

IDENTIFICATION OF FUNGAL ORGANISMS PRESENT IN ELEMENTS CONSIDERED HISTORICAL HERITAGE

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ABSTRACT

In this study, the presence of xylophagous organisms in historical wood present in the temple of Santiago Apostol in Tupátaro, Michoacán, Mexico, was evaluated. Through a visual inspection of three different structural zones in damaged wood of the temple, sampling of various fungal isolates was performed, to be subsequently molecularly identified. Similarly, the temperature and humidity conditions of each site where the samples were taken were recorded, and the laccase and cellulase activities were evaluated for each isolate. The results showed the presence of 14 fungal organisms with well-differentiated morphological characteristics, present in structures such as doors, windows, floors, ceilings, columns, and lintels. Organisms such as *Fusarium*, *Trichoderma*, *Penicillium*, and *Aspergillus* were found. The temperature and humidity conditions in the temple were found to favor fungal growth in different areas of the structure. The fungi found and identified exhibit enzymatic characteristics to degrade and/or generate aesthetic damage in the colonized wood.

KEYWORDS: Xylophagous fungi, wood, historical monuments, chromogenic fungi.

INTRODUCTION

Wood is among the most durable cellulosic materials because it is constituted by macromolecules that form the cell wall: cellulose (40 to 44% of the wood cell wall), lignin (18 to 35% of the wood cell wall), and hemicellulose (15 to 32% of the wood cell wall), as well as by low molecular weight organic and inorganic substances termed extractives (Kracher & Ludwig 2016; Andlar et al. 2018; Goodell et al. 2020; Urtis-Flores et al. 2026). It is important to cite these physicochemical characteristics of wood, as they explain how it became, on a global scale, the most widely used organic material in traditional and modern construction systems, which have been a recurrent practice for hundreds of years. Consequently, this has

brought about a high prevalence of elements manufactured either partially or totally from wood. Wooden structures have been a common choice in the construction of religious buildings, especially in regions with a rich cultural heritage, being fundamental in historical constructions, such as churches with a strong presence of colonial typology in Mexico (Morales 2011), estimated that there are more than 110,000 historical monuments (INAH) of which more than 5,000 are located within the State of Michoacán de Ocampo. However, despite wood being considered a durable material, prolonged exposure to deterioration agents whether biotic, abiotic, or anthropic can accelerate the process of mechanical and structural loss, as well as changes in aesthetics or natural wear, thereby generating losses in its load capacity or modulus of rupture (Zhang et al. 2022; Martín & López 2023).

For instance, in the temple of Santiago Apostol in Tupátaro, Michoacán, wood is one of the mainly employed materials, where it is possible to appreciate the use of traditional techniques specific to the art and architecture of the region. However, the wood has been compromised by humidity and human factors (Forest Products Laboratory 2010; Riggio et al. 2018). Among the most important deterioration agents are xylophagous fungi, characterized by the type of rot or damage they cause (white, brown, soft rot, or chromogenic damage), utilizing the structural components of wood (cellulose, lignin, and hemicellulose) as a carbon source and severely affecting its reliability in use (Díaz-Rivera et al. 2021; Li et al. 2022).

The high prevalence of these fungal organisms in natural and anisotropic environments is due to a great adaptive versatility, growing in a relative humidity equal to or greater than 65% and at temperatures ranging between 10-40°C (ASTM 2016). In addition to possessing a specialized enzymatic capacity (cellulases, laccases, ligninolytic enzymes, manganese peroxidases, lignin peroxidases, and oxalic acid) to catabolize the structural polymers of the plant cell wall (Goodell et al. 2003; Komorowicz et al. 2023). Xylophagous organisms are those possessing the metabolic capacity to degrade lignocellulosic materials and utilize them as a substrate; representatives can be found in divisions such as Ascomycota (*Aspergillus*, *Penicillium*) or Basidiomycota (*Trametes*, *Gloeophyllum*) (Hamed 2013). They can be easily found in historical buildings because these properties-owing to time, their construction systems, and high maintenance costs-generate the appropriate conditions for xylophagous fungi to develop, as reported by various investigations worldwide. Therefore, the identification of deterioration agents is crucial, as it allows us to understand the attack mechanisms and the damage they can cause to wood (Blanchette et al. 2004).

To minimize damage, *in situ* monitoring of environmental conditions is performed in some of these buildings, providing information that is correlated with the conservation of collections of various museum-related and non-structural natures within the property (ICOMOS 2003). Therefore, developing monitoring strategies for properties focused on fungal issues is important, since the development of these organisms can be favored within their interiors. This microbial deterioration risks not only the structural integrity of historical monuments but also their cultural value, as they represent living testimonies of the history and identity of a region (Clausen & Kartal 2003; Held et al. 2005; Held et al. 2006).

Currently, commercial solutions to combat these fungi are not necessarily compatible with the characteristics of historical materials, or with the existing guidelines and criteria for the conservation of built wooden heritage; this can cause additional damage or interfere with

its preservation. For this reason, it is important to identify the fungi present in historical monuments, as well as their current environmental conditions, in order to contribute to the development of comprehensive strategies for the maintenance, care, or restoration.

MATERIAL AND METHODS

Study site

The Religious Complex of Santiago Apostol in Tupátaro dates back to the 18th century; the current space is constituted by the church nave, the atrium, the sacristy, and the museum with its courtyard bounded by the atrium, with the entire complex being delimited by an atrium wall. This property is located just 25 minutes from the city of Morelia (the capital of the State of Michoacán) towards Pátzcuaro, Michoacán (Fig. 1A). Signs of a need for maintenance and repairs were shown by the building, as it was neglected over the years, although it was intervened in the 20th century. Major modifications were undergone by the complex after the colonial period, the most severe being the reduction of the complex due to the “Leyes de Reforma” (Lempérière 2008).

Temperature and humidity

Internal monitoring of the temple was performed at three selected points based on a visual inspection where damage due to the presence of xylophagous fungi was identified (Fig. 1A). An Onset HOBO Data Logger U12-012 with 1 external channel was utilized for this purpose. Active monitoring was maintained for 12 months, and temperature and humidity records were captured every hour. The devices were located as follows: the first in the altarpiece area (H1); the second beneath the wooden floor in the central section that exhibits the floor area of the central nave (H2); and the last in the choir area (H3). This setup was designed to obtain readings from the sites of greatest conservation interest.

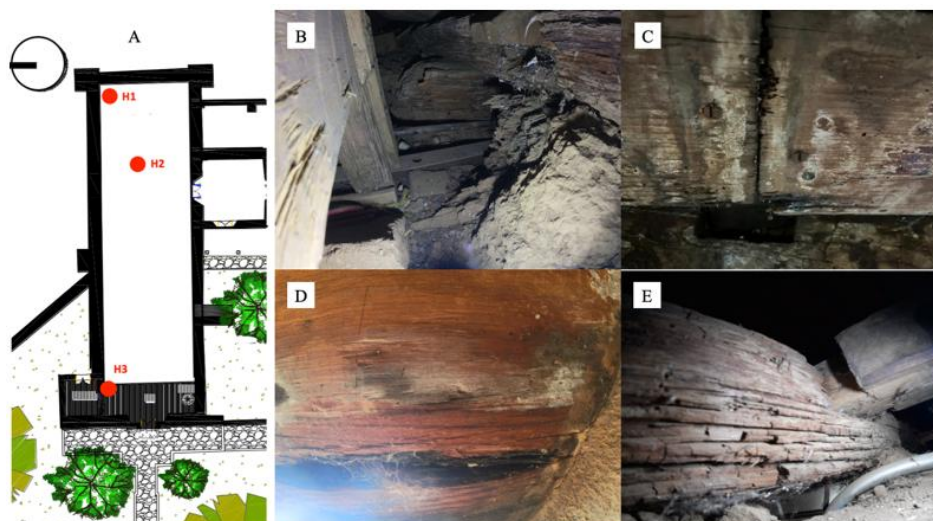


Fig. 1: Plan of the interior of the temple (A) showing the altar altarpiece area (H1), the floor area of the central nave (H2), the choir area (H3). Areas found with wood where fungal damage is detected (B-E).

Sampling for fungal isolation

The collection of existing fungal material was performed in some of the areas where

a structural risk was detected, which corresponds to the location of the temperature and humidity sensors (Fig. 2B-E). At the sites H1, H2, H3, three different wood chip samples were taken from each site, as follows: sampling was conducted using sterile forensic-style personal protective equipment, including latex gloves, masks, safety goggles, and sterilized cutting tools such as blades, scalpels, and forceps. Wood chips of approximately 2x0.5 cm was collected, placed in sterile Petri dishes, and stored in a cooler at approximately 5°C for transportation to the Wood Microbiology Laboratory of FITECMA-UMSNH until further use.

Fungal isolation

The surfaces of the samples (wood chips) were carefully cleaned using a cotton swab moistened with 70% alcohol. Subsequently, the wood chips were fragmented and placed in Petri dishes containing potato dextrose agar (PDA) medium and maintained in a microbiological incubator at 28°C under dark conditions. Every 12 hours, the Petri dishes were inspected to identify fungal growth (colonies) to be sequentially sub-cultured until pure cultures were obtained.

Taxonomic identification of fungal organisms

The pure cultures were characterized through morphological and molecular evaluation. For the morphological evaluation, samples were prepared for observation under an optical microscope using magnifications of 10X, 40X, and 100X.

For molecular identification, DNA was extracted from approximately 100 mg of fungal material using DNEasy Power Soil Pro Kit (QIAGEN) following the manufacturer's instructions. DNA quality and concentration were evaluated by electrophoresis in agarose gel 1% stained with SYBR Safe (Thermo Fischer Scientific) and spectrophotometry (ratio 260/280). Approximately 50ng of DNA was used as a template to amplify the internal transcribed spacer 2 (ITS2) region of ribosomal DNA (rDNA) by PCR by using Terra PCR Direct Polymerase Mix (Takara Bio). The primers used for ITS2 sequencing were 5'-GCATCGATGAAGAACGCAGC-3' and 5'-GTCCTCCGCTTATTGATATGC-3, corresponding to the forward and reverse primers. The reactions were incubated in a Mastercycler Nexus Series (Eppendorf) thermocycler under the following amplification conditions: 98°C for 2 min, followed by 30 cycles of 98°C for 10s, 65°C for 15s, and 68°C for 45s, and a final extension at 68°C for 2 min. The amplified fragments were verified for length (~400 bp) using agarose gel electrophoresis and purified by using the QIAquick Gel Extraction Kit (QIAGEN). The amplified DNA fragments (50-80ng) were sequenced with BigDye Terminator v3.1 Cycle Sequencing Kit (Thermo Fischer Scientific) by using a 3500 Genetic Analyzer (Applied Biosystems) following the manufacturer's instructions. Sequence quality evaluation was carried out by using CHROMAS Version 2.6.6 Software (<https://technelysium.com.au/wp/chromas/>). Subsequently, sequence comparisons were performed against the National Center for Biotechnology Information (NCBI) database using the Nucleotide Basic Local Alignment Search Tool (Blastn) (https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome) and the database UNITE considering a percentage sequence identity higher than 97% (Abarenkov et al. 2024).

The identified organisms were analyzed based on their wood bio-deteriorating potential, their relationship with the environmental conditions of the property, and their capacity to degrade historical materials, particularly wood.

Qualitative enzymatic analysis

Laccase and cellulase enzymatic activities were determined according to the methodology described by Florencio et al. 2012, with some modifications described by Urtis-Flores et al. 2026. Cellulase activity was measured to obtain the enzymatic index (EI) using the following:

$$EI = (\text{Colony diameter}) / (\text{Hydrolysis diameter}) \quad (1)$$

RESULTS

Environmental conditions of the site

From January to December 2024, temperature and humidity monitoring was performed. In the altar altarpiece area (H1), an annual mean temperature of 17.6°C was recorded, with a maximum mean temperature of 22.5°C observed in May and a minimum of 14.4°C in January. In the floor area of the central nave (H2), an annual mean temperature of 15.9°C was recorded, with a maximum mean temperature of 18.6°C observed in May and June, and a minimum of 13.0°C in January. In the area between the choir area (H3), an annual mean temperature of 18.3°C was recorded, with a maximum temperature of 22.9°C observed in May and a minimum of 15.1°C in January (Fig. 2A).

Regarding humidity, an annual mean value of 62.7% was recorded for the altar altarpiece area (H1), with a maximum humidity of 81.1% in September and a minimum of 38.2% in March. For the floor area of the central nave (H2), an annual mean humidity of 69.6% was recorded, with a maximum humidity of 81.8% in September and a minimum of 56.3% in February. For the area between the coffered ceiling and the roof (H3), an annual mean humidity of 58.2% was recorded, with a maximum humidity of 79.8% in September and a minimum of 37.2% in March (Fig. 2B).

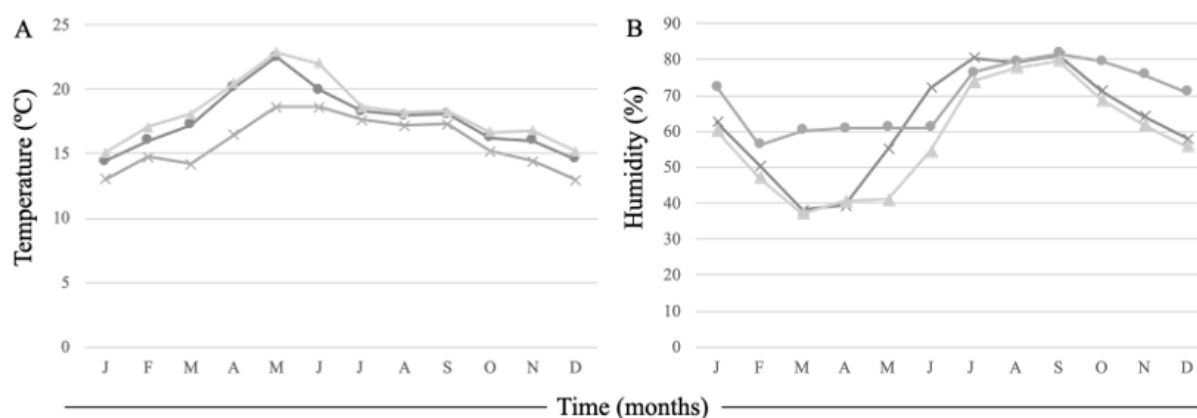


Fig. 2: Temperature and humidity values at sites H1 (Circle), H2 (X), H3 (Triangle).

Samples obtained

A total of fourteen samples was obtained from the chips of wood infected with fungi from

various elements, such as doors, windows, beams, flooring, coffered ceilings, and columns. From these, 14 fungal organisms with well-differentiated morphological characteristics among samples were successfully isolated (Fig. 3).

Colonial description

Different isolates were obtained from the samples (Fig. 3), from which the following macroscopic characteristics were observed and described: *Fusarium oxysporum* (A7-3): A coloration with white-pink, purple, or violet tones was exhibited, along with a dense cottony texture. *Trichoderma* (A3-2): White at the beginning, transforming rapidly into bright yellow-green patches as sporulation occurred, with a white cottony mycelial texture. Upon maturation, compact patches or concentric rings filled with spores were formed. *Fusarium oxysporum* (A4-2A): A highly striking and predominant pigmentation ranging from deep purple to grayish-violet was presented. Small areas or isolated foci of white/cream aerial mycelium were observed scattered across the surface and near the central inoculum. The edges were diffuse, filamentous in appearance, and lighter in color, indicating an active growth phase toward the periphery of the plate. *Trichoderma* (M3-1A1): A pale yellow-green to olive-green color was exhibited in the central zone. It was surrounded by a conspicuous light white/grayish peripheral halo composed of young mycelium that had not yet entered a massive sporulation phase, although the production of conidial heads (reproductive structures) was observed. *Penicillium bilaiae* (M9-3A): A grayish-green or pale bluish-green coloration was presented across most of the colony due to the high concentration of mature conidia. A densely velvety and compact texture was exhibited. Small transparent droplets of metabolic exudate were observed, which is a highly common physiological trait within this genus under optimal conditions of humidity and nutrients. *Fusarium* (A13-2): The colony was characterized as predominantly semi-transparent white to pale cream, maintaining a uniform coloration throughout its body without the presence of colored pigments or dark spores. The texture was fine cottony, radial, and filamentous. Individual hyphae were visible to the naked eye, propagating outward in straight lines from the center, which provided a plumose appearance. *Penicillium* (M6-38A): A grayish-green or bluish-green color was exhibited in the central and intermediate zones of the colony. This greenish region was sharply surrounded by a prominent white-cream perimeter halo, which was conformed by vegetative mycelium. *Penicillium bilaiae* (M11-3AA): A markedly granular and powdery texture was presented in the central and middle zones due to the massive presence of erect conidial heads protruding from the agar. Growth was circular, regular, and symmetrical, maintaining a highly sharp and clean border with the rest of the culture medium. *Aspergillus* (M10-1 A2): Most of the plate surface was covered by a pure white aerial mycelium. A well-delimited central zone of intense black or dark brown color was observed, where the fungus had matured and begun massive sporulation. *Penicillium bilaiae* (M1-182): The central body and nodular accumulations presented a grayish-green or dull olive-green color (sporulation zones). This coloration was surrounded and intertwined by a translucent white to cream vegetative mycelium that extended widely toward the edges, and an irregular floccose and granular texture was observed. *Aspergillus* (M9-1A): The colony presented a predominantly white to pale cream coloration throughout its entire extension. No visible production of diffusible pigments that could stain the culture medium was observed, thereby maintaining

a hyaline and clean appearance. A cottony, fluffy, and markedly heterogeneous texture was exhibited. *Trichoderma* (A4-2B): A heterogeneous coloration was shown, characterized by concentric rings of a bright olive-green color corresponding to maturation and sporulation zones. The olive-green regions alternated with a white to cream vegetative mycelium in the zones of younger or less dense growth. *Penicillium bilaiae* (M11-3AAB): A bluish-green, grayish, or dull emerald-green coloration was presented across most of the colony surface, which was uniform throughout the mature zone. This compact mass of spores was delimited by a very fine whitish/cream peripheral halo that marks the zone of active mycelial growth.



Fig. 3: Fungal isolates obtained correspond to *F. oxysporum* A7-3; M7-IA2; *Trichoderma* A3-2; *F. oxysporum* A4-2A; *Trichoderma* M3-1A1; *P. bilaiae* M9-3A; *Fusarium* A13-2; *Penicillium* M6-38A; *P. bilaiae* M11-3AA; *Aspergillus* M10-1 A2; *P. bilaiae* M1-182; *Aspergillus* M9-1A; *Trichoderma* A4-2B; *P. bilaiae* M11-3AAB.

Taxonomic identity of fungi

A diverse fungal community was shown through the taxonomic identification results using BLAST analysis and taxonomic assignment with UNITE, wherein organisms belonging to the genera *Fusarium*, *Penicillium*, *Trichoderma*, and *Aspergillus* were found (Tab. 1).

Tab. 1: Molecular identification of fungi isolated from the temple of Tupátaro, Michoacán.

Taxonomic identity of fungal isolates			
GAN	Analysis BLAST	Similitude (%)	Analysis UNITE
PX230264	<i>Fusarium oxysporum</i> (A7-3)	100	<i>Fusarium foetens</i>
-	M7-IA2	-	-
PX230401	<i>Trichoderma</i> (A3-2)	100	<i>Trichoderma</i>
PX230264	<i>Fusarium oxysporum</i> (A4-2A)	100	<i>Fusarium oxysporum</i>
PX230401	<i>Trichoderma</i> (M3-1A1)	100	<i>Trichoderma</i>
PX230510	<i>Penicillium bilaiae</i> (M9-3A)	100	<i>Penicillium bilaiae</i>
PX230620	<i>Fusarium</i> (A13-2)	100	<i>Fusarium</i>
PX230511	<i>Penicillium</i> (M6-38A)	100	<i>Penicillium crustosum</i>
PX230510	<i>Penicillium bilaiae</i> M11-3AA	99.65-100	<i>Penicillium</i>
PX230621	<i>Aspergillus</i> M10-1 A2	100	<i>Aspergillus niger</i>
PX230510	<i>Penicillium bilaiae</i> M1-182	99.28-99.64	<i>Penicillium bilaiae</i>
PX230621	<i>Aspergillus</i> M9-1A	100	<i>Aspergillus foetidus</i>
PX230401	<i>Trichoderma</i> A4-2B	99.65-100	<i>Trichoderma</i>
PX230510	<i>Penicillium bilaiae</i> M11-3AAB	99.63-100	<i>Penicillium bilaiae</i>

GAN= GenBank accession number.

The high similarity percentage obtained in BLAST and UNITE (99-100%) for most of the isolates confirmed the reliability of the molecular identification. This aspect is especially relevant in heritage studies, where morphological identification is often limited by atypical or degraded sporulated states.

Cellulase and laccase activity

A significant enzymatic activity related to wood degradation was demonstrated by the found isolates (Tab. 2). Cellulase activity was exhibited by the isolates *F. oxysporum* A7-3, M7-1A2, *Trichoderma* A3-2, *F. oxysporum* A4-2A, *Trichoderma* M3-1A1, *Aspergillus* M10-1 A2, *Aspergillus* M9-1A, and *Trichoderma* A4-2B (Fig. 4: CA). On the other hand, the isolate M7-1A2 was the only one that showed laccase activity in this study (Fig. 4: LA).

Tab. 2: Enzymatic activity index of cellulase and qualitative detection of laccase in the selected fungal isolates.

Isolate	CA	LA
<i>Fusarium oxysporum</i> A7-3	4.9	ND
M7-1A2	4.63	+
<i>Trichoderma</i> A3-2	1.2	ND
<i>Fusarium oxysporum</i> A4-2A	4.01	ND
<i>Trichoderma</i> M3-1A1	1.1	ND
<i>Penicillium bilaiae</i> M9-3A	ND	ND
<i>Fusarium</i> A13-2	2.2	ND
<i>Penicillium</i> M6-38A	ND	ND
<i>Penicillium bilaiae</i> M11-3AA	ND	ND
<i>Aspergillus</i> M10-1 A2	1.1	ND
<i>Penicillium bilaiae</i> M1-182	ND	ND
<i>Aspergillus</i> M9-1A	1.1	ND
<i>Trichoderma</i> A4-2B	1.1	ND
<i>Penicillium bilaiae</i> M11-3AAB	ND	ND

CA=Cellulase Activity LA= Laccase Activity, for LA: (+) indicates a positive reaction, ND= non-detected.

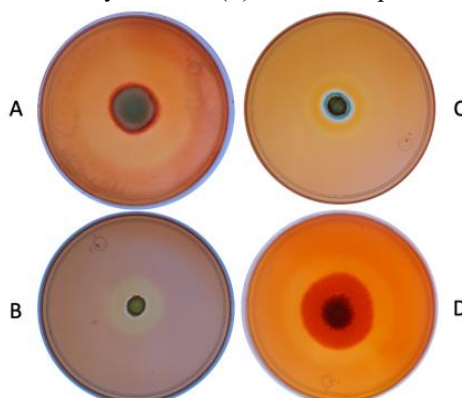


Fig. 4: Representative images of cellulase activity of the isolates (A) *F. oxysporum* A7-3; (B) M7-1A2; (C) *F. oxysporum* A4-2A; (D) *Fusarium* A13-2.

DISCUSSION

The temperature conditions found at the site coincide with environments that favor the growth of microorganisms that utilize wood as a substrate. In natural environments (forests), xylophagous fungi are present in settings with temperatures near 10°C, where they grow and thrive naturally. Fungi are organisms characterized by high metabolic versatility and adaptive capacity to adverse environmental conditions (Stephenson 2022). In this study, because the annual mean temperature was found to range between 15.9°C (H1) and 18.3°C (H3), it was demonstrated that temperature conditions remain ideal for fungal growth throughout the entire year, which consequently allows them to cause damage to the wooden structures of the temple.

Similarly, humidity conditions are directly related to fungal growth and were found to be favorable for development, with annual mean values ranging from 58.2% to 69.6% relative humidity. In wood, due to its anisotropic properties, moisture percentages of 30% can be reached, which was shown to be favorable for fungal proliferation.

In the present study, representativeness of organisms belonging to the genera *Fusarium*, *Penicillium*, *Trichoderma*, and *Aspergillus* was found. This information holds significant scientific value for several reasons: first, information was generated regarding the organisms present in wood from historical monuments and the role they might be playing; second, this knowledge contributes to the development and application of antifungal treatments for infested wood aimed at eliminating these specific organisms, given that the design of a targeted control strategy enhances its success.

The presence of the isolates *Fusarium* is particularly relevant. While organisms of this genus are widely known for their high pathogenicity in plants, their ability to colonize wood with a moisture content above 20% has also been documented, utilizing microscopic fissures and areas with prior biodeterioration (Wang et al. 2024).

It has also been documented that *Fusarium* species produce hydrolytic enzymes, such as cellulases and hemicellulases, which contribute to the degradation of the plant cell wall, thereby mechanically weakening wooden structural elements. In a historical building, their presence is often associated with the loss of surface cohesion, fiber softening, or color changes (such as the presence of pinkish or whitish stains, Fig. 1C). Furthermore, their detection at multiple points was suggested to indicate persistent humidity problems, possibly caused by capillarity, filtration, or condensation. *Fusarium oxysporum* is a filamentous fungus and represents one of the few fungal species that ferment plant carbohydrate polymers to ethanol in a single-step process. It can produce various enzymes that degrade the plant cell wall and ferment D-glucose, D-xylose, cellulose, and hemicellulose into ethanol (Anasontzis et al. 2016).

On the other hand, regarding the genus *Penicillium*, it was documented that these organisms act as early colonizers, which implies the subsequent presence of more aggressive fungi. *Penicillium* species do not necessarily cause severe structural degradation; however, they do generate greenish or bluish surface stains and were shown to indicate inadequate environmental conditions (such as high relative humidity and poor ventilation).

Species of the genus *Penicillium* were shown to be associated with the aesthetic and chemical alteration of wood, modifying surface pH and favoring biodeterioration processes. When acting in synergy with bacteria or other filamentous fungi, these processes generate superficial damage and create the necessity to replace the damaged wood (Seifert & Frisvad 2000).

The presence of *Trichoderma* across several isolates was shown to be ambivalent from a conservation standpoint. On one hand, it is a fungus characterized by antagonistic activity against other microorganisms; however, it also possesses a high capability for cellulose degradation. While *Trichoderma* typically colonizes areas with high moisture content (Mansour & Salem 2015), previously degraded wood, or wood with simple organic treatments, its enzymatic activity was suggested to accelerate weight loss and mechanical strength reduction, especially in non-structural elements such as doors, frames, and coffered ceilings.

The finding of *Aspergillus* isolates was shown to be important; these species are opportunistic fungi characterized by a high tolerance to environmental variations and the capacity to produce organic acids (such as oxalic acid), pigments that darken the material, and enzymes that degrade cellulose and lignin (de Vries & Visser 2001). In wooden elements, *Aspergillus* is associated with surface darkening, localized embrittlement, and respiratory tract health risks (Shah & Panjabi 2014). Its presence was suggested to strengthen the hypothesis of indoor environments with poor air renewal and humidity accumulation (Wirth et al. 2019).

Although the fungi found in this study are not typically categorized as wood-decay fungi (such as *Trametes* and *Gloeophyllum*), they are capable of degrading wood since they produce cellulase and laccase enzymes. This degradation occurs at a slower rate; however, the mycelium can affect the structure through its growth, as well as create suitable conditions for other wood-decay fungi to colonize the substrate (Urtis-Flores et al. 2026).

The detection of laccase activity in isolate M7-IA2 highlights its potential utility across diverse biotechnological applications. These enzymes oxidize both phenolic and non-phenolic lignin-derived compounds, as well as highly recalcitrant environmental pollutants. Consequently, this strain presents valuable prospects for application in the paper and pulp, textile, and bioremediation industries, as well as in xenobiotic degradation and biosensor development (Viswanath et al. 2014). Furthermore, fungal laccases have gained increasing traction in the food industry for the production of cost-effective and healthy products (Brijwani et al. 2010). The implementation of these enzymes minimizes the reliance on toxic solvents while enabling the valorization and reuse of agro-industrial residues under safe, energy-efficient conditions. Although high production costs, limited stability, and low reusability rates currently hinder their widespread industrial adoption, fungal laccases remain ideal biotechnological tools. Their exceptional catalytic versatility as oxidants requiring only molecular oxygen to operate underscores their industrial potential (Loi et al. 2021).

Finally, it is important to mention that a complex legal system for the protection of cultural heritage exists in Mexico (Hiriart 2022). The Federal Law on Archaeological, Artistic, and Historical Zones and Monuments grants authority to the National Institute of Anthropology and History (INAH 2018), outlining the guidelines for the conservation, research, protection, restoration, and recovery of monuments and movable property. For this reason, the generation of knowledge regarding the organisms involved in wood degradation within sites of these characteristics was shown to be essential, as it simplifies and facilitates the development of specific procedures for the control and elimination of the problem.

CONCLUSIONS

In this study, organisms representing the genera *Fusarium*, *Penicillium*, *Trichoderma*, and *Aspergillus* were identified as capable of degrading lignocellulosic materials, as they exhibited laccase and cellulase enzymatic activity. This information shows potential for the design of preventive treatments and the control of damage caused by wood-degrading fungi.

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