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Anthropization Effects on the Filamentous Fungal Community of the Brazilian Catimbau National Park

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ABSTRACT: The *Caatinga* biome features an exclusive endemic biodiversity, and is characterized by the presence of xerophytic, deciduous vegetation, high temperatures, and low rainfall. This important park has undergone anthropization, especially through extraction of firewood and timber and growing plants for raising goats. The objectives of this study were to compare the communities of filamentous fungi present in the preserved area and in the anthropized soil of the Catimbau National Park in Buíque, PE, Brazil, and to evaluate the impacts of anthropization on such communities. A total of 12 collections of soil samples were made, six in the preserved area and six in the anthropic area, and the physicochemical properties of the soil samples were analyzed. Fungi were isolated through suspension and serial dilution methods. After growth, the samples were purified and identified based on classical taxonomy, according to specific literature. The diversity, evenness, richness, dominance, frequency, and similarity among the species of filamentous fungi in both areas were assessed based on ecological indexes. A total of 4,488 colony-forming units of filamentous fungi were obtained, which were distributed into 65 species belonging to 15 genera. In the preserved area, higher abundance and richness of species were observed, with predominance of the genera *Aspergillus* and *Penicillium*. In both areas, diversity and equitability were high, demonstrating that the species are well distributed in these areas. In the preserved area, the dominant genera were *Aspergillus*, *Gongronella*, and *Penicillium*, whereas *Aspergillus* was the dominant genus in the anthropic area. Two distinct communities were observed in the areas analyzed. Principal component analysis showed that *Penicillium simplicissimum* influences the total diversity of both communities. The anthropization that occurred in the Catimbau National Park has changed the composition of the filamentous fungal communities of the site, restricting the number of species and decreasing the abundance of these important microorganisms. This results in ecosystem damage and likely causes relevant major imbalances, with serious consequences, such as possible disappearance of the aforementioned species, as well as of species yet undiscovered by the scientific community.

Keywords: *Caatinga*, diversity, *Aspergillus*, *Gongronella*, *Penicillium*.

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INTRODUCTION

A biome is defined as an area of the geographic space with dimensions about one million square kilometers and characteristics such as a uniform type of environment that is identified and classified according to the macroclimate, the formation of phytophysiognomy, soil, and altitude. All these characteristics confer a peculiar structure and functionality on the biome; in other words, a biome has its own ecology (Coutinho et al., 2010).

Brazil is considered as megadiverse because it has the richest continental biota on the planet (about 15-20 %), comprising six important biomes (Amazonia, *Caatinga*, *Campos Sulinos*, *Cerrado*, Mata Atlântica, and *Pantanal*) and the largest river system in the world (IBGE, 2016). Among the biomes found in Brazil, the *Caatinga* has the unique characteristic of being exclusively Brazilian.

Occupying an area of 844,453 km^2, or about 9.9 % of national territory, the *Caatinga* covers most of the states of Piauí, Ceará, Rio Grande do Norte, Paraíba, Pernambuco, Alagoas, Sergipe, and Bahia and the northeast of the state of Minas Gerais in the Jequitinhonha Valley. This biome is bordered on the east by the Atlantic Forest, on the west by the Amazon Forest, and on the south by the Cerrado (IBGE, 2016). This biome is characterized by xerophilous and deciduous vegetation, directly related to high climatic variations, high temperatures, and low pluviometric indexes (Leal et al., 2005). In addition to being little explored scientifically, the *Caatinga* consists of few conserved areas; approximately 1 % of what remains is protected by conservation units. The Catimbau National Park (Parna Catimbau) is prominent among these areas.

The Parna Catimbau is situated in the central portion of the state of Pernambuco (8° 24' 00" at 8° 36' 35" S and 37° 09' 30" at 37° 14' 40" W). The park was created on December 13, 2002, because it was considered of extreme biological importance by the Ministry of Environment (Siqueira, 2006; ICMBio, 2017). The Catimbau Valley covers an area of 62,294 ha and has an elevation range of 900-1,000 m. It not only includes the typical vegetation of the hyperxerophytic *Caatinga* but also receives influences from other Brazilian ecosystems such as the Atlantic Forest, R*estinga*, *Cerrado*, and *Campos Rochosos* (Siqueira, 2006; Ferreira, 2009).

In general, the *Caatinga* has undergone a marked process of desertification, caused primarily by deforestation and inadequate use of natural resources. Therefore, it is necessary to study microbial communities and the processes they trigger to understand both their diversity and the effects of environmental disturbances or stresses on such communities (Cavalcanti et al., 2006). This aspect can be observed in the Catimbau Valley, where the extraction of wood for firewood is very common, especially in the municipalities of Buíque, Tupanatinga, and Ibimirim. This activity meets the demands of expansion of agricultural practices and production of firewood and charcoal. The expansion of these activities is associated with deforestation and forest fires in the region. This compromises the soil quality of this important archaeological park and the communities of filamentous fungi present in this substrate.

Monitoring the microbial community and its biomass reveals changes in soil quality (Melloni, 2007), and it may be used as a tool to detect more impactful changes (Stenberg, 1999) because it detects changes faster than analysis of organic matter, making a diagnosis possible before a decrease in soil quality is more severe (Tótola and Chaer, 2002).

The hypotheses of the present study were that the intense anthropization undergone by the Parna Catimbau can decrease the diversity of filamentous fungi present in the soils of this important area and that such activity may lead to extinction of rare species and/or species that have not yet been described by the scientific community. In this context, the objectives of the present study were to compare the filamentous fungal communities present in the preserved and in the anthropized soils in the Catimbau Valley, Buíque, PE, Brazil, and to evaluate the ecological aspects of these communities.

MATERIALS AND METHODS

Study area

This study was carried out at the Catimbau National Park (Parna Catimbau) in Pernambuco, Brazil. With an area of 62,294 ha, the Parna Catimbau occupies part of the municipalities of Buíque, Ibimirim, and Tupanatinga. The climate in the Parna Catimbau is semi-arid tropical, with average annual temperature of 23 °C and average annual rainfall of 300-500 mm. The vegetation is typical of the *Caatinga*, with high diversity of species and structure. The Parna Catimbau is also the second largest archaeological site in Brazil. It contains 30 archaeological sites registered with cave paintings and other human artifacts dating back at least 6,000 years (Geise et al., 2010; Santos et al., 2013).

Collections of soil samples from anthropized Caatinga and preserved Caatinga in the municipality of Buíque, Pernambuco, Brazil

Twelve collections of soil samples were made. Six collections were made in the preserved area (08° 31' 56.1" S and 37° 15' 03.2" W, elevation 924 m) and six in the anthropized area (08° 34' 5.0" S and 37° 14' 4.3" W, elevation 744 m), in which goats are raised. The soil samples were collected in three 4 × 25 m transects, at a depth of 0.00-0.20 m, making for a total of three composite samples, formed of 10 subsamples each. Based on the number of transects established in this study, 36 samples were obtained. All samples were stored in sterile plastic bags, kept at room temperature, and transported to the laboratory.

Isolation and purification of filamentous fungi

Fungi were isolated using the suspension method according to Clark (1965). All 36 composite soil samples were suspended in sterile distilled water, and serial dilutions were performed. Suspensions were then obtained at the concentration of 1:10,000 g mL^{-1}. Each of the aqueous suspension soil samples was inoculated into five different Petri dishes containing Sabouraud agar supplemented with 50 mg L^{-1} of chloramphenicol (SA-C), and into five Petri dishes containing Dichloran Rose Bengal agar supplemented with 50 mg L^{-1} of chloramphenicol (DRB-C). In all, 90 Petri dishes were inoculated and maintained at 28±2 °C for 72 h.

For purification of the filamentous fungal isolates, fragments of fungal colonies were transferred to Petri dishes containing SA-C medium. After confirming the purity of the cultures of fungi of the *Aspergillus* and *Penicillium* genera, they were cultured in malt extract agar, and the other genera were cultured in potato dextrose agar at 25±2 °C.

Identification of species through classical taxonomy

Macroscopic characteristics (color, appearance, and diameter of the colonies) and microscopic characteristics (somatic and reproductive microstructures) were identified through classical taxonomy of all fungal samples. Fungi were identified according to specific literature, such as Raper and Thom (1949), Ellis (1971; 1976), Schipper (1978), Carmichael et al. (1980), Benny (1982), Schipper (1984), Klich and Pitt (1988), Schipper (1990), Pitt (1991), Klich (2002), Samson and Frisvad (2004), Domsch et al. (2007), Hoffmann et al. (2007), Zheng et al. (2007), Houbraken and Samson (2011) and Samson et al. (2011).

Soil physical and chemical properties

The pH was obtained from the mixture of soil in water at the ratio of 1:2.5. The Al^{3+}, Ca^{2+}, and Mg^{2+} contents of the soil were extracted using a of 1 mol L^{-1} KCl solution in the proportion 1:10 and quantified by titration. Potassium, Na, and P were extracted using Mehlich-1 solution at the ratio of 1:1 (soil:solution). Potassium and Na contents were determined by flame photometry, and the P content was determined by a spectrophotometer at a wavelength of 725 nm. The potential acidity (H+Al) was extracted with calcium acetate and quantified by titration. All analyses were performed in triplicate (Embrapa, 2009).

Analysis of ecological data

Statistical analysis of the diversity of filamentous fungal species in both areas (preserved and anthropized) was performed using the Shannon-Wiener index (H'), and equitability was quantified by the Pielou index (Pinto-Coelho, 2002). Richness was calculated based on the index established by Magurran (2004). The relative dominance was given by the equation DA = NA/NA + NB + NC ... NN × 100, where DA stands for species dominance, and NA + NB + NC ... NN indicates the number of species A, B, C .... N. The species whose percentages were higher than 50 % are considered dominant (Magurran, 1988). The frequency of species during dry and rainy seasons was calculated by the equation FA = PA/P × 100, where F stands for species A frequency, PA is the number of samples in which species A is present, and P is the total number of samples. According to Magurran (1988), F ≥50 % = constant species, 10 % < F ≤ 49 % = common species, and F ≤10 % = rare species.

The similarity and dissimilarity of the filamentous fungal species among the soil samples of the analyzed areas were tested based on the Bray-Curtis distance, ranging from 0 (similarity) to 1 (dissimilarity), using the density matrix of the species (Pinto-Coelho, 2002). The analysis was performed between collections and transects, and the method of dendrogram binding was the Weighted Pair Group Method with Arithmetic Mean (Rohlf and Fisher, 1968). These calculations were performed using the Numerical Taxonomy and Multivariate Analysis System from Exeter Software (USA).

RESULTS

A total of 4,488 colony-forming units (CFUs) of filamentous fungi were obtained, which were distributed into 65 species belonging to 15 genera (Table 1). The largest number of CFUs (2,840) was obtained in the preserved area, which were distributed among 48 species. In the anthropized area, 1,648 CFUs were obtained, which were distributed among 23 species (Table 2). The genera *Aspergillus* P. Micheli and *Penicillium* Link were the most representative, with 22 and 27 species, respectively. Forty-one species occurred exclusively in the preserved area and 16 exclusively in the anthropized area. *Aspergillus terreus*, *Gongronella butleri*, *P. citreonigrum*, *P. decumbens*, *P. glabrum*, *P. implicatum*, *P. simplicissimum*, and *Talaromyces minioluteus* were common to both areas (Table 2).

The diversity of species in both the evaluated areas was high, because results from the Shannon-Wiener index (H') were higher than 3.0 bits per ind. The Pielou equitability index was higher than 0.5 in both the anthropized area and the preserved area, demonstrating that the species are well distributed in the areas studied (Figure 1). However, the preserved area presented higher species richness (49) in relation to the anthropized area (23) (Table 2).

Table 1. Abiotic factor analysis of soil samples from preserved and anthropized areas of the Parna Catimbau, Buíque, Pernambuco, Brazil

Factor	Preserved area						Anthropized area					
	C1	C2	C3	C4	C5	C6	C1	C2	C3	C4	C5	C6
Temperature (°C)	30	32	33	32	32	32	32	35	33	35	33	32
pH(H_2O)	4.07	4.19	4.15	4.15	4.15	4.19	7.50	6.32	6.37	7.40	6.50	5.80
P (mg kg^{-1})	0.10	0.30	0.23	0.18	0.23	0.28	54.60	21.30	22.30	23.50	50.15	52.30
Al^{3+} ($cmol_c$ kg^{-1})	0.01	0.02	0.05	0.15	0.18	0.05	0.20	0.20	0.23	0.40	0.20	0.10
Na^+ ($cmol_c$ kg^{-1})	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015	0.015
K^+ ($cmol_c$ kg^{-1})	0.010	0.010	0.013	0.010	0.015	0.012	0.035	0.010	0.085	0.085	0.085	0.085
Ca^{2+} ($cmol_c$ kg^{-1})	0.60	0.70	0.80	1.00	1.30	0.90	0.80	0.50	0.50	0.50	0.70	0.60
Mg^{2+} ($cmol_c$ dm^{-3})	0.90	0.70	0.80	0.60	1.20	0.80	0.40	0.60	0.50	0.40	0.60	0.80
H+Al ($cmol_c$ dm^{-3})	3.01	2.45	2.65	3.12	3.15	3.13	0.82	1.43	1.34	1.37	0.95	0.99

C1: collection 1; C2: collection 2; C3: collection 3; C4: collection 4; C5: collection 5; C6: collection 6; pH(H_2O): pH in water, 1:2.5 soil:solution ratio; P, K^+, Na^+: extracted by Mehlich-1; Al^{3+}, Ca^{2+}, and Mg^{2+} extratec by 1 mol L^{-1} KCl; H+Al: potential acidity, extracted by 0.5 mol L^{-1} calcium acetate.

Table 2. Number of filamentous fungal isolates collected in the preserved and anthropized areas of the PARNA Catimbau (Caatinga) and Relative Dominance, according to Magurran (1988).

Specie	Preserved Area									Anthropized area									Overall total
	C1	C2	C3	C4	C5	C6	T	RD	FR	C1	C2	C3	C4	C5	C6	T	RD	FR	
								%									%		
Absidia cylindropora Hagem	10	10	9	3	5	6	43	1.51	100	0	0	0	0	0	0	0	0.00	0	43
Acremonium terricola (J.H. Mill., Giddens & A.A. Foster) W. Gams	3	3	3	4	3	4	20	0.70	100	0	0	0	0	0	0	0	0.00	0	20
Aspergillus aculeatus Lizuga	0	0	0	0	0	0	0	0.00	0	0	0	0	0	0	5	5	0.30	16,6	05
A. avenaceus G. Sm.	15	10	13	6	7	12	63	2.22	100	0	0	0	0	0	0	0	0.00	0	63
A. awamori Nakaz.	0	0	0	0	0	0	0	0.00	0	12	12	18	15	14	17	88	5.36	100	88
A. candidus Link	0	0	0	0	0	0	0	0.00	0	13	16	22	25	27	25	128	7.79	100	128
A. carbonarius (Bainier) Thom	0	0	0	0	0	0	0	0.00	0	22	23	23	18	16	19	121	7.36	100	121
A. carneus Smith	0	0	0	0	0	0	0	0.00	0	18	15	13	13	13	13	85	5.17	100	85
A. flavofurcatus Bat. & H. Maia	13	15	16	18	12	12	86	3.03	100	0	0	0	0	0	0	0	0.00	0	86
A. flavus Link	45	15	25	25	28	35	173	6.09	100	0	0	0	0	0	0	0	0.00	0	173
A. fumigatus Fresen.	0	5	0	5	0	0	10	0.35	16.6	0	0	0	0	0	0	0	0.00	0	10
A. niger Tiegh.	38	33	11	32	28	24	166	5.85	100	0	0	0	0	0	0	0	0.00	0	166
A. ochraceus G. Wilh.	32	63	43	33	32	28	231	8.13	100	0	0	0	0	0	0	0	0.00	0	231
A. parasiticus Speare	35	42	25	33	32	36	203	7.15	100	0	0	0	0	0	0	0	0.00	0	203
A. sclerotiorum G.A. Huber	98	98	20	25	28	23	292	10.28	100	0	0	0	0	0	0	0	0.00	0	292
A. stromatoides Raper & Fennel	0	0	0	0	0	0	0	0.00	0	17	22	23	26	13	10	111	6.76	100	111
A. sulphureus (Fresen.) Thom & Church	0	0	0	0	0	0	0	0.00	0	13	14	16	13	13	14	83	5.05	100	83
A. sydowii (Bainier & Sartory) Thom & Church	0	0	0	0	0	0	0	0.00	0	13	13	13	13	12	11	75	4.56	100	75
A. tamari Kita	0	0	0	0	0	0	0	0.00	0	11	11	12	16	13	13	76	4.63	100	76
A. terreus Thom	23	25	22	18	15	20	123	4.33	100	13	13	13	13	13	13	78	4.75	100	201
A. terreus var. aureus Thom & Raper	15	12	12	12	12	13	76	2.68	100	0	0	0	0	0	0	0	0.00	0	76
A. ustus (Bainier) Thom & Church	0	0	0	0	0	0	0	0.00	0	15	17	18	12	13	13	88	5.36	100	88
A. versicolor (Vuill.) Tirab.	0	0	0	0	0	0	0	0.00	0	5	6	6	6	6	6	35	2.13	100	35
A. viridinutans Ducker & Thrower	0	0	0	0	0	0	0	0.00	0	7	8	9	4	7	6	41	2.50	100	41
Chaetomium cupreum L.M. Ames	15	13	6	7	7	6	54	1.90	100	0	0	0	0	0	0	0	0.00	0	54
Curvularia pallescens Boedijn	0	0	0	0	0	0	0	0.00	0	3	3	3	3	3	3	18	1.10	100	18
Eupenicillium shaerii Stolk & D.B. Scott	5	5	8	5	5	7	35	1.23	100	0	0	0	0	0	0	0	0.00	0	35
Fusarium redolens Wollenw.	4	13	13	14	17	18	79	2.78	100	0	0	0	0	0	0	0	0.00	0	79
F. solani (Mart.) Sacc.	9	7	5	4	6	6	37	1.30	100	0	0	0	0	0	0	0	0.00	0	37
F. oxysporum E.F. Sm. & Swingle	10	7	7	6	7	9	46	1.62	100	0	0	0	0	0	0	0	0.00	0	46
Gliomastix murorum (Corda) S. Hughes	3	3	3	7	7	8	31	1.09	100	0	0	0	0	0	0	0	0.00	0	31
Gongronella butleri (Lendn.) Peyronel & Dal Vesco	10	9	3	7	7	7	43	1.51	100	13	13	16	13	13	15	83	5.05	100	126
Neocosmospora vasinfecta E.F. Sm.	2	2	2	2	2	2	12	0.42	100	0	0	0	0	0	0	0	0.00	0	12
Neosartorya fischeri (Wehmer) Malloch & Cain	2	2	2	2	2	2	12	0.42	100	0	0	0	0	0	0	0	0.00	0	12
Papulaspora immersa Hotson	0	0	1	0	0	0	1	0.04	33.3	0	0	0	0	0	0	0	0.00	0	01
Penicillium adametzii K.M. Zaleski	12	9	2	7	6	6	42	1.48	100	0	0	0	0	0	0	0	0.00	0	42
P. aurantiogriseum Dierckx	12	4	6	5	6	6	39	1.37	100	0	0	0	0	0	0	0	0.00	0	39
P. brevicompactum Dierckx	13	12	12	12	12	12	73	2.57	100	0	0	0	0	0	0	0	0.00	0	73
P. canescens Sopp	0	0	0	0	0	0	0	0.00	0	23	12	14	17	14	14	94	5.72	100	94
P. citreonigrum Dierckx	15	18	18	12	15	14	92	3.24	100	9	8	8	8	8	8	49	2.98	100	141
P. citrinum Sopp	12	12	12	12	12	15	75	2.64	100	0	0	0	0	0	0	0	0.00	0	75
P. decumbens Thom	18	14	15	13	13	12	85	2.99	100	13	1	13	13	15	16	71	4.32	100	156
P. funiculosum Thom	13	13	13	14	15	18	86	3.03	100	0	0	0	0	0	0	0	0.00	0	86
P. glabrum (Wehmer) Westling	5	6	4	7	7	8	37	1.30	100	12	12	12	15	15	15	81	4.93	100	118
P. griseofulvum Dierckx	0	0	0	0	0	0	0	0.00	0	3	3	2	2	0	0	10	0.61	66.6	10
P. implicatum Biourge	4	4	6	6	6	6	32	1.13	100	13	13	3	15	14	14	72	4.38	100	104
P. janczewskii Zaleski	2	1	5	3	3	3	17	0.49	100	0	0	0	0	0	0	0	0.00	0	23
P. lanosum Westling	12	10	12	10	12	12	68	2.39	100	0	0	0	0	0	0	0	0.00	0	68
P. lapidosum Raper & Fennell	3	2	3	3	3	3	17	0.60	100	0	0	0	0	0	0	0	0.00	0	17
P. lividum Westling	3	3	6	12	12	12	48	1.69	100	0	0	0	0	0	0	0	0.00	0	48
P. melinii Thom	3	3	3	3	1	1	14	0.49	100	0	0	0	0	0	0	0	0.00	0	14
P. miczynskii K.M. Zaleski	1	1	1	1	1	1	06	0.21	100	0	0	0	0	0	0	0	0.00		06
P. montanense M. Chr. & Backus	3	3	3	5	5	5	24	0.85	100	0	0	0	0	0	0	0	0.00	0	24
P. oxalicum Currie & Thom	4	4	4	3	3	3	21	0.74	100	0	0	0	0	0	0	0	0.00	0	21
P. pinophilum Hedgc.	0	1	0	5	5	5	16	0.56	66.6	0	0	0	0	0	0	0	0.00	0	16
P. restrictum .C. Gilman & E.V. Abbott	3	3	0	3	3	3	15	0.53	83.3	0	0	0	0	0	0	0	0.00	0	15
P. simplicissimum (Oudem.) Thom	17	17	13	13	16	14	90	3.17	100	13	13	13	18	19	23	99	6.03	100	189
P. spinulosum Thom	0	0	0	0	0	0	0	0.00	0	13	12	12	11	0	8	56	3.41	83.3	56
P. waksmanii Zaleski	4	3	3	4	7	7	28	0.99	100	0	0	0	0	0	0	0	0.00	0	28
*P. sp*1	2	3	3	2	2	2	14	0.49	100	0	0	0	0	0	0	0	0.00	0	14
*P. sp*2	1	0	0	1	1	1	4	0.14	66.6	0	0	0	0	0	0	0	0.00	0	04
*P. sp*3	2	3	3	3	3	2	16	0.56	100	0	0	0	0	0	0	0	0.00	0	16
Rhizopus oryzae Went & Prins. Geerl.	3	3	3	3	3	6	21	0.74	100	0	0	0	0	0	0	0	0.00	0	21
Talaromyces minioluteus (Dierckx) Samson, N. Yilmaz, Frisvad & Seifert	2	2	2	2	2	2	12	0.42	100	0	0	0	0	0	1	1	0.06	16.6	12
T. purpurogenus Samson, Yilmaz, Houbraken	0	0	0	4	4	4	12	0.42	50.0	0	0	0	0	0	0	0	0.00	0	12
Total species: 65	556	546	401	436	440	461	2,840	100	-	274	260	282	289	261	282	1,648	100	-	4,488

C1: collection 1; C2: collection 2; C3: collection 3; C4: collection 4; C5: collection 5; C6: collection 6. RD: Relative Dominance; FR: Frequency.

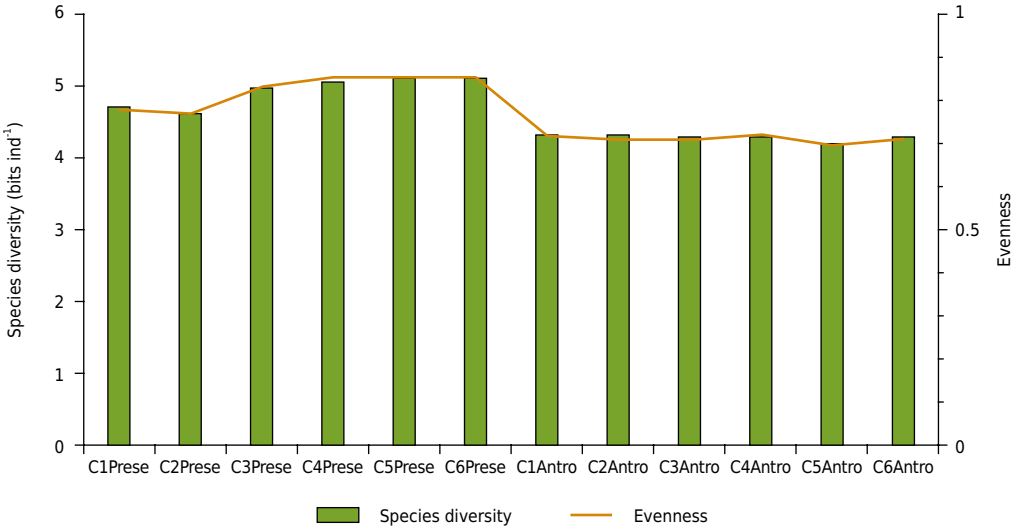

Figure 1. Diversity (bits per ind) of the species of filamentous fungi in the preserved area (Prese) in the anthropic area (Antro), in six sample collections (C1, C2, C3, C4, C5, and C6); and Evenness statistical analysis based on the Shannon index. C1: collection 1; C2: collection 2; C3: collection 3; C4: collection 4; C5: collection 5; C6: collection 6.

In the preserved area, the dominant species were *Aspergillus awamori*, *A. candidus*, *A. carbonarius*, *A stromatoides*, *A. sulphureus*, *A. sydowii*, *A tamarii*, *A. terreus*, *A. ustus*, *G. butleri*, *P. canescens*, *P. decumbens*, *P. glabrum*, *P. implicatum*, and *P. simplicissimum*. The species that dominated the community of filamentous fungi in the anthropized area were *A. flavus*, *A. niger*, *A. ochraceus*, *A. parasiticus*, and *A. sclerotiorum* (Table 2).

In the preserved area, 46 of the 49 identified species were considered constant, which included *Absidia cylindropora*, *Acremonium terricola*, *Aspergillus avenaceus*, *A. flavofurcatus*, *A. flavus*, *A. niger*, *A. ochraceus*, *A. parasiticus*, *A. sclerotiorum*, *A. terreus*, *A. terreus* var. aureus, *Chaetomium cupreum*, *Eupenicillium shaerii*, *Fusarium oxysporum*, *F. redolens*, *F. solani*, *Gliomastix murorum*, *Gongronella butleri*, *Neocosmospora vasinfecta*, *Neosartorya fischeri*, *Penicillium adametzii*, *P. aurantiogriseum*, *P. brevicompactum*, *P. citreonigrum*, *P. citrinum*, *P. decumbens*, *P. funiculosum*, *P. glabrum*, *P. implicatum*, *P. janczewskii*, *P. lanosum*, *P. lapidosum*, *P. lividum*, *P. melinii*, *P. miczynskii*, *P. montanense*, *P. oxalicum*, *P. pinophilum*, *P. restrictum*, *P. simplicissimum*, *P. waksmanii*, *P. sp1*, *P. sp2*, *P. sp3*, *Rhizopus oryzae*, *Talaromyces minioluteus*, and *T. purpurogenus*. Two species were considered common, *Aspergillus fumigatus* and *Papulaspora immersa*.

In the anthropized area, 22 species were considered constant, including *Aspergillus awamori*, *A. candidus*, *A. carbonarius*, *A. carneus*, *A. stromatoides*, *A. sulphureus*, *A. sydowii*, *A. tamarii*, *A. terreus*, *A. ustus*, *A. versicolor*, *A. viridinutans*, *Curvularia pallescens*, *Gongronella butleri*, *P. canescens*, *P. citreonigrum*, *P. decumbens*, *P. glabrum*, *P. griseofulvum*, *P. implicatum*, *P. simplicissimum*, and *P. spinulosum*. Only *Talaromyces minioluteus* was considered common in the anthropized area.

After the application of the Bray-Curtis index or the Bray-Curtis distance, a dendrogram of the relationship between the soil fungus samples from the preserved and anthropized areas was generated, which resulted in two large groups (Figure 2). The same index was applied to evaluate the proximity between the species, which generated another dendrogram, resulting in the formation of distinct groups (Figure 3). Principal component analysis (PCA) revealed that *Penicillium simplicissimum* influences the total diversity of both communities (Figure 4). The populations of *Acremonium terricola* and *Penicillium citreonigrum* directly correlated with temperature, as well as with H+Al, Mg^{2+}, and Ca^{2+} contents. All these factors inversely correlated with *Penicillium glabrum*, *Gongronella butleri*, and *Penicillium implicatum* populations and were influenced directly by pH and P, Al^{3+}, and K^{+} contents (Figure 4).

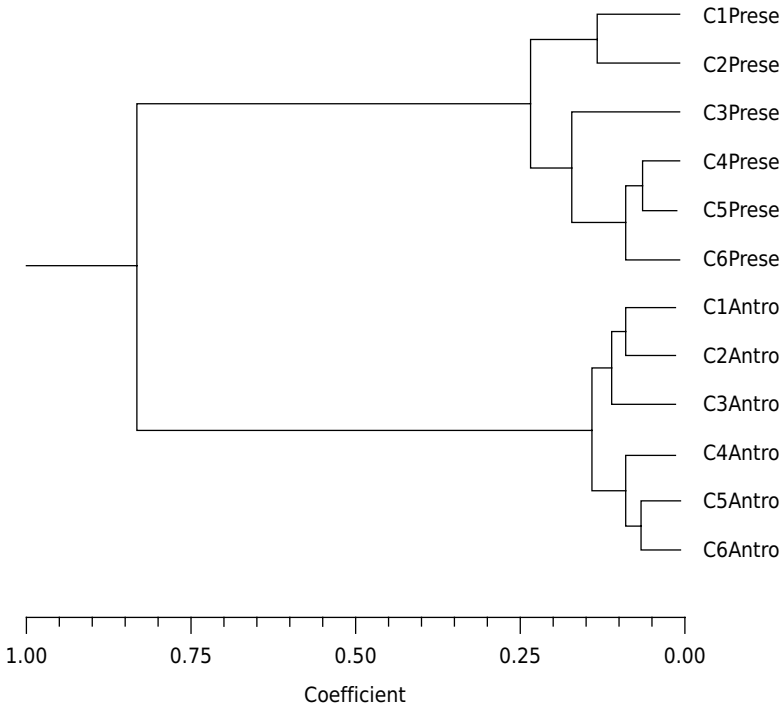

Figure 2. Dendrogram of relation between soil fungi samples from the Preserved (Prese) and Anthropized (Antro) areas of the Parna Catimbau, *Caatinga*, Pernambuco, Brazil, during the six sample collections (C1, C2, C3, C4, C5, and C6) performed. Bray-Curtis Index; Method of Weighted Pair-Group Method (WPGM). Coperetic analysis: Rf = 0.8. C1: collection 1; C2: collection 2; C3: collection 3; C4: collection 4; C5: collection 5; C6: collection 6.

DISCUSSION

Soil is a natural resource essential for the functioning of the terrestrial ecosystem and represents a balance between physical, chemical, and biological factors (Atlas and Bartha, 1993; Melloni et al., 2013). The biological fraction is primarily composed of microorganisms (bacteria and fungi, especially filamentous fungi), as well as worms, insects, and nematodes. One of the primary functions performed by microorganisms present in the soil is the cycling of organic matter during the decomposition process (Atlas and Bartha, 1993). In this context, filamentous fungi play a prominent role because they are excellent decomposers of organic matter (Schimel et al., 2007).

The presence of a specific microbial species in a specific soil depends on the dominant environmental conditions, as well as the genetic background of the species (Pereira et al., 1996). Thus, there are abiotic factors that limit the survival and activity of soil microorganisms. The primary abiotic soil factors are temperature, pH, salinity, energy sources, organic substrates (decomposing plant and animal remains), nutrients (C- and N-containing molecules), and toxic elements. In addition, there are the effects of the anthropogenic impact on the soil microbiota, Such as management change and soil cultivation (Pimentel et al., 2008). By physicochemical analysis of the soils, differences in the properties analyzed can be observed, both among the collections and between the areas. Higher values of pH and K^+ were observed in the anthropized area, indicating an environment of greater eutrophism. Higher values of H+Al were observed in the preserved area, due to the greater amount of organic matter. Considering that physicochemical properties are very important factors for microorganisms, oscillations in these factors may contribute to the success of certain populations, as well as their decline (Atlas and Bartha, 1993).

Soil must be understood as an integral part of specific functions in the ecosystem, given that the biological fraction is dynamically and easily affected by agricultural management (Kimpe and Warkentin, 1998). The anthropogenic effect on filamentous

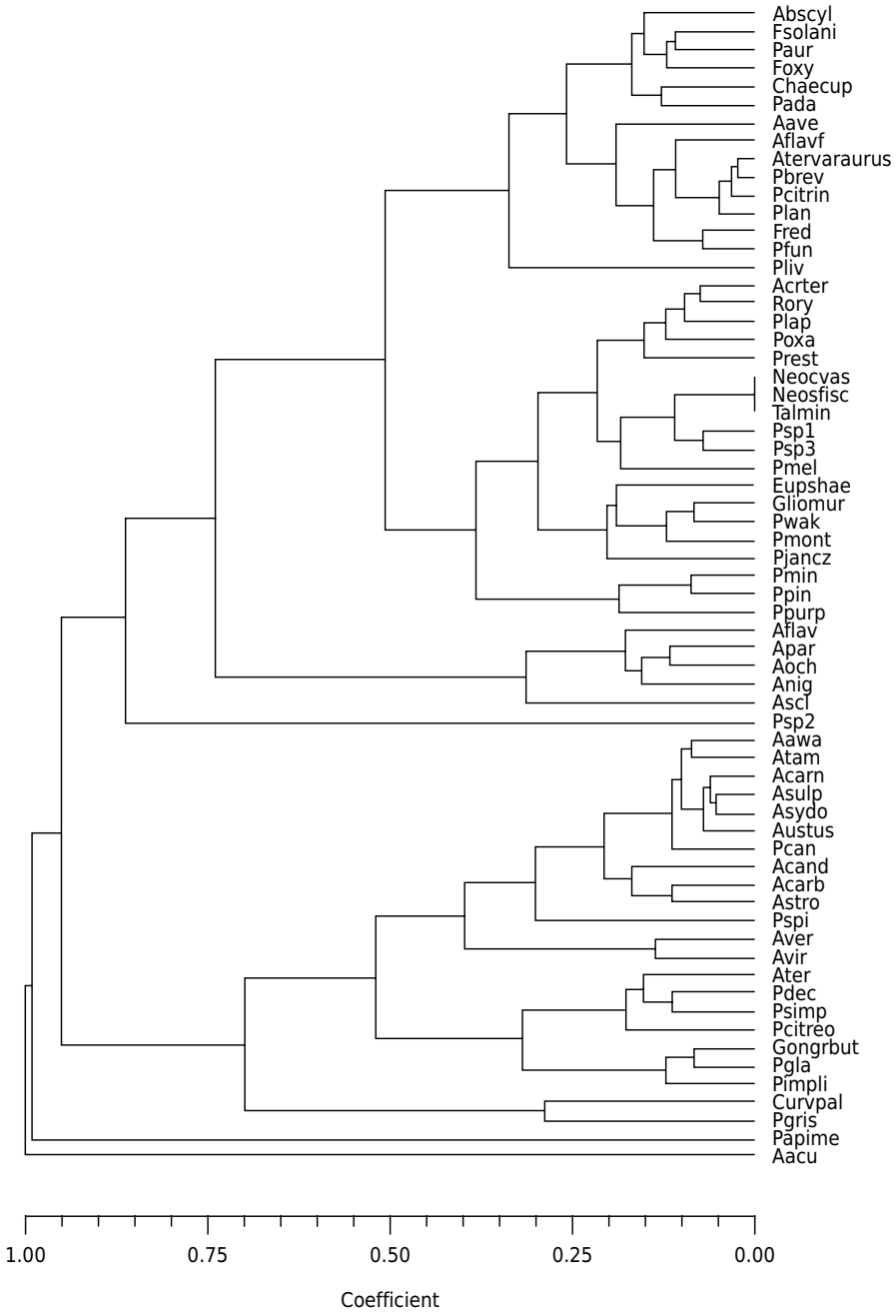

Figure 3. Proximal dendrogram among filamentous fungi species from a Preserved and Anthropized area of the Parna Catimbau, *Caatinga*, Pernambuco, Brazil. Statistical analysis based on the Bray-Curtis index; Proportional weight binding method (WPGM: Weighted Pair-Group Method; Arithmetic Average). Coperetic analysis: Rf = 0.8. Abscyl: *Absidia cylindrospora*; Fsolani: *Fusarium solani*; Paur: *Penicillium aurantiogriseum*; Foxy: *Fusarium oxysporum*; Chaecup: *Chaetomium cupreum*; Pada: *Penicillium adametzii*; Aave: *Aspergillus avenaceus*; Aflavf: *Aspergillus flavofurcatus*; Atervaraurus: *Aspergillus terreus* var. aureus; Pbrev: *Penicillium brevicompactum*; Pcitrin: *Penicillium citrinum*; Plan: *P. lanosum*; Fred: *Fusarium redolens*; Pfun: *Penicillium funiculosum*; Pliv: *P. lividum*; Acrter: *Acremonium terricola*; Rory: *Rhizopus oryzae*; Plap: *Penicillium lapidosum*; Poxal: *P. oxalicum*; Prest: *Penicillium restrictum*; Neocvas: *Neocosmospora vasinfecta*; Neosfics: *Neosartorya fischeri*; Talmin: *Talaromyces minioluteus*; Psp1: *Penicillium sp*1; Psp3: *P. sp*3; Pmel: *P. melinii*; Eupshae: *Eupenicillium shaerii*; Gliomur: *Gliomastix murorum*; Pwak: *Penicillium waksmanii*; Pmont: *P. montanense*; Pjancz: *P. janczewskii*; Pmin: *P. miczynskii*; Ppin: *P. piniphilum*; Ppurp: *P. purpurogenum*; Aflav: *Aspergillus flavus*; Apar: *A. parasiticus*; Aoch: *Aspergillus ochraceus*; Anig: *A. niger*; Ascl: *A. sclerotiorum*; Ps2: *Penicillium sp*2; Aawa: *Aspergillus awamori*; Atam: *A. tamarii*; Acarn: *A. carneus*; Asulp: *A. sulphureus*; Asydo: *A. sydowii*; Austus: *A. ustus*; Pcan: *Penicillium canescens*; Acand: *Aspergillus candidus*; Acarb: *A. carbonarius*; Astro: *A. stromatoides*; Pspi: *Penicillium spinulosum*; Aver: *Aspergillus versicolor*; Avir: *A. viridinutans*; Ater: *A. terreus*; Pdec: *Penicillium decumbens*; Psimp: *P. simplicissimum*; Pcitreo: *P. citreonigrum*; Gongrbut: *Gongronella butleri*; Pgla: *Penicillium glabrum*; Pimpli: *P. implicatum*; Curvpal: *Curvularia pallescens*; Pgris: *Penicillium griseofulvum*; Papime: *Papulaspora imersa*; Aacu: *Aspergillus aculeatus*.

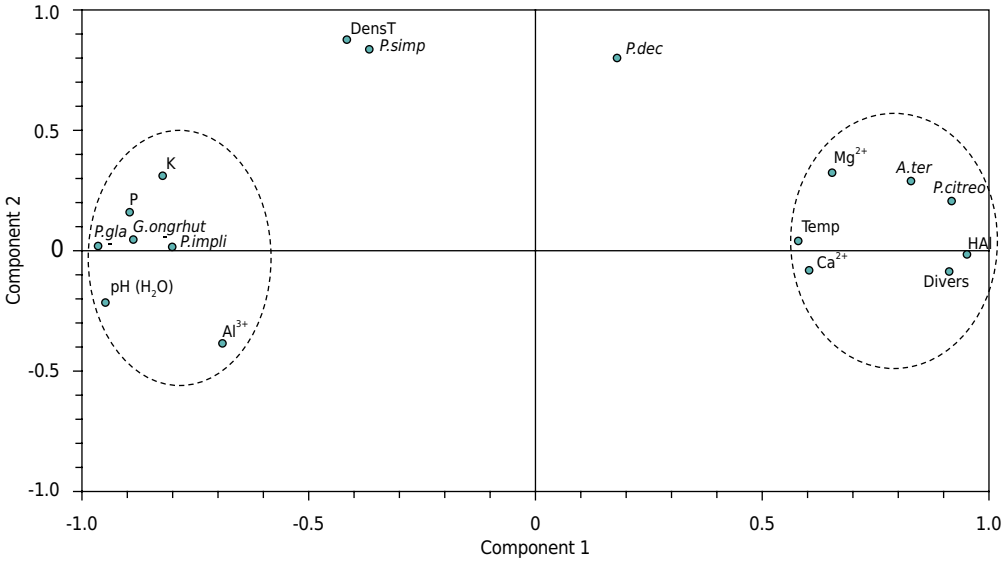

Figure 4. Two-dimensional projection of the Principal Component Analysis of soil samples from preserved and anthropized areas of the Parna Catimbau, Buíque, Pernambuco, Brazil. Factor 1 (Component 1) and Factor 2 (Component 2). P. gla: *Penicillium glabrum*; G. ongrbut: *Gongronella butleri*; P. impli: *Penicillium implicatum*; P. simpli: *P. simplicissimum*; Pdec: *P. decumbens*; A ter: *Aspergillus terreus*; P. cítreo: *Penicillium citreonigrum*.

fungus communities present in soils was observed in the present study. The preserved area of the Parna Catimbau showed greater species richness (48 species) and abundance (2,840 CFUs) than the anthropized area, with 23 species and 1,648 CFUs.

A series of factors may be related to the species richness of a community (Begon et al., 1990). Among these, geographical factors such as latitude, altitude, and soil depth. Other important factors are the productivity, climate variability, and age of the environment. Finally, there are biological factors, such as the intensity of predation and competition, the heterogeneity of biological origins of space and habitat, and the status of ecological succession in the community. Although all these factors are considered secondary, and depend on influences external to the community, they may play a relevant role in the definitive structuring of the community (Rodrigues et al., 2011).

The environmental conditions inherent to preserved *Caatinga* can explain the high richness and abundance of species. However, the Parna Catimbau has been considerably influenced by local human communities, and such an influence may explain the decrease in the richness and abundance of fungal species in the soil of the cultivated area. According to Pereira and Quirino (2008), anthropization and soil management reduce the richness and the abundance of species.

The genera with the highest richness and abundance of species were *Aspergillus* and *Penicillium*. This fact was already observed by Cruz et al. (2013), who studied the diversity of fungi in the soil of the Parna Catimbau and identified 23 species of *Aspergillus* and 26 species of *Penicillium*. Unlike the present study, Cruz et al. (2013) evaluated the diversity of filamentous fungi in only one area, analyzing the influence of seasonality on the community. Oliveira et al. (2013) carried out studies on the community of filamentous fungi in Catimbau Valley soils and identified 85 species of filamentous fungi, of which 28 belonged to the genus *Aspergillus* and 18 to the genus *Penicillium*, in contrast with the results found in the present study, in which *Penicillium* exhibited more species. This difference may be due to the fact that the studies were carried out in different areas, although within the Parna Catimbau. According to Atlas and Bartha (1993), it is difficult to attribute generalized adaptive characteristics to the soil microbiota. Soils have several microhabitats, and in a given microhabitat, there may be specific situations favoring certain endogenous communities. In the areas evaluated in the present study,

the conditions seem to be more favorable to the physiological abilities of species of the genus *Penicillium*, since this genus shows greater richness. For three isolates belonging to the genus *Penicillium*, it was not possible to identify morphological characteristics in a satisfactory way; they could be new species and molecular analyses comprising polyphase taxonomy were necessary.

Some species of *Aspergillus* and *Penicillium* are recognized for their harmful effects, primarily because they cause deterioration of food and produce mycotoxins. However, several species are widely used in biotechnological processes for producing numerous metabolites, such as enzymes, antibiotics, and antitumor substances (Houbraken and Samson, 2011). In this context, *Caatinga* soils constitute an excellent reservoir of filamentous fungi with biotechnological potential, with possible new species for science. According to Chambergo and Valencia (2016), so far, only 100,000 species of fungi have been described, although it is estimated that there are 5.1 million species of fungi on the planet.

In the present study, in the soil of both areas analyzed, some species were of low occurrence and may be considered autochthonous microorganisms (Atlas and Bartha, 1993). Few species were common to both areas; common occurrence would indicate that they have high adaptability to the different environmental conditions observed between the areas, such as the physical and chemical conditions of soils.

The indexes that measure diversity can serve as indicators of the equilibrium of ecological systems, functioning as tools for their management (Machado et al., 2005). The high diversity of the indexes found in the present study, for both the preserved area and the anthropized area, can be attributed to the probable maturity of their communities. The maturity of a community is closely related to diversity and productivity (Atlas and Bartha, 1993). A highly diverse community allows several relationships between different species, and there is a lower energy requirement, which is reflected by a lower rate of primary production of biomass per unit, and diversity remains stable. Based on the Pielou equitability index, a homogeneous pattern of distribution of individuals was observed among all species, indicating that the communities evaluated are in ecological equilibrium.

In the preserved area, we observed the codominance of species belonging to the genera *Aspergillus*, *Gongronella*, and *Penicillium*. However, in the anthropized area, only the genus *Aspergillus* was dominant. Five of the 12 *Aspergillus* species found in this area dominate the entire filamentous fungal community. The dominant species *A. flavus*, *A. niger*, *A. ochraceus*, *A. parasiticus*, and *A. sclerotiorum* have been reported as typical of soil and resistant to adverse environmental conditions (Klich, 2002; Cruz et al., 2013). In both communities (preserved area and anthropized area), species classified as constant and common were found, with no rare species.

Thus, soil must be recognized as an integral part of specific functions in the ecosystem, in which the biological fraction is dynamically and easily affected by agricultural management (Kimpe and Warkentin, 1998). The Bray-Curtis distance (Magurran, 1988) was used to graphically visualize the proximity between the two communities analyzed. When it was applied to the collected samples, we observed the formation of two large groups (preserved area and anthropized area), indicating the individuality of each community. This can be observed in the dendrogram shown in figure 2. When the same analysis was applied to the species, two large groups were formed (preserved area and anthropized area) and, within each, three subgroups. Such groupings may indicate that the closest species have similar ecological niches in the community and are therefore closely related (Figure 3). Such species likely require the same nutrients and have a similar enzymatic apparatus. The PCA allows biological properties to be more easily detected and interpreted (Blackith and Reyment, 1971; Reis, 1997) and allows verification of the discriminatory capacity of the original variables in the grouping process and interpretation of the results translated by the value of the correlation between properties (Pimentel et al., 2008). The feasibility of a PCA can be

visualized by the amount of information from the original variables retained by the first three principal components (percentage of the total explanation of the variables accumulated by the first three components). In the present study, PCA revealed that *P. simplicissimum* influences the total diversity of both communities (Figure 4). For their part, the populations of *Acremonium terricola* and *P. citreonigrum* directly correlated with temperature and concentrations of H+Al, Mg^{2+}, and Ca^{2+}. All these factors inversely correlated with the populations of *P. glabrum*, *P. implicatum*, and *Gongronella butleri*, which are directly influenced by pH(H_2O) and P, Al^{3+}, and K^+ concentrations (Figure 2). In other words, the populations of *Acremonium terricola* and *P. citreonigrum* are antagonistic to those of *P.glabrum*, *P. implicatum*, and *Gongronella butleri*, probably competing for some type of nutrient.

CONCLUSIONS

The Parna Catimbau is an important biodiversity reserve of the microbiota of the *Caatinga*, harboring high diversity of filamentous fungi in its soils.

The anthropization of areas of the Parna Catimbau changes the composition of the local filamentous fungi, restricting the species, and reducing the abundance of these important microorganisms.

This important ecosystem has been impaired and may undergo great imbalances with serious consequences, such as possible disappearance of the species described, as well as species not yet discovered by the scientific community.

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