



Penicillium and *Talaromyces* endophytes from *Tillandsia catimbauensis*, a bromeliad endemic in the Brazilian tropical dry forest, and their potential for L-asparaginase production

Leticia F. Silva¹ · Karla T. L. S. Freire¹ · Gianne R. Araújo-Magalhães² · Gualberto S. Agamez-Montalvo³ · Minelli A. Sousa¹ · Tales A. Costa-Silva⁴ · Laura M. Paiva¹ · Adalberto Pessoa-Junior⁴ · Jadson D. P. Bezerra¹ · Cristina M. Souza-Motta¹

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Abstract

This study was conducted to report the richness of endophytic *Penicillium* and *Talaromyces* species isolated from *Tillandsia catimbauensis*, a bromeliad endemic in the Brazilian tropical dry forest (Caatinga), to verify their ability to produce the enzyme L-asparaginase and to partially optimise the production of biomass and L-asparaginase of the best enzyme producer. A total of 184 endophytes were isolated, of which 52 (29%) were identified through morphological and phylogenetic analysis using β -tubulin sequences into nine putative species, four in *Penicillium* and five in *Talaromyces*. *Talaromyces diversus* and *T. cf. cecidicola* were the most frequent taxa. Among the 20 endophytic isolates selected for L-asparaginase production, 10 had the potential to produce the enzyme (0.50–2.30 U/g), especially *T. cf. cecidicola* URM 7826 (2.30 U/g) and *Penicillium* sp. 4 URM 7827 (1.28 U/g). As *T. cf. cecidicola* URM 7826 exhibited significant ability to produce the enzyme, it was selected for the partial optimisation of biomass and L-asparaginase production. Results of the 2³ factorial experimental design showed that the highest dry biomass (0.66 g) was obtained under pH 6.0, inoculum concentration of 1×10^8 and 1% L-proline. However, the inoculum concentration was found to be statistically significant, the pH was marginally significant and the concentration of L-proline was not statistically significant. L-Asparaginase production varied between 0.58 and 1.02 U/g and did not reach the optimal point for enzyme production. This study demonstrates that *T. catimbauensis* is colonised by different *Penicillium* and *Talaromyces* species, which are indicated for enzyme production studies.

Keywords Bromeliad · Biomass optimisation · Fungi ecology · Endophytes · Enzyme

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✉ Jadson D. P. Bezerra
jadsondpb@gmail.com

✉ Cristina M. Souza-Motta
cristina.motta@ufpe.br

¹ Departamento de Micologia Prof. Chaves Batista, CB, Universidade Federal de Pernambuco, Av. Professor Nelson Chaves, s/n, Cidade Universitária, Recife, Pernambuco CEP: 50670-901, Brazil

² Programa de Pós Graduação em Biociência Animal, Departamento de Morfologia e Fisiologia Animal, Universidade Federal Rural de Pernambuco, Rua Manoel de Medeiros, s/n, Dois Irmãos, Recife, Pernambuco CEP: 52171-900, Brazil

³ Departamento de Estatística e Matemática Aplicada, Universidade Federal do Ceará, Av. Mister Hull, s/n, Pici, Fortaleza, Ceará CEP: 60455-760, Brazil

⁴ Faculdade de Ciências Farmacêuticas, Universidade de São Paulo, Av. Prof. Lineu Prestes, 580, B16, Cidade Universitária, São Paulo, SP CEP: 05508-000, Brazil

Introduction

Endophytes are microorganisms that colonise the host plant tissues at both intracellular and inter-cellular levels without causing disease symptoms (Tan and Zou 2001). Through this symbiotic interaction, microorganisms can produce compounds that provide resistance to phytopathogens, prevent being eaten by herbivores and enhance the development of the host plant (Arnold et al. 2003; Waqas et al. 2012; Zhou et al. 2016). Furthermore, the host provides an environment with less competition and greater nutritional source to the endophytic fungi (Peixoto Neto et al. 2004). Strobel and Daisy (2003) described that of about 300,000 existing plant species, each individual plant host harbours one or more endophytic microorganisms; however, only a few of these plants have been investigated for their endophytic microbiota. Therefore, there are tremendous possibilities of identifying new endophytes with biotechnological potential in plants from different environments.

Although only a few studies have confirmed the fungal endophytic associations of plants from desert, semi-arid, arid and dry tropical rainforest environments, these surveys have reported a remarkable diversity of endophytes (Fisher et al. 1994; Suryanarayanan et al. 2005; Khidir et al. 2010; Loro et al. 2012; Sun et al. 2012; Bezerra et al. 2012a, b, 2013). Few studies from Brazil have also contributed to the knowledge of the endophytic mycobiota of Caatinga plants, such as the studies on the cacti *Opuntia ficus-indica* (Bezerra et al. 2012a; Freire et al. 2015), *Cereus jamacaru* (Bezerra et al. 2013) and *Tacinga inamoena* (Bezerra et al. 2017); on *Mandevilla catimbauensis* (Apocynaceae) (Crous et al. 2017) and on the Fabaceae species *Indigofera suffruticosa* (Santos et al. 2015a).

Endophytic microorganisms have been considered as a major source of bioactive compounds as they occupy unique biological niches (Strobel and Daisy 2003). Chapla et al. (2013) reported that endophytic fungi have an excellent potential to produce yet unidentified bioactive substances that have been reported to have the potential to produce enzymes (Bischoff et al. 2009; Bezerra et al. 2012a, 2015), antimicrobials (Pinheiro et al. 2013; Kusari et al. 2013; Bezerra et al. 2015; Pires et al. 2015), plant growth hormones (Silva et al. 2006; Ting et al. 2008; Hwang et al. 2011) and other compounds of medicinal interest (Meng et al. 2011) such as the enzyme L-asparaginase (Theantana et al. 2007; Kalyanasundaram et al. 2015; Santos et al. 2015b).

Some studies on the diversity of endophytes in dry environments (Bezerra et al. 2012a, 2013, 2015; Freire et al. 2015) have reported the presence of the endophytic species of the genera *Penicillium* and *Talaromyces*, which were also proven to be promising sources for the production of L-asparaginase. For example, the endophyte *Talaromyces pinophilus* isolated from *Curcuma amada* can be considered as a

potential candidate for industrial and clinical trials on the production of the enzyme L-asparaginase (Krishnapura and Belur 2016). Theantana et al. (2009) also verified that the endophytic *Penicillium* and *Talaromyces* species exhibited a high enzymatic activity when isolated from medicinal plants in Thailand. Another study by Chow and Ting (2015) also demonstrated that endophytes associated with plants have anticancer properties and further reported *P. simplicissimum* as one of the best producers of L-asparaginase. Another study from Brazil on the endophytes from the Caatinga cactus *C. jamacaru* also confirmed the enzymatic potential of *Penicillium* isolates, highlighting *P. brevicompactum* as the best L-asparaginase producer (Santos et al. 2015b).

L-asparaginase is an enzyme that catalyses the hydrolysis of the amino acid asparagine in ammonia and aspartic acid (Jain et al. 2012; Jha et al. 2012; Nomme et al. 2012). This enzyme has been used as an important drug in the treatment of several types of cancers (Devi and Azmi 2012; Guilleme et al. 2013). Its mechanism of action results in the extracellular reduction of the amino acid asparagine, which inhibits protein synthesis and induces apoptosis of neoplastic cells (Guilleme et al. 2013). The enzyme is mainly derived from bacteria, and its long-term use may cause hypersensitivity and lead to allergic reactions and anaphylaxis (Duval et al. 2002; Sarquis et al. 2004). In addition to its medicinal importance, this enzyme has been used in the food industry as an alternative for the reduction of acrylamide in foods (Hendriksen et al. 2009; Kornbrust et al. 2009). Acrylamide has been classified as a potentially carcinogenic compound for humans, which is formed in cooked and fried foods, especially in carbohydrate-rich foods that are heat-treated (Kumar et al. 2014; Zuo et al. 2015). L-asparaginase can reduce the level of free asparagine by hydrolysis, thus removing one of the essential compounds for the formation of acrylamide, but not affecting most of the amino acids (Hendriksen et al. 2009; Kornbrust et al. 2009). This enzyme has been commercially produced from two fungal sources, *Aspergillus oryzae* and *A. niger* (Krishnakumar and Visvanathan 2014). According to Jha et al. (2012), there is a need for a greater search by the food and pharmacological industries to meet the demands of this enzyme. However, no study has yet investigated the potential of L-asparaginase production by *Penicillium* and *Talaromyces* isolates from the bromeliad *Tillandsia catimbauensis*.

Tillandsia catimbauensis is an endemic bromeliad in the Brazilian tropical dry forest (Caatinga). However, due to its restricted distribution and conservation status of protected areas of the Caatinga in the conservation units, this species is under a critical risk of extinction (Santos et al. 2011; Fabricante et al. 2014; Ferreira et al. 2015). The Catimbau National Park is the only Caatinga region that has records of *T. catimbauensis* in its natural environment, protecting about 62,000 ha of the forest that occupies 54% of the north-east region and 11% of the country, presenting a remarkable

diversity of flora and fauna with several endemic species (Leal et al. 2003; Alves et al. 2009; Fabricante et al. 2014; Ferreira et al. 2015; ICMBio 2018).

Considering the uniqueness of the bromeliad *T. catimbauensis* in the Brazilian tropical dry forest (Caatinga) and the significance of the verification of the biotechnological capacity of L-asparaginase production by the endophytes, this study was conducted with the following aims: (a) to report the richness of the endophytic *Penicillium* and *Talaromyces* isolates from *T. catimbauensis*, (b) to investigate the potential of the isolates for the production of L-asparaginase and (c) to use the most promising endophytic fungus in terms of the enzymatic activity in the partial optimisation stage of fungal biomass and L-asparaginase production.

Materials and methods

Plant material collection

The plant material was collected from the areas of the Caatinga forest in the Catimbau National Park, Buíque, Pernambuco, Brazil (8°36'35" S, 37°14'40" W). The Caatinga forest is primarily characterised by a shrub, spiny and branched vegetation, consisting of several bromeliads, cacti and euphorbiaceous plants (Leal et al. 2005). This forest has a warm and semi-arid climate, with rainfall < 1000 mm/year distributed within a range of 3–6 months (Velloso et al. 2002) and an average annual temperature between 20 and 28 °C (Maracajá and Benevides 2006). The leaves of the bromeliad *T. catimbauensis* (Fig. 1) were collected from 15 individual plants during the dry season in May 2015. The collections were authorised by the Ministério do Meio Ambiente (MMA)/Instituto Chico



Fig. 1 *Tillandsia catimbauensis*, an endemic bromeliad in Brazil and native to the Caatinga forest, in its natural environment in the Catimbau National Park, Pernambuco, Brazil (8°36'35" S, 37°14'40" W)

Mendes para Conservação da Biodiversidade (ICMBio), the approval being issued on 10 April 2015; permission number: 48641-1 and authentication code: 17827693.

Endophytic fungi isolation

The plant material was used within 48 h of collection, and the endophytic fungi were isolated as described by Bezerra et al. (2015). Briefly, the leaves of the bromeliad were cut into fragments measuring about 10 cm and washed with water containing neutral detergent. Subsequently, the asepsis of the leaves was achieved by soaking them in 70% ethanol for 60 s, sodium hypochlorite (2–2.5% active chlorine) for 180 s and 70% ethanol for 30 s, followed by washing three times with distilled and sterilised water. Under aseptic conditions, 28 fragments measuring about 1 cm² were cut from the plant tissue of each individual (totalling 420 fragments), transferred to Petri dishes containing potato dextrose agar (PDA) supplemented with the antibiotics chloramphenicol (100 mg/L) and tetracycline (50 mg/L) and then incubated at 28 °C ± 2 °C for up to 30 days. To verify the effectiveness of asepsis, 1-mL aliquots of the last water wash were transferred to Petri dishes containing the same culture medium and incubated under the same conditions.

Endophytic fungi identification

All the endophytic fungi that were morphologically identified as *Penicillium* sp. were cultured on malt extract agar (MEA) for 7 days at 25 °C. Slides were prepared using lactic acid, and the fungal microstructures (conidiophores, phialides, conidia, etc.) were analysed. Representative endophytic strains are deposited in the URM culture collection (*Micoteca URM Prof. Maria Auxiliadora Cavalcanti*) at the Federal University of Pernambuco, Recife, Brazil.

Genomic DNA was extracted for molecular analysis from all the endophytic fungi that were morphologically grouped as *Penicillium* spp. The genomic DNA was obtained from the colonies grown on MEA for 7 days at 25 °C using the Wizard® Genomic DNA Purification Kit (Promega, Madison, WI) according to the manufacturer's instructions. DNA amplification of a part of the gene β -tubulin was performed using the primers Bt2a and Bt2b (Glass and Donaldson 1995), and PCR was carried out as described by Visagie et al. (2014). Sequencing and sequence analyses were performed as described by Bezerra et al. (2017).

The sequences obtained in this study were used for conducting searches using the tool BLASTn in the GenBank database at NCBI for verifying the previous identity with sequences deposited in the database. After these searches, an alignment was constructed using the sequences from the type material or the reference strains according to Houbraken and Samson (2011), Yilmaz et al. (2014) and Visagie et al. (2014,

2016). The online MAFFT interface (Kato and Standley 2013) was used to perform the alignment, and MEGA v. 7.0 (Kumar et al. 2016) was used for sequence adjustments. The maximum likelihood (ML) analysis was performed using MEGA v. 7.0 with 1000 bootstrap replicates, and gaps were treated as missing data. The general time-reversible (GTR) nucleotide substitution model was estimated using the online tool Findmodel (<http://www.hiv.lanl.gov/content/sequence/findmodel/findmodel.html>). The tree that was obtained was printed using TreeView v. 1.6.6 (Page 1996). Newly generated β -tubulin sequences were deposited in the GenBank database (MG906521–MG906572).

L-Asparaginase production in liquid medium

A total of 20 endophytes belonging to the genera *Penicillium* and *Talaromyces* (10 for each genus) were randomly selected for evaluating the production of L-asparaginase. First, the biomass production was carried out using Czapek Dox's medium (CDM) modified by adding L-asparagine (Saxena and Sinha 1981), modified by Gulati et al. (1997). Erlenmeyer flasks (250 mL) containing 50 mL of CDM were inoculated with 1 mL of spore suspension (1×10^8). These flasks were incubated at 30 °C for 96 h at 120 rpm. Then, the cultures were filtered using Whatman no. 1 filter paper, and the biomass thus obtained was used for analysing enzyme production. The biomass obtained in the first step was inoculated into the modified CDM as described previously, but with two differences, i.e. the glucose concentration was adjusted from 14.0 to 2.0 g/L, and no $(\text{NH}_4)_2\text{SO}_4$ (2.0 g/L) was added. The inoculated media were incubated at 30 °C for 96 h at 120 rpm. Finally, the cultures were filtered using Whatman no. 1 filter paper, and the biomass thus obtained was used for quantification of the enzymatic activity (Loureiro et al. 2012, modified).

L-Asparaginase activity

L-asparaginase activity was determined according to Drainas et al. (1977) with the following modifications: 1.5 mL Tris–HCl buffer (20 mM, pH 8.6) and 0.1 g of mycelium from each culture obtained during the fermentation step were macerated and vortexed. To the samples, 0.2 mL of L-asparagine solution (100 mM) and 0.2 mL of stock hydroxylamine solution (1 M, pH 7.0) were added and incubated at 37 °C at 150 rpm. After 30 min, the reaction was stopped by adding 0.5 mL of ferric chloride reagent [10% (w/v) FeCl_3 plus 5% (w/v) trichloroacetic acid in 0.66 mol/L HCl] to all the samples and the blank samples (Tris–HCl and mycelium). The reaction mixture was centrifuged at 6000 rpm for 15 min at 4 °C to remove the precipitates. Absorbance was measured at 500 nm against the blank samples that received L-asparagine and hydroxylamine solutions after 30 min of

incubation. One unit of L-asparaginase was defined as the amount of enzyme that releases 1 μmol of β -hydroxamic aspartic acid per minute.

Partial optimisation of fungal biomass and L-asparaginase production

For determining the best producer of L-asparaginase, a statistical experimental design was used to optimise the fungal biomass production. In this study, the 2^3 factorial design (Myers and Montgomery 1995; Box et al. 2005) was selected to evaluate the influence of the variables on biomass production. This experimental design comprised 12 trials, three variables with two levels for each variable (2^3) and four replications at the central point. The variables that were analysed in this study were L-proline concentration, pH and inoculum (spore) concentration (Suppl. Table 1). L-proline was chosen as the substrate based on analyses of previous experiments (unpublished data), which had demonstrated it as the best inducer of fungal biomass production. At this stage, 100 mL of CDM was added to the Erlenmeyer flasks (250 mL), and the culture media were adjusted according to the specific conditions for each trial design. These flasks were incubated under the same pre-fermentation conditions as mentioned above. After the incubation period, the fungal biomass was filtered, dried at 60 °C and the weight was checked.

The 2^3 factorial design was also used to partial optimise L-asparaginase production. The initial experimental process was given by the conditions established during the pre-fermentation stage, which provided higher biomass production. This experimental design and the corresponding dependent variables described above, except the inoculum concentration (spores mL^{-1}), which was replaced by fungal biomass in grams, are presented in Table 2 of the Supplementary Material. The fungus was inoculated as described above, and the flasks were incubated at 120 rpm for 120 h at 30 °C. After the incubation period, the fungal biomass was filtered and used to determine enzyme activity (Drainas et al. 1977).

Data analyses: richness of endophytes and L-asparaginase production

The absolute (fa) and the relative (fr) frequencies of the endophytes were calculated. The absolute frequency was expressed by the number of times that each taxon was isolated from the plant, and the relative frequency was defined as the absolute frequency divided by the total number (m) of endophytes isolated ($fr = fa/m * 100$).

All the results obtained during L-asparaginase production were subjected to the non-parametric Kruskal–Wallis test to verify whether any statistically significant difference existed ($p < 0.05$) between the enzymatic activities produced by the endophytes isolated from *T. catimbauensis*.

The results obtained in the partial optimisation of fungal biomass and L-asparaginase production were analysed by the F-test (ANOVA) to verify and evaluate the relationship between the selected independent variables and the biomass. Finally, the response surface theory was used to visualise trends among the variables. All statistical analyses were conducted using the R software (R Development Core Team 2015).

Results

A total of 184 endophytic fungi were isolated from the leaves of the bromeliad *T. catimbauensis*, of which 52 endophytes were identified as *Penicillium* and *Talaromyces* spp. (Table 1). Phylogenetic analysis using β -tubulin sequences from these isolates recognised a total of nine putative species. These data indicated the richness of four *Penicillium* species, and the other five species were grouped in the genus *Talaromyces*, both in the Trichocomaceae (Fig. 2). The most frequently isolated species in *Talaromyces* was *T. diversus* (20 isolates), and *Penicillium* sp. 4 (8 isolates) was the more frequently recovered *Penicillium* putative new species. Other species such *P. decaturense* were isolated once or twice and were reported as rare isolation. Other isolates were identified up to the genus level, and they were considered as putative new species in both genera.

Of the total 20 endophytic fungi tested in the liquid medium, 10 exhibited the capacity to produce the enzyme L-asparaginase, with the enzymatic activity varying between 0.50 and 2.30 U/g. L-Asparaginase production was statistically analysed using the non-parametric Kruskal–Wallis test to determine whether any statistically significant difference existed between the isolates. This test resulted in a *p* value of 0.00483, based on which we can confirm that at least one value of the enzymatic activity of one isolate was statistically different from the others (Table 2). In addition, we

Table 1 Endophytic fungi frequency (absolute and relative) isolated from leaves of the bromeliad *Tillandsia catimbauensis* in the Brazilian tropical dry forest (Caatinga)

Endophytic fungi	<i>fa</i>	<i>fr</i>
<i>Talaromyces diversus</i>	20	10.8
<i>T. sayulitensis</i>	1	0.5
<i>Talaromyces</i> sp.	1	0.5
<i>T. cf. cecidicola</i>	13	7
<i>Penicillium decaturense</i>	2	1
<i>Penicillium</i> sp. 1	2	1
<i>Penicillium</i> sp. 2	2	1
<i>Penicillium</i> sp. 3	3	1.6
<i>Penicillium</i> sp. 4	8	4.3

can observe that the following five groups can be formed between the endophytes used for enzyme production: A (URM 7826 and URM 7827), B (URM 7828, URM 7829 and URM 7830), C (URM 7831 and URM 7667), D (URM 7832, URM 7833 and URM 7665) and E (T106, T114, T12, T82, T20, T63, T95B, T95A, T10A and T124 isolates). There was no statistically significant difference between the isolates from the same group; however, a statistically significant difference was observed between the isolates from different groups. The best results were obtained with the isolates *T. cf. cecidicola* URM 7826 and *Penicillium* sp. 4 URM 7827 from the group A, which produced 2.30 and 1.28 U/g of the intracellular enzyme, respectively. Based on the results obtained in the L-asparaginase activity, the endophyte *T. cf. cecidicola* URM 7826, which demonstrated the best enzymatic activity (2.30 U/g), was selected for the partial optimisation of fungal biomass and L-asparaginase production.

In the experimental 2³ factorial design, the biomass production ranged from 0.16 to 0.66 g after 96 h of incubation, which demonstrated the significance of the variables used for the partial optimisation process of biomass production (Table 3). The results of the experimental design showed that the concentration of the inoculum was statistically significant (*p* < 0.05), whereas the variable pH was marginally significant (*p* < 0.1), and the concentration of L-proline was not statistically significant (*p* > 0.1) (Suppl. Table 3). The model adequately adjusts the data, since the independent variables explained 92.74% of biomass production variation, the lack of fit was not statistically significant and the predicted values were close to the observed values (Table 3 and Suppl. Table 3). Based on the experimental design used in this study, the best conditions for biomass production were pH 6.0, inoculum concentration of 1×10^8 and 1% of L-proline concentration, which produced 0.66 g of biomass. The analysis based on the experimental design showed that the maximum point has possibly not yet reached; however, there are clearly marked trends (Fig. 3).

L-Asparaginase production using the experimental 2³ factorial design varied between 0.58 and 1.02 U/g (Table 4). The adjusted statistical model did not explain the production of L-asparaginase, as the *p* value for the lack of fit was significant (*p* < 0.05) (Suppl. Table 4). The optimal point for enzyme production was not reached, demonstrating that further studies and detailed analyses are required to verify the influence of the variables on L-asparaginase production.

Discussion

According to Strobel and Daisy (2003), plants of unique environments, endemic and occupying areas of great biodiversity must be collected for the purpose of isolating

Fig. 2 Maximum Likelihood (ML) tree obtained by phylogenetic analysis using β -tubulin sequences from 52 endophytic *Penicillium* and *Talaromyces* putative species isolated from leaves of the bromeliad *Tillandsia catimbauensis* in the Brazilian tropical dry forest (Caatinga). ML bootstrap values above 70% are shown at nodes. Endophytic fungi obtained in this study are in blue colour. *Trichocoma paradoxa* CBS 247.57 was used as outgroup

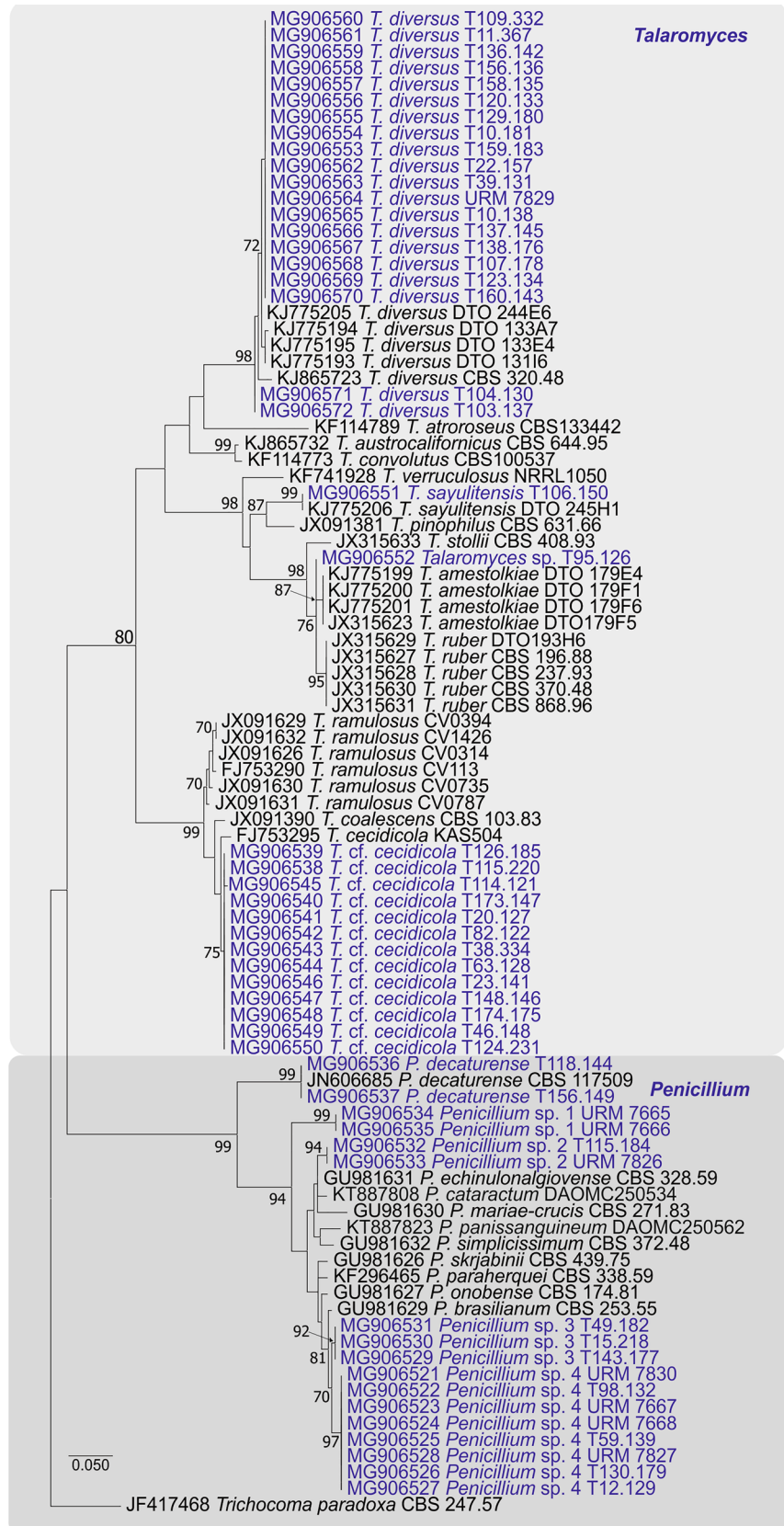


Table 2 L-asparaginase enzymatic activity (U/g) of endophytic fungi from *Tillandsia catimbauensis*, a bromeliad endemic in the Brazilian tropical dry forest

Endophytic fungi	URM accession	Absorbance activity 1	Absorbance activity 2	Average
<i>Talaromyces cf. cecidicola</i>	7826	2.46	2.14	2.30 ^a
<i>Penicillium</i> sp. 4	7827	1.08	1.47	1.28 ^a
<i>Penicillium</i> sp.	7828	0.81	0.77	0.79 ^b
<i>T. diversus</i>	7829	0.82	0.69	0.76 ^b
<i>Penicillium</i> sp. 4	7830	0.79	0.72	0.75 ^b
<i>P. decaturense</i>	7831	0.60	0.60	0.60 ^c
<i>Penicillium</i> sp. 4	7667	0.60	0.71	0.65 ^c
<i>Penicillium</i> sp.	7832	0.52	0.54	0.53 ^d
<i>Penicillium</i> sp.	7833	0.50	0.55	0.52 ^d
<i>Penicillium</i> sp. 1	7665	0.50	0.50	0.50 ^d

Non-parametric test of Kruskal–Wallis ($p=0.00483$). Averages followed by the same letter do not differ statistically from each other. The endophytes listed (group E) did not show L-asparaginase activity: *Penicillium* sp. 4 (T12.129), *Talaromyces* sp. (T95.126, T95.126a), *T. cf. cecidicola* (T114.121, T82.122, T20.127, T63.128, and T124.231), *T. diversus* (T10.181), and *T. pinophilus* (T106.150)

Table 3 Biomass produced by *Talaromyces cf. cecidicola* URM 7826 in the 2³ factorial experimental design with four central points after 96 h of incubation

Assay	L-Proline concentration (%)	pH	Inoculum concentration (spores mL ⁻¹)	Biomass (g)	
				Experimental	Predicted
1	1	6.0	1 × 10 ⁶	0.21	0.2538
2	2	6.0	1 × 10 ⁶	0.21	0.2463
3	1	8.0	1 × 10 ⁶	0.16	0.1713
4	2	8.0	1 × 10 ⁶	0.16	0.1638
5	1	6.0	1 × 10 ⁸	0.66	0.6413
6	2	6.0	1 × 10 ⁸	0.60	0.6338
7	1	8.0	1 × 10 ⁸	0.50	0.5588
8	2	8.0	1 × 10 ⁸	0.53	0.5513
9	1.5	7.0	5.05 × 10 ⁷	0.40	0.4025
10	1.5	7.0	5.05 × 10 ⁷	0.49	0.4025
11	1.5	7.0	5.05 × 10 ⁷	0.49	0.4025
12	1.5	7.0	5.05 × 10 ⁷	0.42	0.4025

endophytes and discovering natural products. The present study demonstrated a high frequency of *Penicillium* and *Talaromyces* isolates when exploring the fungal endophytic richness associated with the bromeliad *T. catimbauensis*. Similar studies using Caatinga plants have reported the presence of *Penicillium* isolates as endophytes. For example, Freire et al. (2015) reported the presence of *P. funiculosum*, *P. citrinum* and *P. janthinellum* in healthy *Opuntia ficus-indica* and infested by *Dactylopius opuntiae*. Other studies on cacti species from the Caatinga forest have also reported the isolation of *P. aurantiogriseum* and *P. glandicola* from *O. ficus-indica* (Bezerra et al. 2012a) and nine endophytic *Penicillium* species from *Cereus jamacaru*, with the latter isolates corresponding to 5% of

the endophytic community (Bezerra et al. 2013). In contrast, the study of Santos et al. (2015a) on *Indigofera suffruticosa* in the Caatinga forest did not report *Penicillium* and *Talaromyces* species as endophytes.

Endophytic *Penicillium* species have also been isolated from plants from warm and dry environments (Loro et al. 2012; Sun et al. 2012), but there was no association of *Talaromyces* species (Suryanarayanan et al. 2005; Khidir et al. 2010). In an interesting study on *Cannabis sativa* in the Netherlands, > 90% of the endophytic fungi isolated belonged to the genus *Penicillium* (Kusari et al. 2013). *Talaromyces* species have been described as endophytes of plants from different environments, such as *Amomum siamense* in Thailand (Bussaban et al. 2001), medicinal plants in Thailand (Theantana et al. 2009), *Dactylis glomerata* in Spain (Márquez et al. 2007), *Cupressus sempervirens* in Iran (Soltani and Moghaddam 2015) and *Bauhinia forficata* in Brazil (Bezerra et al. 2015). These studies may also help in understanding the relationship between these microorganisms and their hosts and the protection of plants living in stressful environments.

The endophytic fungi isolated from *T. catimbauensis* possess the biotechnological potential for the production of the enzyme L-asparaginase. Endophytic microorganisms are considered as the major sources of bioactive natural products with potential use in agriculture, medicine, pharmaceuticals and industries (Jalgaonwala et al. 2011), and among these microorganisms, fungi have been reported as potential producers of novel secondary metabolites (Schulz et al. 2002). Some studies have demonstrated the potential of endophytic fungi for the production of the enzyme L-asparaginase (Chow and Ting 2017; Kalyanasundaram et al. 2015; Manasa and Nalini 2014; Theantana et al. 2007, 2009; Thirunavukkarasu et al. 2011).

Fig. 3 Response surface and contour for a biomass of *Talaromyces cf. cecidicola* URM 7826 in function of pH and L-proline (a), inoculum and L-proline (b), and inoculum and pH (c) setting the missing variable to its midpoint

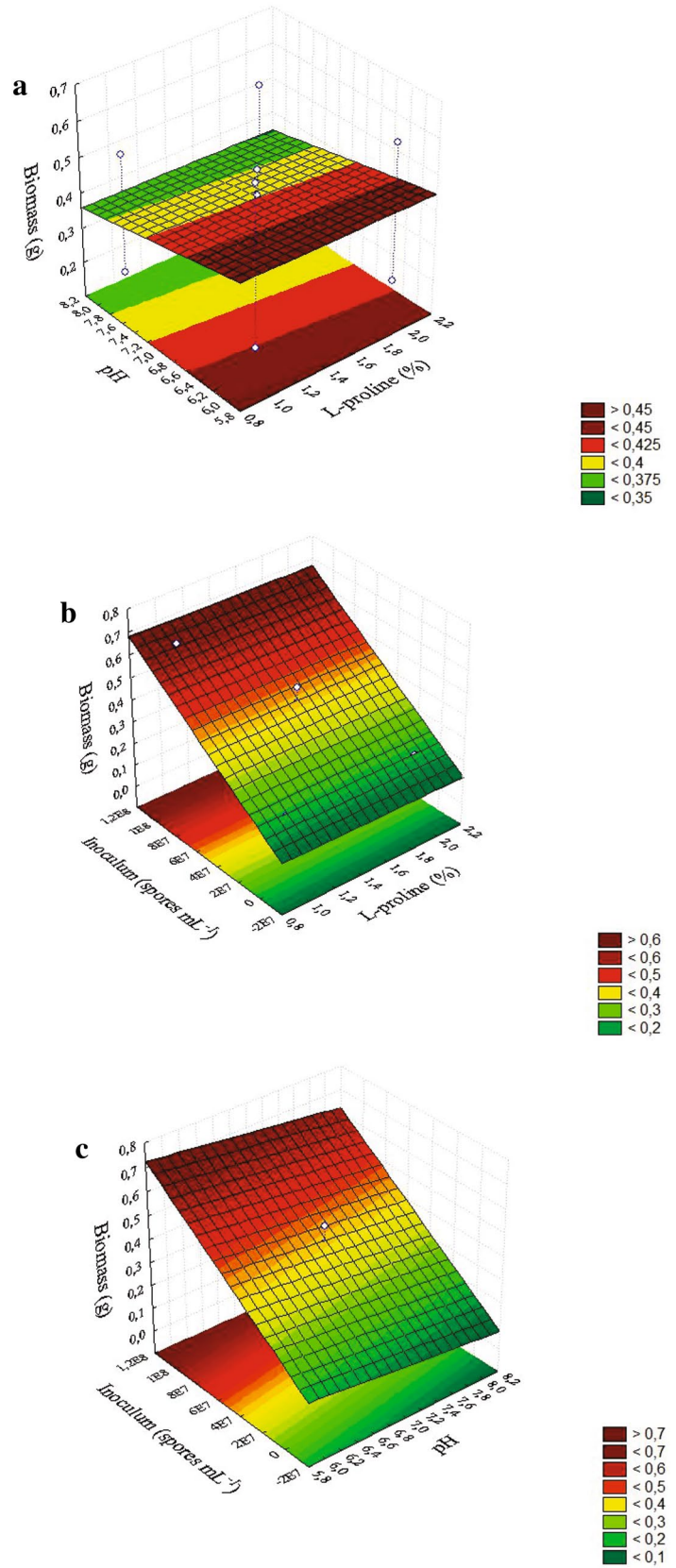


Table 4 L-Asparaginase production by *Talaromyces cf. cecidicola* URM 7826 in the 2³ factorial experimental design with four central points after a 120 h incubation

Assay	L-Proline concentration (%)	pH	Inoculum concentration (biomass g)	L-Asparaginase activity (U/g)
1	0.5	5.0	1.5	0.68
2	1.5	5.0	1.5	0.00
3	0.5	7.0	1.5	0.00
4	1.5	7.0	1.5	0.98
5	0.5	5.0	3.5	0.63
6	1.5	5.0	3.5	1.01
7	0.5	7.0	3.5	1.02
8	1.5	7.0	3.5	0.58
9	1	6.0	2.5	0.92
10	1	6.0	2.5	0.89
11	1	6.0	2.5	0.87
12	1	6.0	2.5	0.96

The genera *Penicillium* and *Talaromyces* have been emphasised in the production of L-asparaginase. For example, Theantana et al. (2009) using fungi isolated from medicinal plants reported an enzymatic activity varying between 0.014 and 1.530 U/mL from 53 endophytes, highlighting the high activity of *Penicillium* and *Talaromyces* isolates. Similarly, Santos et al. (2015b) investigated the potential of endophytic fungi isolated from *C. jamacaru* in Brazil and found that of nine *Penicillium* isolates tested, four showed activity for L-asparaginase, with *P. brevicompactum* being considered as one of the largest producers of the enzyme (2.54 U/mL). Chow and Ting (2015) confirmed the enzymatic activity of 25 endophytic fungi, reporting *P. simplicissimum* as the third largest producer of L-asparaginase. Similar results were obtained by Krishnapura and Belur (2016) who investigated the endophytic fungus *T. pinophilus* isolated from the rhizomes of *Curcuma amada* and partially purified and characterised the enzyme produced by the endophyte, which was considered as a potential candidate for industrial and clinical trials because of its biochemical properties and high efficiency. However, these studies used different methodologies to verify the enzymatic activity (e.g. the use of the culture filtrate and the nesslerisation technique to evaluate the enzymatic production), due to which the results may not be comparable with the results obtained in the present study, wherein fungal biomass and quantification of β -hydroxamic aspartic acid were used to determine the enzymatic activity. Similar to this study, Drainas et al. (1977) used the biomass of *A. nidulans* to quantify the enzymatic activity based on the formation of β -hydroxamic aspartic acid. Based on the studies of Drainas et al. (1977), Kumar and Manonmani (2013) and Kumar et al. (2013), using the extracellular enzyme, the fungal enzymatic production can be verified

through the quantification of β -hydroxamic aspartic acid (see Suppl. Tables 5 and 6).

According to Kumar et al. (2010), most of the microorganisms accumulate the enzyme L-asparaginase as an intracellular product. Similar to this study, other studies have also verified the production of intracellular L-asparaginase by fungi from the genus *Penicillium*. Using the nesslerisation technique, Elshafei et al. (2012) evaluated the intracellular and extracellular enzymatic activity of filamentous fungi and verified that the isolates had the highest activities at the intracellular level, highlighting *P. brevicompactum* (1.7 U/mg) and *P. purpurescens* (1.24 U/mg). They further demonstrated L-asparaginase as an intracellular enzyme. Other researchers such as Gupta et al. (2009) who analysed fungi from the mangrove ecosystem reported that 85 isolates had intracellular enzymatic activity and only 20 other isolates had extracellular enzymatic activity, especially the intracellular production of *Penicillium* sp. PF 52 and *Penicillium* sp. RF2, with activities of 16.71 and 5.41 U/g, respectively. In addition, Patro and Gupta (2012) using the nesslerisation method to verify L-asparaginase activity demonstrated enzymatic activity in the cellular biomass of *Penicillium* sp.

In the present study, the best biomass production conditions were identified as inoculum concentration of 1×10^8 spores, pH 6.0 and 1% of L-proline. According to Amena et al. (2010), optimisation of the inoculum concentration is essential because few spores can lead to insufficient biomass, whereas numerous spores can result in an increased biomass production, leading to rapid nutrient depletion. In addition, the growth of microorganisms can be drastically affected by pH (Niharika and Supriya 2014). Similar to this study, Niharika and Supriya (2014) analysed the influence of the variable proline on the growth of *Fusarium oxysporum* and found that proline (1%) was the best among all nitrogen sources for mycelial growth. However, Sarquis et al. (2004) reported that proline (2%) was the second largest source of nitrogen for *A. tamarii*. Using soil samples from Egypt, Bedaiwy et al. (2016) demonstrated that pH 7.0 was ideal for the growth of *A. tamarii* and for the production of L-asparaginase. Gbolagade et al. (2006) using submerged conditions to optimise the biomass production of *Pleurotus florida*, an edible fungus, reported that the fungus produced the highest biomass at pH 6.5 and at a temperature of 30 °C.

According to Thakur et al. (2013), the initial pH of the culture medium can affect enzyme production, as it affects nutrient availability. According to Hosamani and Kaliwal (2011), it is necessary to optimise the inoculum because an excess biomass can lead to nutrient depletion of the substrate or the accumulation of substances that inhibit formation of the product. Sarquis et al. (2004) suggested that the production of L-asparaginase is regulated by nitrogen; whereas Elshafei et al. (2012) reported that pH 6.0 was ideal to produce intracellular L-asparaginase from *P.*

brevicompatum. Similarly, Kumar et al. (2013) discovered that pH 5.8 was optimal for the production of L-asparaginase by *Cladosporium* sp. As shown in the present study, Thakur et al. (2013) found that pH 7.0 was the best condition for enzymatic production by *Mucor hiemalis*. In this study, the optimal concentrations of L-proline and the inoculum were 0.5% and 3.5 g, respectively. However, Baskar and Renganathan (2012) optimised the production of L-asparaginase and observed that a concentration of 1.7% L-proline was ideal for enzymatic production by *A. terreus*. Dias and Sato (2016) optimised L-asparaginase production by *A. oryzae* and obtained optimum conditions of pH 8.0, 2% L-proline, and 3×10^7 spores/mL as the inoculum concentration. In this study, the experimental design provided the guidelines to reach optimal enzyme production. Our results suggest that future experiments should fix one of the variables (inoculum or pH) and vary the others, as the range of inoculum and L-proline concentrations in some assays resulted in different effects on enzymatic production.

The results of the present study show that the bromeliad *T. catimbauensis*, which is endemic in the Brazilian tropical dry forest, is an important host for endophytic species belonging to the genera *Penicillium* and *Talaromyces*. To our knowledge, this is the first record of the production of the enzyme L-asparaginase by endophytic fungi isolated from *T. catimbauensis*, which demonstrates the importance of the study on the richness of endophytes in arid environments. Among the 10 isolates that exhibited enzymatic activity (0.50–2.30 U/g), the endophytes *T. cf. cecidicola* URM 7826 (2.30 U/g) and *Penicillium* sp. 4 URM 7827 (1.28 U/g) were found to be the most promising. In the partial optimisation stage of the biomass production of *T. cf. cecidicola* URM 7826, pH (6.0) was found to be marginally significant and the inoculum concentration was found to be significant (1×10^8), whereas the concentration of L-proline (1%) was not significant. Furthermore, L-asparaginase production by *T. cf. cecidicola* URM 7826 varied between 0.58 and 1.02 U/g when using the experimental 2^3 factorial design and did not reach the optimal point for enzyme production. Considering the industrial importance of the enzyme L-asparaginase, it is necessary to search for new sources of enzyme production, as there is a growing demand for this enzyme in Brazil, and the endophyte *T. cf. cecidicola* URM 7826 is indicated for further optimisation studies to produce L-asparaginase.

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Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

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