

A novel rapid screening method for identifying aflatoxin B₁-degrading Agaricales

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Abstract

Aflatoxin B₁ (AFB₁) is one of the most toxic and widespread mycotoxins, representing a serious threat to food safety and public health. In this study, a rapid screening method was developed to identify fungal strains capable of degrading AFB₁, using mushrooms belonging to the order Agaricales. Fifteen strains were evaluated, including isolates obtained from different regions of Argentina as well as commercially used strains. The fungi were inoculated onto Coconut Milk Agar (CMA), with and without the addition of AFB₁. Fungal growth on both media was assessed, and toxin degradation was evaluated by the reduction of fluorescence under UV light (365 nm), subsequently confirmed by high-performance liquid chromatography with diode array detection (HPLC-DAD).

All strains exhibited a reduction in growth rate in the presence of AFB₁. Among the 15 strains analyzed by HPLC-DAD, ten achieved complete degradation of AFB₁ to undetectable levels (>99% degradation), while three showed partial degradation (84%, 62%, and 20%). Notably, two strains (*Cyclocybe cylindracea* and *Stropharia* sp.) degraded AFB₁ despite the absence of visible mycelial growth, suggesting the involvement of extracellular enzymatic activity. These results demonstrate that several Agaricales species exhibit a high potential for AFB₁ degradation. The proposed method represents a rapid, low-cost, and effective tool for the preliminary identification of aflatoxin-degrading strains, showing a high concordance with quantitative HPLC-DAD results, and highlighting its promising applicability in bioremediation programs.

Introduction

Mycotoxins are secondary metabolites produced by diverse fungal species whose presence in food and subsequent ingestion can cause adverse effects on human and animal health (Iheshiulor et al., 2010). It is estimated that between 60 and 80% of food crops worldwide are contaminated with at least one type of mycotoxin (Eskola et al., 2020), with aflatoxins (AFs) standing out due to their high toxicity and wide distribution. These toxins are mainly associated with species of the genus *Aspergillus*, particularly those belonging to section *Flavi*, and are frequently detected in plant-derived products, such as cereals, nuts, and peanuts, among others. However, they may also be found in foods of animal origin, including milk, dairy products, and meat (Jallow et al., 2021; Sharafi et al., 2024). Aflatoxins are responsible for estimated economic losses of approximately USD 1.2 billion annually, mainly due to the devaluation of contaminated agricultural products (Gbashi et al., 2018).

Once produced, AFs are difficult to eliminate because they exhibit high stability to heat and conventional food processing treatments (Loi et al., 2023). In addition, their occurrence may take place at different stages of the food production chain, which considerably complicates their control (Jallow et al., 2021). The International Agency for Research on Cancer (IARC, 2002) has classified aflatoxins as Group 1 carcinogens, and they are estimated to contribute up to 28% of global cases of hepatocellular carcinoma, the most common type of liver cancer (Tai et al., 2020). Moreover, exposure to aflatoxins

may cause acute intoxication, immunosuppression, and growth retardation. Among all aflatoxins, aflatoxin B₁ (AFB₁) is considered the most toxic (Li et al., 2022).

The incidence and severity of AF contamination depend on multiple factors, among which water activity, temperature, and pH are particularly important (Shabeer et al., 2022). Throughout the food production chain, different aflatoxin mitigation strategies have been developed and can be broadly classified as physical, chemical, and biological. Physical methods include oxidation-based technologies; chemical approaches involve agents, such as organic acids, ozone, or adsorbents, whereas biological methods rely on the use of microorganisms and enzymes capable of transforming aflatoxins into metabolites with lower toxicity (Kinyoro & Kaale, 2024).

In recent years, bioremediation has attracted considerable interest due to its high efficiency in neutralizing contaminants without altering the organoleptic properties of foods or posing risks to human health. Microorganism-mediated degradation has been established as an ecological, economical, and efficient alternative for the removal of different contaminants (Zapašník et al., 2025a).

Fungi of the order Agaricales constitute the most diverse group among fruiting body-forming fungi, comprising thousands of described species and many more yet to be discovered (Hawksworth & Lücking, 2017). More than half of the global production of edible mushrooms is concentrated in four genera within this order: *Agaricus*, *Flammulina*, *Lentinula*, and *Pleurotus* (Royse, 2014).

The production of edible and medicinal mushrooms has increased markedly in recent years, which has also led to a global rise in the generation of residues associated with this industry (Bisht & Negi, 2026). The main by-product of this process is spent mushroom substrate (SMS), the residual substrate remaining after fructification, which is often disposed of through various practices, some of them with negative environmental impacts (Leong et al., 2022). In recent years, SMS has been the focus of numerous studies aimed at its valorization, including its application in bioremediation processes (Pérez-Chávez et al., 2022). This residue can be used as a source of enzymes, since Agaricales are white-rot fungi capable of synthesizing ligninolytic enzymes, such as laccases and peroxidases, which are involved in the degradation of aromatic and potentially toxic compounds (Söylemez et al., 2025). In addition, some mycotoxins have chemical structures similar to lignin monomers, suggesting that these enzymes could be effectively employed for their degradation (Qin et al., 2021). Mushroom production has thus become a key component of the circular economy, as these fungi are able to grow on lignocellulosic agro-industrial residues, transforming them into high-value fungal biomass (Grimm & Wösten, 2018), while generating residues with a reduced environmental impact that could be used as enzymatic sources for industrial or bioremediation processes.

The use of Agaricales fungi for the degradation of AFs has been previously reported, identifying ligninolytic enzymes, particularly laccases, as the main catalytic agents involved (Lou et al., 2023). However, most studies have focused on commercial strains belonging to the genus *Pleurotus* (Motomura, 2003; Alberts, 2009; Das, 2014; Loi et al., 2016; Branà et al., 2017; Jackson & Pryor, 2017; Branà et al., 2020; Song et al., 2021; Lou et al., 2023; Zapašník et al., 2025), and to a lesser extent on

Agaricus (Hussain et al. 2020) and *Cyclocybe* (Guo et al., 2024). Despite these advances, available information regarding the capacity of Agaricales to degrade aflatoxins remains limited.

In this context, the development of rapid and efficient methodologies for the detection and selection of fungal strains with AFB₁-degrading activity is essential. Coconut milk medium has previously been used to detect AFB₁ production in *Aspergillus* strains (Davis, 1987), taking advantage of its ability to enhance toxin fluorescence and facilitate visual observation.

The aim of the present study was to develop a low-cost and easily applicable screening method for the detection of AFB₁-degrading activity in Agaricales strains, as well as to evaluate this capacity in 15 strains belonging to nine families within this order.

Materials and Methods

Isolation of wild fungal strains

Basidiome samples of Agaricales fungi were collected from different areas of Argentina.

From the collected basidiomes, axenic cultures were obtained on 60-mm Petri dishes containing malt extract agar (MEA). Under a laminar flow hood, a small piece of tissue from the inner portion of the basidiome was excised and transferred onto the culture medium. Isolates were incubated at 24°C in darkness until complete colonization. Strains were selected based on their taxonomic position, aiming to cover the largest possible number of families within the order Agaricales, as well as on their growth rate.

In the case of newly collected specimens, species identification was performed following the methodology described by Lechner (2021). Sections of the hymenophore, the outermost cellular layers of the pileus, and the stipe were prepared and examined microscopically. After compiling all relevant morphological characteristics, taxonomic identification was achieved using specialized literature.

For the screening assay, two commercially used strains were included.

Preparation of the screening medium

For medium preparation, 40 g of powdered coconut milk, 20 g of bacteriological agar, and 1 L distilled water were mixed and sterilized by autoclave at 121°C for 15 min. The medium was then cooled to approximately 50°C and dispensed into sterile 60-mm Petri dishes (10 mL per plate). For the CMA + AFB₁ medium, an aflatoxin B₁ standard (Sigma-Aldrich, purity > 98%) was added to reach a final concentration of 4 µg/mL (40 µg AFB₁ per plate). Plates were allowed to solidify at room temperature under aseptic conditions in a laminar flow hood.

Fungal strains and experimental conditions

A total of 15 fungal strains belonging to nine different families within the order Agaricales were used for the screening test. Thirteen corresponded to wild isolates and two to commercially used strains. All strains are preserved in the CHA (Cepario Hongos Agaricales) and BAFC (Buenos Aires Fungal Collection) culture collections under their respective accession codes.

The complete list of species, taxonomic family, collection site, substrate of development, and identification code is provided in Table 1.

Strains were subcultured two weeks prior to the experiment to ensure the use of young and metabolically active mycelium. Petri dishes containing Coconut milk agar (CMA) and CMA added with aflatoxin B₁ (CMA + AFB₁) were inoculated using 5-mm-diameter agar plugs. Each treatment was performed in duplicate, and plates were incubated at 24°C in darkness.

During incubation, two perpendicular colony radii were measured per plate over a period of 20 days. The values of both radii were averaged for each plate and subsequently averaged between replicates. Results were graphically represented as a function of incubation time.

Table 1

Species included in the study, taxonomic family, province of collection, substrate of occurrence, and BAFC culture collection accession number.

Species	Family	Province/source	Substrate	Code
<i>Agrocybe perfecta</i>	Strophariaceae	Jujuy	Manure	BAFC4834
<i>Cyclocybe cylindracea</i>	Tubariaceae	Buenos Aires	Wood	BAFC4832
<i>Gymnopilus junonius</i>	Hymenogastraceae	Buenos Aires	Wood	BAFC4828
<i>Lepista nuda</i>	Tricholomataceae	Tucuman	Leaf litter, soil	BAFC4831
<i>Macrolepiota colombiana</i>	Agaricaceae	Jujuy	Soil	BAFC4829
<i>Mycena niveipes</i>	Mycenaceae	Buenos Aires	Wood	BAFC4827
<i>Oudemansiella canarii</i>	Physalacriaceae	Jujuy	Wood	BAFC4826
<i>Pleurotus black pearl king (BPK)*</i>	Pleurotaceae	Commercial strain	Wood	CHA114
<i>Pleurotus djamor</i>	Pleurotaceae	Commercial strain	Wood	CHA113
<i>Pleurotus ostreatus</i>	Pleurotaceae	Commercial strain	Wood	CHA116
<i>Psilocybe cubensis</i>	Hymenogastraceae	Tucumán	Manure	CHA117
<i>Psilocybe sp.</i>	Hymenogastraceae	Salta	Soil	BAFC4835
<i>Stropharia rugosoannulata</i>	Strophariaceae	Buenos Aires	Soil	BAFC4833
<i>Stropharia sp.</i>	Strophariaceae	Misiones	Wood	CHAFC115
<i>Volvariella bombycina</i>	Pluteaceae	Buenos Aires	Wood	BAFC4830

*A hybrid commercial strain known as Shimofuri Hiratake in Japan.

Screening of AFB degradation by UV fluorescence revelation

After 20 days of incubation, the plates were placed under UV light (365 nm), and the presence/absence of fluorescence was visually recorded. To reduce the objective factor of the method, the plates were photographed. Images were processed to enhance the contrast, using ImageJ software by adjusting brightness until the negative control plates (CMA without mycelium) appeared completely black.

Plates were considered positive for AFB₁ degradation when a reduction in fluorescence intensity was observed with respect to the positive control (CMA + AFB₁ without mycelium). Maximum degradation was observed when fluorescence levels were comparable to those of the negative control.

Extraction and quantification of AFB₁ by HPLC-DAD

Confirmation of AFB₁ degradation was carried out by high-performance liquid chromatography (HPLC) coupled with diode array detection (DAD).

After 20 days of incubation at 24°C in darkness, the entire culture medium from each Petri dish was recovered. The medium was cut into fragments of approximately 5 × 5 mm and quantitatively transferred into 50 mL Falcon tubes. The extraction and detection of AFB₁ was performed following the protocol described by Mochamad and Hermanto (2017) with minor modifications. Briefly, 10 ml acetonitrile (ACN) were added to each tube as extraction solvent. Samples were homogenized by vortexing for 30 s, followed by orbital shaking at 1300 rpm for 60 min at room temperature to promote complete extraction of AFB₁ from the agar-based medium.

Subsequently, the tubes were centrifuged at 1300 × g for 10 min at room temperature to sediment solid residues of the culture medium. The supernatant was carefully recovered and filtered through Whatman No. 1 filter paper to remove coarse particles. Finally, 1 mL of the filtrate was filtered again through a 0.45 µm PTFE syringe filter to ensure the removal of fine particles prior to injection into the chromatographic system.

Chromatographic separation was performed using a Waters HPLC system equipped with a diode array detector (DAD) and a reverse-phase C18 column (250 mm × 4.6 mm, 5 µm particle size). The mobile phase consisted of an isocratic mixture of water:methanol:acetonitrile (63:26:11, v/v/v) at a flow rate of 1.0 mL/min. The injection volume was 20 µL, the column temperature was maintained at 30°C, and AFB₁ quantification was carried out at 354 nm. The detection limit of the method (LOD) was defined as the minimum concentration of AFB₁ which could be confirmed by the diode array detector (0.05 µg/ml). The limit of quantification (LOQ) was calculated as five times the noise, defined as the standard deviation of the linear regression of the drift at the selected time range (0.2 µg/ml).

Results

Growth on CMA and CMA + AFB₁

Figure 1 shows the growth of the different strains, expressed as colony radius (mm) as a function of time on CMA and CMA + AFB₁ media. On CMA, *Pl. ostreatus* and *O. canarii* reached complete colonization in the shortest time, both achieving full plate coverage within five days. *A. perfecta*, *Pl. BPK*, *Pl. djamor*, and *V. bombycina* reached complete colonization by day nine of incubation. Overall, eight of the fifteen strains tested were able to completely cover the surface of the medium.

The addition of AFB₁ to the medium negatively affected the growth rate of all evaluated strains. On CMA + AFB₁, all strains exhibited a longer lag phase (from 3 up to 20 days). The effect was the least evident for *Pl. djamor*, which initiated growth after three days of incubation in the presence of the mycotoxin. However, subsequently, its growth almost completely ceased.

The strains *Pl. ostreatus* and *V. bombycina* showed the shortest colonization times (20 days), whereas *A. perfecta*, *C. cylindracea*, and *Stropharia* sp. failed to grow.

Visual screening by UV fluorescence

Representative plates from the screening assay, visualized under UV light and subsequently processed by brightness adjustment, are shown together with the controls in Fig. 2. In cases where complete degradation occurred (Fig. 2.a), plates displayed dark, nearly black tones. In contrast, when no degradation was observed, plates retained an intense bluish fluorescence similar to that of the negative control (Fig. 2.c). Finally, in cases of partial degradation (Fig. 2.b), intermediate blue tones were observed.

The visual screening results are presented in Table 2. In nine of the fifteen species analyzed (*G. junonius*, *Ma. colombiana*, *My. niveipes*, *O. canarii*, *Pl. ostreatus*, *P. BPK*, *Ps. cubensis*, *Psilocybe* sp., and *V. bombycina*), a complete reduction in fluorescence intensity was observed compared to the negative control. Four strains (*A. perfecta*, *L. nuda*, *C. cylindracea*, and *Stropharia* sp.) showed partial fluorescence reduction, while two strains (*P. djamor* and *S. rugosoannulata*) maintained an intensity similar to that of the negative control, indicating a presuntive absence of AFB₁ degradation.

Table 2
Visual screening results for aflatoxin B₁ (AFB₁)
degradation under UV light by the fungal strains evaluated
in this study.

Strain	UV fluorescence
<i>A. perfecta</i>	±
<i>C. cylindracea</i>	+
<i>G. junonius</i>	+
<i>L. nuda</i>	±
<i>Ma. colombiana</i>	+
<i>My. niveipes</i>	+
<i>O. canarii</i>	+
<i>Pl. bpk</i>	+
<i>Pl. djamor</i>	–
<i>Pl. ostreatus</i>	+
<i>Ps. cubensis</i>	+
<i>Psilocybe sp.</i>	+
<i>S. rugosoannulata</i>	–
<i>Stropharia sp.</i>	±
<i>V. bombycina</i>	+
Note: + (positive), - (negative) and ± (partially positive).	

Quantification of residual AFB₁ by HPLC-DAD

The results obtained through HPLC-DAD analysis are presented in Fig. 3. Of the 15 strains evaluated, ten achieved complete AFB₁ degradation, showing no detectable chromatographic peaks: *C. cylindracea*, *G. junonius*, *Ma. colombiana*, *My. niveipes*, *O. canarii*, *Pl. ostreatus*, *Pl. bpk*, *Psilocybe sp.*, *V. bombycina*, and *Ps. cubensis*. This corresponds to a degradation rate exceeding 99% of the initial mycotoxin concentration.

Three strains exhibited partial degradation with varying levels of efficiency. *Stropharia sp.* reached 84% degradation, with a residual concentration of 0.65 µg/mL. *L. nuda* showed a residual concentration of 1.52 µg/mL, equivalent to 62% degradation.

The strains *A. perfecta* and *Pl. djamor* presented a low degradation rate of 20%, and 19%, respectively, with a residual concentration of 3.20 µg/mL and 3.25 µg/mL. Finally, *S. rugosoannulata* showed no degradation capacity, maintaining a concentration of 4.0 µg/mL (0% degradation) under the tested conditions. These results confirm that these strains are not efficient AFB₁ degraders.

The overall agreement between the results of the visual screening under UV light and the quantification by HPLC-DAD was high, validating the utility of the preliminary method. Cases such as *A. perfecta*, which yielded a negative result in the UV screening and showed only 20% degradation by HPLC, reinforce the consistency between both methodologies in identifying strains with low or null activity. Furthermore, the total degradation (ND) observed in *C. cylindracea* and the 84% in *Stropharia* sp. are particularly noteworthy, as these strains did not show visible growth on the medium with the toxin, suggesting the action of persistent extracellular enzymes.

Discussion

The strong agreement between the visual screening and HPLC-DAD quantification highlights the robustness of the proposed method as a reliable tool for the rapid screening of AFB₁-degrading fungi. This is particularly relevant given the need for low-cost and high-throughput approaches to assess large fungal collections for biotechnological applications, where rapid preliminary screening methods are limited. Species previously described as AFB₁ degraders, such as *C. cylindracea* and *Pl. ostreatus*, (Branà et al., 2020; Song et al., 2021; Söylemez & Yamaç, 2021; Guo et al., 2024; Zapašnik et al., 2025) also exhibited degradation capacity in this study, further supporting the reliability of the experimental approach.

Beyond method validation, the differential responses observed among the evaluated strains provide insights into the mechanisms underlying AFB₁ transformation. The results clearly distinguish between fungal tolerance to the toxin and its actual biodegradation. For instance, *Stropharia rugosoannulata* was able to grow on CMA supplemented with AFB₁ without showing detectable degradation, suggesting physiological tolerance rather than active detoxification. In contrast, strains such as *Stropharia* sp. and *C. cylindracea* were able to reduce AFB₁ levels despite the absence of visible mycelial growth. This observation is particularly noteworthy, as it suggests that AFB₁ transformation may occur through extracellular enzymatic activity independent of active fungal proliferation. Such behavior reinforces the potential applicability of enzyme-based detoxification systems, even under conditions that limit biomass development.

Interactions between fungi and toxic compounds may involve different mechanisms, including tolerance, adsorption, or enzymatic transformation, depending on the metabolic capabilities of each strain (Harms et al., 2011). In this context, the enzymatic repertoire of fungi is strongly influenced by their ecological role and the substrates they colonize. Wood-decaying basidiomycetes are well known for producing extracellular oxidative enzymes involved in lignin degradation, such as laccases and peroxidases, which are capable of transforming a wide range of aromatic and xenobiotic compounds (Pointing, 2001;

Janusz et al., 2017). Because AFB₁ possesses a conjugated aromatic structure, these oxidative systems have been proposed as key mediators of its transformation (Alberts et al., 2009). However, the results obtained here indicate that AFB₁ degradation is not restricted to ligninolytic fungi. Species associated with soil, litter, or dung environments also exhibited degradation capacity, suggesting that exposure to diverse aromatic compounds may select for metabolically versatile enzymatic systems capable of modifying structurally complex molecules.

Within this framework, species of the genus *Stropharia* have been reported to produce oxidative enzymes associated with the degradation of lignocellulosic substrates and environmental pollutants (Pozdnyakova et al., 2018). Nevertheless, the *S. rugosoannulata* strain evaluated in this study did not show detectable AFB₁ degradation under the tested conditions, indicating that the enzymatic potential described for the genus does not necessarily translate into effective transformation of this mycotoxin in the *in vitro* testing conditions. This finding is consistent with the well-documented intra-specific variability in Agaricales. For example, different isolates of *Pleurotus ostreatus* have been shown to exhibit significant variation in the production of ligninolytic enzymes, which directly affects their capacity to degrade aromatic compounds (Baldrian, 2006). Such variability highlights the importance of strain-level screening, as species identity alone is not sufficient to predict AFB₁-degrading capacity.

It is also important to consider that the products generated during the biological degradation of AFB₁ may retain varying degrees of toxicity (Song et al., 2022). This may help explain the behavior observed in strains such as *Stropharia* sp. and *C. cylindracea*, which were able to degrade AFB₁ but did not recover normal mycelial growth. In these cases, growth inhibition may not be solely associated with the presence of the parent toxin, but also with the accumulation of intermediate degradation products that still exert toxic effects. Therefore, AFB₁ transformation does not necessarily imply effective detoxification. Further studies focusing on the identification and toxicological evaluation of degradation products are essential before practical applications can be considered.

In agreement with previous reports (Zapaśnik et al., 2025), AFB₁ exposure negatively affected the growth of all evaluated strains, regardless of their ecological origin. This inhibitory effect reinforces the relevance of identifying strains capable not only of tolerating but also of transforming the toxin under adverse conditions.

One limitation of the present study is that the AFB₁-degrading activity was evaluated under a single set of culture conditions. Both culture medium composition and incubation temperature are known to influence fungal growth and the production of extracellular enzymes involved in the degradation of complex organic compounds (Janusz et al., 2017). Consequently, some strains may not have expressed their maximum degradation potential under the experimental conditions employed.

Therefore, the results obtained should be interpreted as a comparative screening performed under standardized experimental conditions, which allows the identification of promising strains for further studies but do not necessarily represent the optimal conditions for the expression of their AFB₁-degrading capacity.

In summary, this study demonstrates that Agaricales fungi constitute a promising and still underexplored resource for AFB₁ biodegradation. The combination of a rapid screening method validated through a quantitative analytical method provided an effective framework for identifying candidate strains with biotechnological potential. These findings open new avenues for the development of sustainable strategies aimed at mitigating mycotoxin contamination in food and agricultural systems.

Conclusions

This study presents a rapid, low-cost, and reliable screening method for the identification of AFB₁-degrading Agaricales strains, based on fluorescence reduction in coconut milk agar and validated by HPLC-DAD analysis. The high level of agreement between the two approaches supports its applicability as a preliminary tool for large-scale screening programs.

The results demonstrate that several Agaricales species possess a strong capacity to degrade AFB₁, including strains capable of achieving complete toxin removal under the tested conditions. Notably, the ability of certain strains to degrade AFB₁ in the absence of visible growth suggests the involvement of extracellular enzymatic systems, highlighting their potential for enzyme-based detoxification strategies.

In addition, the variability observed among strains emphasizes the importance of strain-level evaluation, as degradation capacity cannot be inferred solely from species identity or ecological group.

Overall, the proposed methodology provides an effective framework for the selection of fungal candidates with biotechnological potential, contributing to the development of sustainable approaches for mycotoxin mitigation in food and agricultural systems.

Declarations

Ethics approval and consent to participate:

All authors confirm that this study did not involve research with human participants or animals. Therefore, no issues related to human or animal welfare apply to this study, and no ethical approval or consent to participate was required.

Consent for publication:

All authors have given explicit consent to the submitted paper and to the inclusion of their data in it.

Competing interests:

The authors declare no competing interests.

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Author contributions:

All authors contributed to the studies described in the paper and read and approved the final manuscript.

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Availability of data and materials:

The strains used in this study were deposited in the BAFC and CHA fungal culture collections.

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38. Advances in screening of edible fungi capable of secreting laccase and degradation of aflatoxin B1 by laccase from edible fungi

Figures

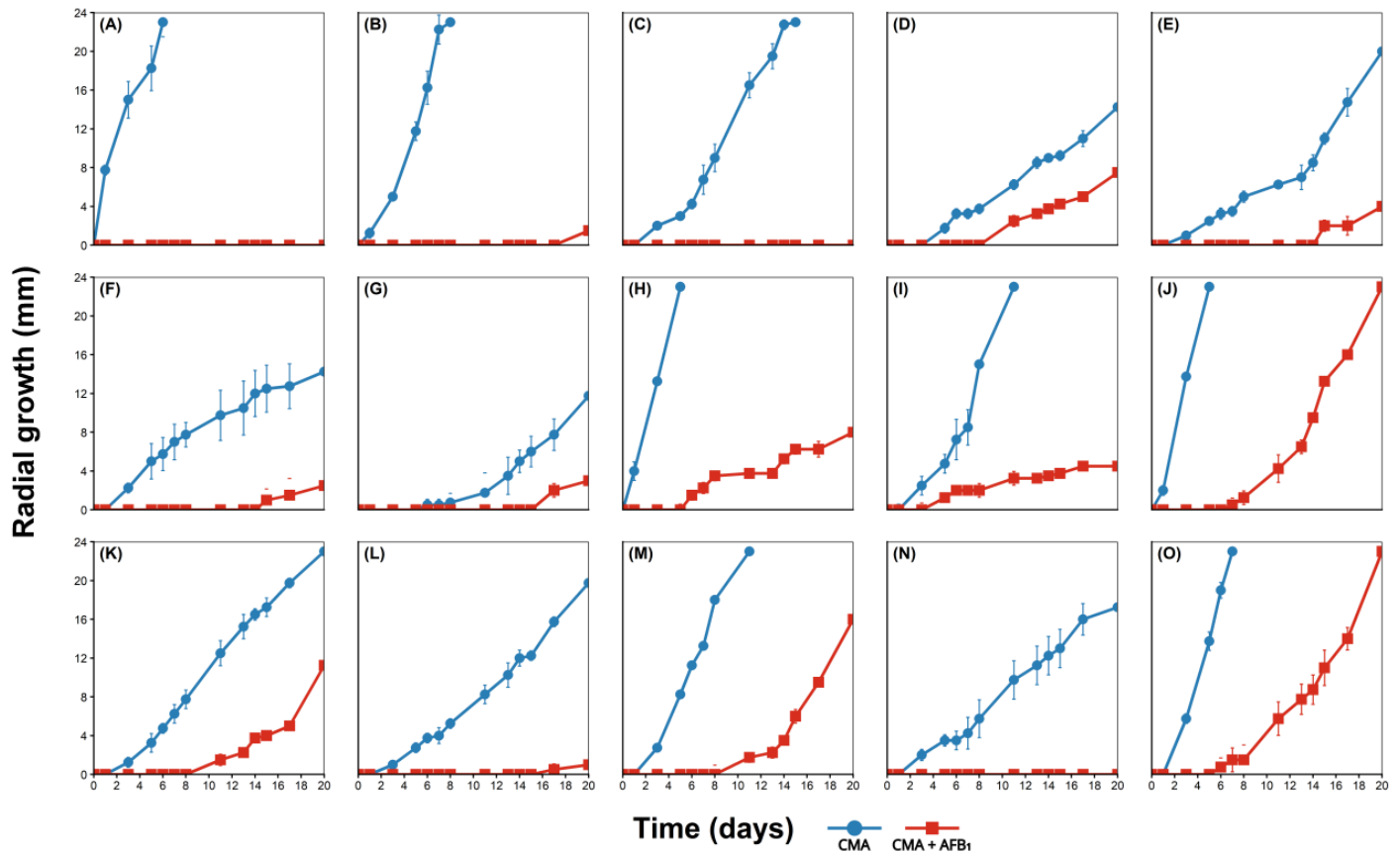


Figure 1

Radial growth curves of the strains used in this study on CMA medium and CMA supplemented with AFB₁ (CMA + AFB₁). A: *A. perfecta*; B: Black Pearl King, C: *C. cylindracea*; D: *G. junonius*; E: *L. nuda*; F: *Ma. colombiana*; G: *My. niveipes*; H: *O. canarii*; I: *Pl. djamor*; J: *Pl. ostreatus*; K: *Ps. cubensis*; L: *Psilocybe sp.*; M: *S. rugosoannulata*; N: *Stropharia sp.*; O: *V. bombycina*.

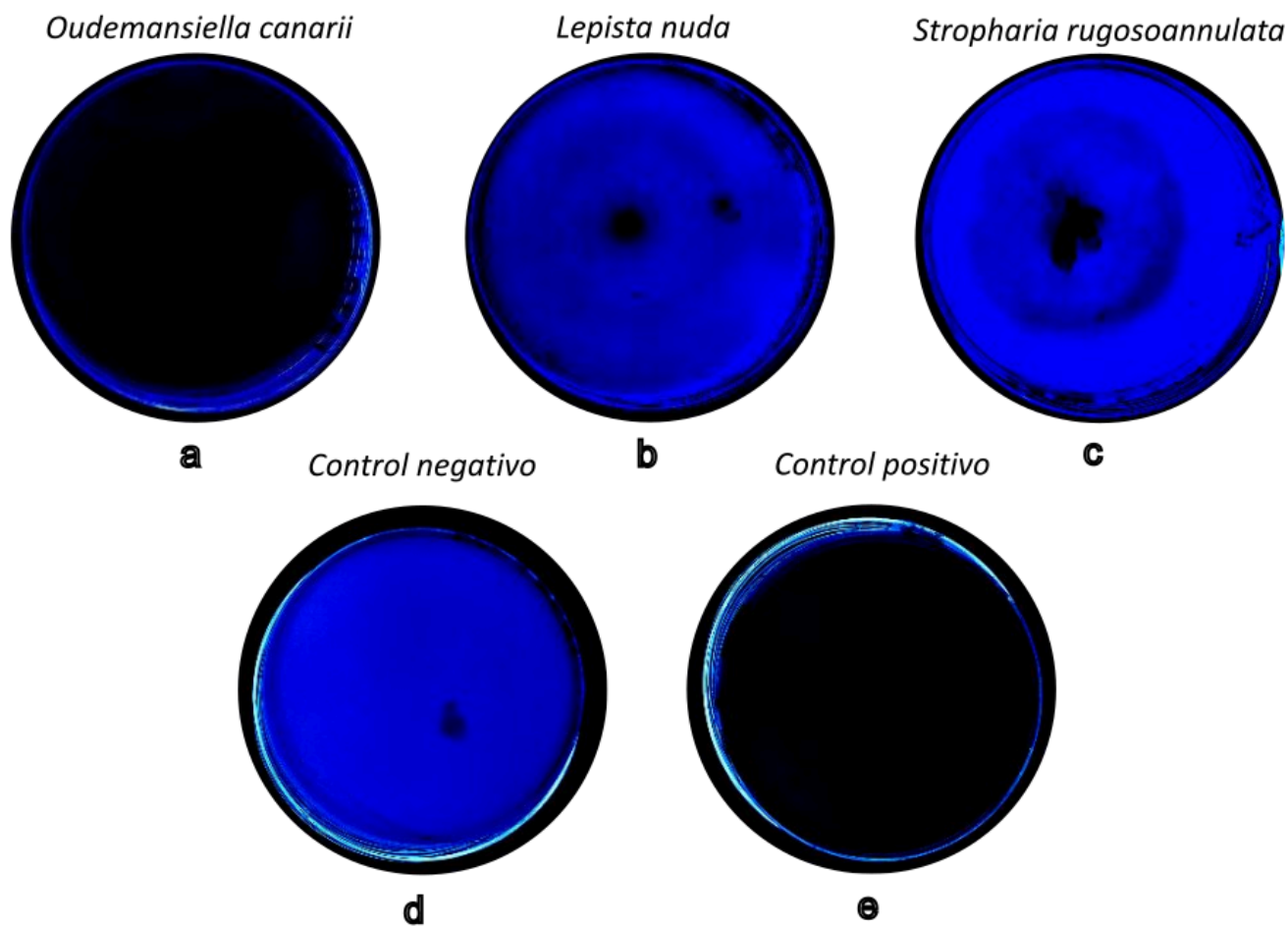


Figure 2

Representative visual outcomes of the AFB₁ degradation screening assay. (a) Positive result, showing complete degradation of AFB₁. (b) Partial degradation. (c) Negative result, with no visible degradation. (d) Negative control (CMA supplemented with AFB₁, without fungal inoculation). (e) Positive control (CMA without AFB₁).

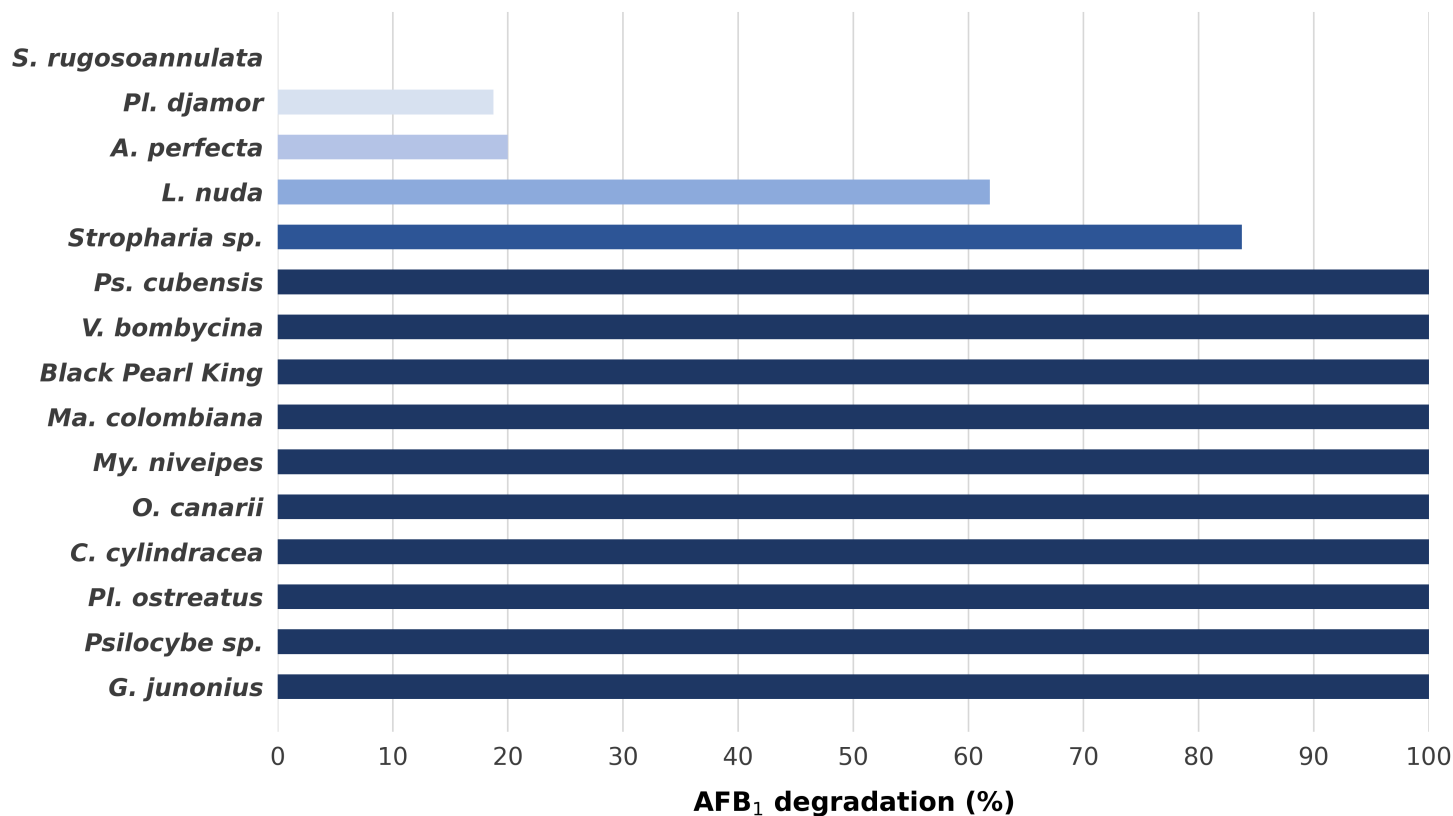


Figure 3

Percentage of AFB₁ degradation by the Agaricales strains included in the screening determined by HPLC-DAD analysis.

Supplementary Files

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