulated at each time incubation period. Thus, catalase and superoxide dismutase gene induction could also be used as clues for reactive oxygen species localization, i.e., *Bbsod1* encodes for a Cu/Zn-dependent superoxide dismutase localized in the cytoplasm (Xie et al., 2010) and *Bbsod3* encodes for a mitochondrial Mn-isoform (Xie et al., 2012), whereas *Bbcatb*, *Bbcatc*, and *Bbcatp* encode for cytoplasmic, secreted, and peroxisomal catalases, respectively (Wang et al., 2013). In fact, the peroxisomal isoform was the most induced gene from the antistress response system in mycelial pellets. However, gene expression data is not sufficient to fully

comprehend if the observed upregulation is useful to protect cells against potential antagonists (both biotic and abiotic) or if it is a result to cells differentiation into mycelial pellets, or both. Targeted single-gene knockout strategies and/or enzymatic studies in subcellular fractions will be needed to confirm this point.

Peroxisomes are known to be the organelles where the last hydrocarbon degradation reactions take place in *B. bassiana* (Pedrini et al., 2007). The biogenesis of peroxisomes involves the action of several proteins, named peroxins, which are encoded by *pex* genes (Li et al., 2016; Smith and Aitchison, 2013). In this study, *Bbpex7*, *Bbpex14/17*, and *Bbpex19* were induced after 3 and/or 7 days of culture. In addition to gene expression patterns, mycelial pellets staining reaction with DAB gave strongly brown stained cells inside the pellet structure, but also inside the individual cells, indicating high catalase/peroxidase activity and peroxisomal proliferation. Moreover, the high number of small black dots found inside alkane-grown cells and the induction of *pex* genes are suggesting that the peroxisome biogenesis pathway is being activated under this growth condition, as it was reported for alkane-grown yeast (Fukui and Tanaka, 1979; Monosov et al., 1996; Smith and Aitchison, 2013; Tanaka and Ueda, 1993).

We conclude that two cellular populations are present in fungi grown in liquid minimal media supplemented with *n*-hexadecane. Both fungal propagules have different molecular and physiological characteristics between them and also compared to cells grown in rich media. In this sense, several unknown direct or indirect responses to hydrocarbon supplementation might be acting as triggers to initiate pellet formation since they are not present in rich media in the same incubation conditions. For other filamentous fungi, pellets formation in liquid cultures are preferred for the non-vicuos rheology of the broth, better

mass transfer and easier pellet separation than with mycelial cultures (Wucherpfenning et al., 2010). In alkane-grown fungi, hydrocarbon droplets in liquid media might be acting as initial nucleation for pellets formation since these structures might assure fungal cells of an easy access to the hydrophobic carbon source in the interface. However, additional studies are needed to better understand the relationship between fungal metabolic adaptations in hydrocarbon-supplemented cultures and pellet formation.

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448

451	Figure legends
452	Fig. 1. A) Mycelial pellets in aqueous solution in a test tube. B) Phase-contrast microscopy
453	of an isolated pellet formed by hyphae cumulates (40× magnification). C) Hexadecane
454	droplets surrounding the mycelial pellet (10× magnification). D) Mycelial pellet stained
455	with DAB (10× magnification). E) Mycelial pellet stained with DAB (20× magnification).
456	
457	Fig. 2. Cell surface hydrophobicity of CM and MM-C16 conidia after 3, 5 and 7 days of
458	culture. * $(p < 0.05)$ , ** $(p < 0.01)$ .
459	
460	Fig. 3. A) Optical observation of a semi-thin section of a mycelial pellet showing the
461	hyphal cumulate structure (40× magnification). B) Ultrastructure of mycelial pellets at
462	50,000× magnification. C) Ultrastructure of MM-C16 biomass at 30,000× magnification.
463	D) Ultrastructure of CM biomass at 30,000× magnification. E), F) Ultrastructure of
464	mycelial pellets at $30,000 \times$ magnification stained with DAB. The reaction appears as black
465	dots (white arrow), and several peroxisomes are visible. Hairpin-like structures are found in
466	the cell surface (black arrow). G), H) Ultrastructure of CM biomass at $30,000 \times$
467	magnification stained with DAB. The reaction is positive mainly in vacuoles, and fewer or
468	none peroxisomes are visible. V: vacuole. N: nucleus. M: mitochondrium. P: peroxisome.
469	

470	Fig. 4. Atomic force microscopy images of MM-C16 conidia (A, C, E) and CM conidia
471	(B, D, F) obtained in tapping mode. Images have a resolution of 512 x 512 pixels. The
472	height is expressed in color scale (right bar).
473	
474	<b>Fig. 5.</b> Gene expression ratios of 3 days and 7 days of s of <i>B. bassiana</i> grown in MM-C16
475	or CM (control). A) Oxidative stress marker genes in mycelial pellets. B) Peroxin genes in
476	mycelial pellets. C) Hydrophobin genes in mycelial pellets (MP) and MM-C16 biomass.
477	Error bars represent standard errors of four independent assays. Dashed line showed a
478	relative expression ratio = 1. **( $p$ < 0.01), *** ( $p$ < 0.001).

 Table 1. Oligonucleotides used in this study.

Name	Forward primer	Reverse primer	Effici ency	$\mathbb{R}^2$	Name/Function	Reference
Bbact	ATGGAGGAAGAAGTTGCTGC	ACACGGAGCTCGTTGTAGAA	(%) 112.7	0.992	γ-Actin	Zhou et. al. (2012)
Bbsod1	ACAACACCAACGGCTGCACC	ACGGCCAACAACGCTGTGAG	116	0.997	Cu/Zn- superoxide dismutase / O <sub>2</sub> - scavenging	Forlani et. al. (2014)
Bbsod2	CCAGTGTTTGGCATTGACATG	TCAGCCGTCTTCCAGTTGATG	105.6	0.996	Mn-superoxide dismutase / O <sub>2</sub> <sup>-</sup> scavenging	Forlani et. al. (2014)
Bbsod3	ACATCAATCACACTCTCTTCTG	GCGTTGGTCTGCTTCTTG	103.1	0.992	Mn-superoxide dismutase / O <sub>2</sub> <sup>-</sup> scavenging	Forlani et. al. (2014)
Bbgpx	CAAGGTCGTCCTCGTCAAC	CTTGTCGCCATTGACCTCCACC	122.5	0.994	Glutathione peroxidase / GSH protection system	Forlani et. al. (2014)
Bbgst	TCTTGTAGCCAGCCCTCCATCG	AGAGATGTGGTCGCGGAACGA	115.5	0.969	Glutathione-S- transferase / GSH protection system	Forlani et. al. (2014)
Bbcata	GAAAGCCGCGCAAGTGAAAG	TCTCTGGCAAAGACATCCAG	107.2	0.993	Spore-specific catalase/ H <sub>2</sub> O <sub>2</sub> scavenging	Forlani et. al. (2014)
Bbcatb	GAAGACGCCCATGTTTGTTCG	AAAGTTGCCCTCATCGGTATAGC	117.3	0.987	Secreted catalase/ H <sub>2</sub> O <sub>2</sub> scavenging	Forlani et. al. (2014)
Bbcatc	TGCTGGACGATGTGTCTGAC	CACGCACCGTATCGCTAGAG	108.6	0.991	Cytoplasmic catalase/ H <sub>2</sub> O <sub>2</sub> scavenging	Forlani et. al. (2014)
Bbcatd	GCGCTCGCAGTGACTGTAC	CTAGCACGGCCCTGTATAATGG	113.3	0.998	Secreted peroxidase/catalase / H <sub>2</sub> O <sub>2</sub> scavenging	Forlani et. al. (2014)
Bbcatp	TGTACTGGGGCTCCGAACC	ATGAGACCTGTGTAGCGTTAGC	105.7	0.967	Peroxisomal catalase/ β-oxidation pathway	Forlani et. al. (2014)
Bbpex5	AATGCCGGGCCGAATATGC	CAGGCTGGCTGTTGAAATCGTG	130.2	0.991	Peroxisomal	This study

					biogenesis factor 5/ PTS1 import receptor	
					<b>.</b>	
Bbpex7	TCGCTTCGGCTGCCAATTTC	TGCGACAATGAGCTGGTTCTCG	111.1	0.993	Peroxisomal	This study
					biogenesis factor 7/	
					PTS2 import	
			8		receptor	
Bbpex14/	TCGCCAACCTCGTCAGACACTG	CCTCGACGCCCTTTGACTTGAG	114.3	0.991	Peroxisomal	This study
17					biogenesis factor	
					14/17/ Receptor	
					docking complex	
Bbpex19	AAGTTCCCTGTCTGGCTGTCGG	CCGGCAAAGGCTTCTTGTGC	114.3	0.993	Peroxisomal	This study
					biogenesis factor	
					19/ soluble	
					chaperone and	
D11 11			100.7	0.006	receptor	7D1 ' 4 1
Bbhyd1	CACCATGGTGGAAAGGATCTGCAC	CCGAGAAGGTGGGAAAGAAGACCA	108.5	0.996	Hydrophobin 1 /	This study
		<u> </u>			cell surface	
Bbhyd2	TGTCAAGACTGGCGACATTTGCG	TCGATGGGGACAAGCTGGTTGA	117.7	0.985	hydrophobicity Hydrophobin 2 /	This study
Donya2	TOTCAAGACTOGCGACATTIGCG	ICUATUUUACAAUCTUUTTUA	11/./	0.903	cell surface	Tills study
					hydrophobicity	

**Table 2.** Determination of humid biomass ratio and pH of the remaining media at different time periods. For both assays, values in each column followed by different lowercase letters and values in each line followed by different uppercase letters indicate significant differences (p<0.05).

Day	Bioma	ss ratio	pH		
	MM-C16	CM	MM-C16	CM	
3	$1.2 \pm 0.2$ aA	$6.1 \pm 0.8$ aB	$6.1 \pm 0.4$ aA	$3.6 \pm 0.1$ aB	
5	$1.2 \pm 0.2$ aA	$7.4 \pm 1.4$ aB	$5.4 \pm 0.7$ aA	$6.5 \pm 0.1$ bA	
7	$1.1 \pm 0.3$ aA	$5.4 \pm 1.9$ aB	$4.9 \pm 0.5$ aA	$7.1 \pm 0.1$ cB	

**Table 3.** Pathogenicity bioassay. Cumulative percentage mortality  $\pm$  SEM of *Tribolium* castaneum and *Tenebrio molitor* larvae treated with *Beauveria bassiana* mycelial pellets and corrected for control mortality using the Abbott's formula. For both insects, different letters indicate significant differences (p < 0.05).

Day	Mortality (%)			
	Tribolium castaneum	Tenebrio molitor		
0	$0 \pm 0a$	$0 \pm 0a$		
2	$0 \pm 0a$	$0 \pm 0a$		
5	$70.2 \pm 11.9$ b	$53.3 \pm 10.7$ b		
8	$67.3 \pm 13.1$ b	$96.7 \pm 1.9c$		









