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Impact of Distillate Diesel Oil on the Growth of Mold Involved in Soil Bioremediation at an Electric Power Plant in Ouagadougou

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Abstract

Hydrocarbon compounds are among the most persistent pollutants globally, contributing significantly to the degradation of soil, air, and water, and posing serious environmental risks to ecosystems and human health. Molds, through their ability to degrade, dissolve, immobilize, or mobilize pollutants like petroleum hydrocarbons, are among the main microorganisms playing a crucial role in soil remediation. This study aimed to evaluate the effect of Distillate Diesel Oil (DDO) on the growth behavior of mold strains isolated from hydrocarbon-contaminated soils at an electric power plant in Ouagadougou. During an eight-month study, two soil samples were randomly collected each month from two hydrocarbon-polluted soil piles undergoing off-site biotreatment, resulting in a total of 18 samples analyzed. Using standard microbiological techniques, 31 mold strains were isolated on Sabouraud agar and incubated at 37˚C for 5 to 7 days. The isolates were purified and preliminarily identified based on macroscopic and microscopic morphological characteristics. Their colony diameter and radial growth rate were determined on Sabouraud culture medium supplemented with 5% (w/v) DDO. The isolates were identified as belonging to four genera: *Aspergillus* spp. (48.39%), *Penicillium* spp. (25.81%), *Fusarium* spp. (22.58%), and *Geotrichum* spp. (3.23%).

Despite a significant reduction in colony diameter (from 19.44% to 87.27%) and average radial growth rate (from 21.05% to 86.49%), all isolates showed the ability to grow, revealing adaptive and enzymatic potential favorable to petroleum hydrocarbon biodegradation. Among the isolates, ten isolates (C, E, L, R, S, X, AA, BB, CC, EE) presented less than 50% reduction in colony diameter, with isolate C showing the highest tolerance (only 19% reduction). These mold isolates are promising candidates for future bioremediation applications in hydrocarbon-contaminated environments.

Keywords

Molds, Hydrocarbons, Distillate Diesel Oil, Bioremediation, Contaminated Soil

1. Introduction

Petroleum pollution remains a major environmental concern worldwide, with hydrocarbon compounds from industrial activities, oil spills, and fuel storage contaminating soils, air, and water bodies. These pollutants pose serious risks to ecosystems and human health due to their toxicity, persistence, and low biodegradability [1] [2]. To address this challenge, various remediation strategies have been developed, including physico-chemical and biological methods (bioremediation, bioaugmentation, phytoremediation…) [3] [4]. Compared to physico-chemical remediation methods, bioremediation offers a more sustainable, cost-effective, and environmentally friendly approach by harnessing the natural metabolic capabilities of microorganisms to degrade pollutants without altering soil structure or generating toxic residues [5]-[8].

In Burkina Faso, over 80% of the national electricity supply is provided by the National Electricity Company of Burkina (SONABEL), which relies on fossil fuels such as Heavy Fuel Oil (HFO), Distillate Diesel Oil (DDO), and various industrial lubricants [2]. The combustion, handling, and accidental release of these substances lead to the emission of complex hydrocarbon mixtures that are both toxic and environmentally persistent. These pollutants, such as used oils, hydrocarbon sludge, contaminated wastewater, and greenhouse gases, pose significant threats to soil fertility, water quality, and air purity, while also endangering the health of workers and nearby communities. To mitigate these impacts, an environmental management system (EMS) has been established at SONABEL's power plants to prevent, monitor, and reduce pollution. This system involves the systematic collection, disposal, and treatment of waste to minimize its harmful impact on the environment. As part of this process, soils contaminated by hydrocarbons undergo bioremediation procedures designed to restore their ecological functionality [2] [9].

Molds play a pivotal role in the remediation of contaminated environments due to their remarkable adaptability and metabolic versatility. These fungi can thrive under extreme conditions, including elevated temperatures and low water activity, while exhibiting a strong capacity to degrade a wide range of organic compounds and pollutants. Notably, several isolated mold strains have demonstrated the ability to utilize Distillate Diesel Oil (DDO)—a light petroleum fraction commonly encountered in industrial soils—as a carbon and energy source [8] [10]-[14]. Indeed, Okrasińska *et al.* [15] reported that the presence of DDO in polluted environments influences fungal physiology, affecting growth dynamics, sporulation, and metabolic pathways, which may in turn modulate their biodegradation potential. In Burkina Faso, several investigations have explored the biodegradation potential of various microorganisms in hydrocarbon-contaminated soils and water [16]-[20]. However, specific research on molds remains limited, particularly regarding their direct responses to Distillate Diesel Oil exposure under local environmental conditions.

This study aims to evaluate the effects of Distillate Diesel Oil (DDO) on mold isolates from hydrocarbon-contaminated soils in a thermal power plant in Ouagadougou. It focuses on their growth, sporulation, tolerance, and potential morphological adaptations to better understand their role in bioremediation strategies applied to polluted sites of these power plants.

2. Materials and Methods

2.1. Study Site

The research was conducted in the thermal power plants Ouaga I and Ouaga III, operated by SONABEL (the National Electricity Company of Burkina Faso), both located in Ouagadougou, the capital city in central Burkina Faso.

The Ouaga I thermal power plant is the oldest in Ouagadougou, having been commissioned in 1954. It is located in Paspanga at an altitude of 300.53 meters (coordinates: N12˚23.031', W1˚30.927'). This plant runs on heavy fuel oil (HFO), distilled diesel fuel (DDO), lubricants, and cooling water [21].

Soil sampling at this site revealed significant hydrocarbon contamination, with concentrations ranging from 9.83 to 136.13 g/kg [9] [17] [20]. Contaminated soil samples were collected at this location and transported to the Ouaga III thermal power plant, which houses an experimental platform for the bioremediation of polluted soils.

The Ouaga III power plant is located in Kossodo, northeast of Ouagadougou (coordinates: N11˚14.906', W000˚42.230'; altitude: 254.20 meters). Treated soil samples were collected and analyzed periodically at the microbiology and microbial biotechnology laboratory of the Joseph KI-ZERBO University [9].

2.2. Soil Biotreatment

The soil collected from the Ouaga I thermal power plant and transported to Ouaga III was divided into two piles, placed on a dedicated platform, and subjected to an "off-site bioremediation" process. This treatment combined the application of mineral fertilizers, straw, and water, along with periodic soil turning, following the method described by Ouédraogo *et al.* [9].

2.3. Soil Sampling

During the biotreatment process, ten composite soil samples were taken randomly from each of the two soil heaps. The samples from each stack were mixed separately to create the analysis samples. A total of eighteen (18) bioremediation soil samples were collected [9].

2.4. Soil Microbiological Analyses

The samples taken from polluted soils in biotreatment [9] were used for microbiological analyses. Within five hours of sampling, they were subjected to isolation and preliminary identification of mold isolates. In addition, the influence of distilled diesel fuel (DDO) on mold growth was evaluated.

2.4.1. Mold Strain Isolation

The mold isolates were obtained from soils contaminated by hydrocarbons undergoing biotreatment, using Sabouraud agar in Petri dishes as a medium. Sabouraud's agar medium is a selective medium used for the isolation of filamentous fungi, limiting bacterial proliferation. Isolation was carried out by spot and serial inoculation, followed by incubation for at least 3 days at 37˚C under aerobic conditions, according to ISO 4833-1:2013 (suitable for soils). The isolates were purified by subculturing distinct colonies after 3 to 5 days of incubation under the same conditions. The selection of the colonies was based on macroscopic traits (color, texture, elevation, margin) observed visually or with a magnifying glass. The isolates were coded with alphabetical letters for identification and tracking during experiments.

2.4.2. Preliminary Identification of Molds

The preliminary identification of mold isolates was based on several criteria. These included cultural parameters (such as growth conditions and growth rate), macroscopic characteristics (including colony appearance, elevation, size, color, margin, diffusible pigment production, and the presence of exudates, observed at the surface and on the back after 24 to 96 hours of incubation), and microscopic characteristics. The microscopic observations focused on specific mold structures—such as vegetative mycelium, reproductive organs, and spores—examined in fresh preparations without staining using a 400-fold optical microscope. Reference taxonomic keys were used to obtain a preliminary classification of isolates at the genus level [22]-[28].

To facilitate the macroscopic analysis of mold isolates, the colonies were diagrammed from the center to the periphery, following the representation described by Carlile and Watkinson (1996) in The Fungi [23]: (**Figure 1**)

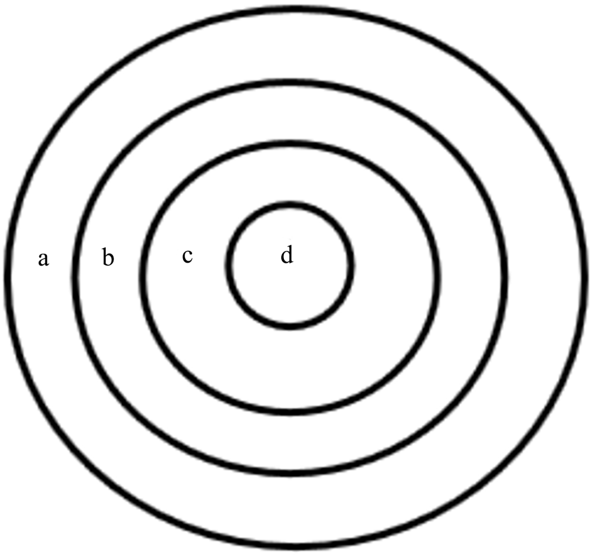

Figure 1. Diagram of a fungal colony illustrating the different differentiation zones on an agar surface, as presented by Carlile and Watkinson (1996) in "The Fungi". a: Extension zone, the part of the hypha that advances into unexplored areas of the culture medium; b: Productive zone, where the highest biomass production occurs; c: Fruiting zone, where biomass no longer increases; d: Aging zone, where hyphae are highly vacuolated or empty due to cytoplasmic mobilization toward spores or younger parts of the colony.

For this study, we designated "a" for "Z4", "b" for "Z3", "c" for "Z2", and "d" for "Z1".

2.4.3. Evaluation of DDO Effect on Mold Colony Development

The culture medium was enriched with 5% distilled diesel oil (DDO) by adding 0.75 ml to 15 ml of Sabouraud agar. The Sabouraud agar was sterilized by autoclaving at 121˚C for 15 minutes. The DDO was then sterilized separately by sterile filtration using a Millipore filter with a pore size of 0.22 µm and subsequently incorporated aseptically into the cooled medium (45˚C - 50˚C) after autoclaving. After homogenization, the mixture was poured into Petri dishes. Isolated mold strains were inoculated in the center of each dish in triplicate. The inoculated plates were incubated at 37˚C under aerobic conditions for four days. Colony growth was monitored by measuring the diameter every 24 hours over a period of 72 to 96 hours. The growth rate (V) was calculated and expressed in centimeters per hour (cm/h) using the following formula:

$$V = \frac{D_1 - D_0}{24 \text{ hours}}$$

D_1 = Final diameter, D_0 = Initial diameter

The values obtained allowed for an evaluation of the ability of the isolates to tolerate and survive in a hydrocarbon-enriched environment.

Distillate Diesel Oil (DDO)

The physical parameters of DDO used to generate electricity at the SONABEL power plant are presented in **Table 1**.

Table 1. Physical parameters of Distillate Diesel Oil (DDO).

Parameter	Valeur (10^{-3})
Density at 29.5˚C	845
Density at 15˚C	854
Average viscosity	3400

2.5. Data Analysis

The interaction between incubation time and the presence of distilled diesel oil (DDO) was assessed using linear regression models, fitted independently for each experimental condition. Colony diameter or growth rate was treated as the response variable, with time as the predictor. A comparison of the regression slopes enabled the evaluation of the combined influence of incubation time and DDO treatment on mold growth kinetics. In parallel, Multiple Correspondence Analysis (MCA) was applied to qualitative data from colony characterization to explore associations among variable categories and reduce the dimensionality of the dataset.

3. Results

3.1. Mold Isolation

During the study, 31 mold isolates were obtained based on their macroscopic characteristics. Preliminary identification of these isolates was conducted using both macroscopic and microscopic characteristics to determine the dominant genera present in the bioremediated hydrocarbon-contaminated soils.

3.2. Preliminary Identification of Mold Isolates

3.2.1. Macroscopic Characteristics

All 31 mold colonies exhibited concentric, radiating morphologies with centrifugal growth, displaying distinct zones of differentiation. After 96 h of incubation, all colonies had developed mycelium, with or without the production of a powdery substance. The location, intensity, and color of this powder varied according to differentiation zones and incubation time. Overall, 19 isolates produced powdery deposits on the colony surface.

Mycelial growth in all mold isolates was apical, with variable growth rates depending on the isolate. The morphology of the colony surface, observed from above, was heterogeneous. Eighteen isolates formed flat colonies, while the remaining isolates (C, E, F, H, I, L, O, R, T, U, Y, AA, CC) showed elevated profiles, sometimes with a depression, peak, or bulge in the center (Figure 2).

Figure 2 illustrates the distribution of isolates across six qualitative variables (Aspect, Margin, Transparency, Exudate, Streak, and Diameter) using comparative charts with confidence ellipses. This visual representation highlights the variability among mold colonies and the clustering of isolates based on distinct morphological traits.

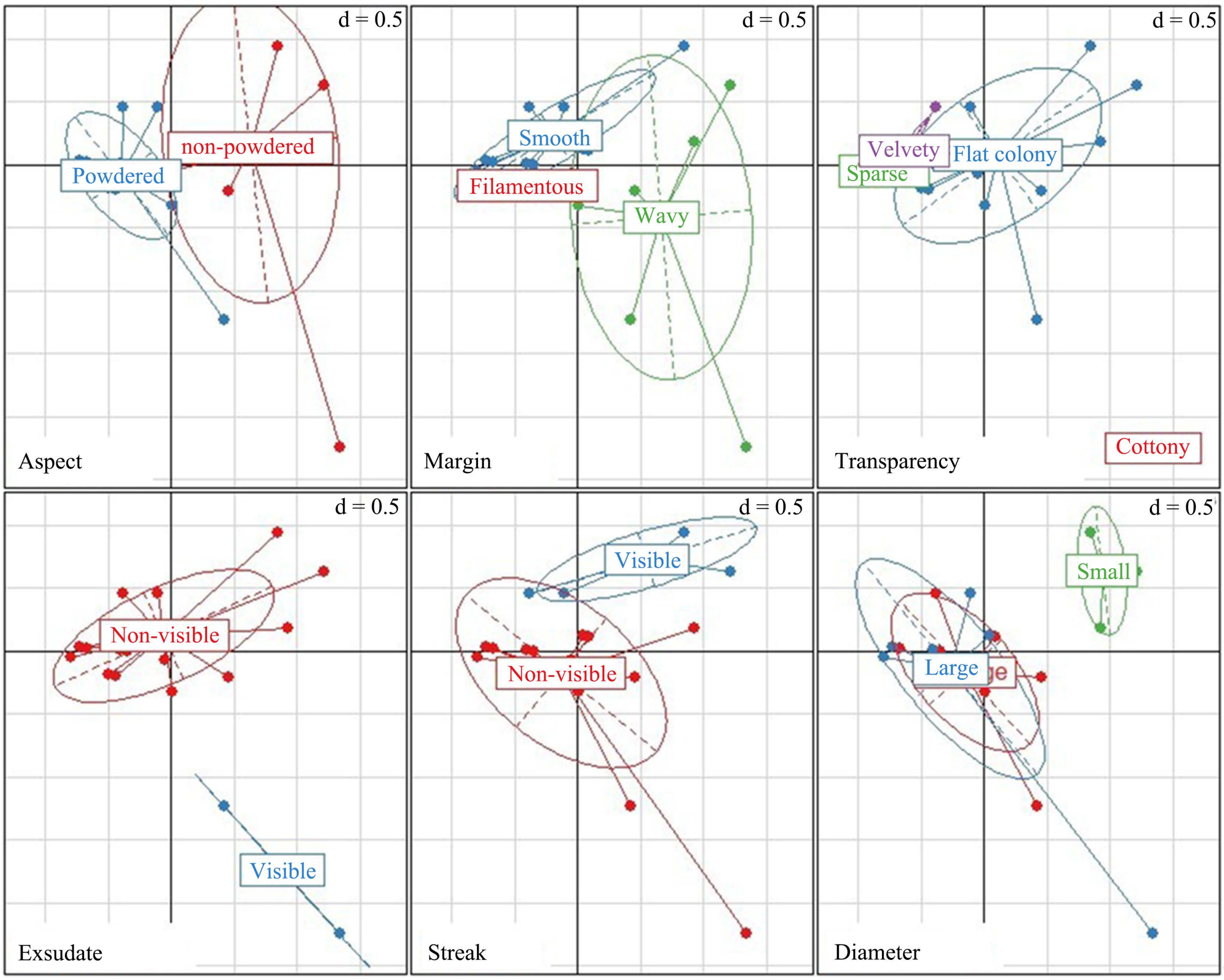

Figure 2. Projection of mold isolates along the first two principal factorial axes, based on the macroscopic characteristics of their colonies.

Indeed, based on colony aspect, two distinct groups of mold isolates were identified: powdery (A, B, D, E, I, K, M, O, Q, R, S, V, W, Y, Z, BB, CC, DD, EE) and non-powdery (C, F, G, H, J, L, N, P, T, U, X, AA). This distinction reflects differences in surface texture and sporulation patterns (Figure 2-**Aspect**).

Colony margins presented three distinct morphotypes: smooth (C, E, F, G, I, J, L, M, O, Q, R, T, W, Y, Z, BB, CC, DD), filamentous (A, B, D, K, N), and wavy (H, P, S, U, V, X, AA, EE). Smooth-edged colonies represented 55% of the isolates, while irregular margins (filamentous or wavy) accounted for 45%. This distribution was independent of colony aspect (powdery vs. non-powdery), as illustrated in Figure 2-**Margin**.

In addition, colony texture and density varied among the isolates. The majority revealed a matted appearance (81%), while a smaller proportion displayed a cottony texture (3%) or a velvety surface (16%), occasionally with or without a powdery layer. One isolate (BB) was characterized by sparse growth (Figure 2-**Transparency**). Moreover, exudate production was rare, observed in only 6% of colonies (Figure 2-**Exudate**).

Figure 2 shows that striation distribution varied according to colony differentiation zones. Colonies were classified based on the presence or absence of visible streaks. Most isolates (52%) lacked streaks on either surface, whereas 38% revealed radial striations on both the upper and underside surfaces, and 10% displayed them exclusively on the underside (Figure 2-**Streak**).

Colony diameters were classified into three levels: small, medium, and invasive. After 96 hours of incubation, the sporulation extent revealed small colonies (isolates P, L, J, T, AA, U) with diameters ranging from 1 cm to just under 3 cm; medium-sized colonies (isolates B, EE, O, Y, R, V, X, C, S, W) measuring between 3 and 5 cm; and large colonies ≥ 5 cm, which were either expansive (isolates Z, CC, DD, K, F, M, E, I, A, D, N, G) or invasive (isolates H, Q, BB). These measurements are directly related to the growth rate and invasive potential of each isolate (Figure 2-**Diameter**).

Figure 3 illustrates the diversity of pigmentation patterns among 31 mold isolates, observed 96 hours after incubation. Each sub-graph (CZ1F to CZ4F) highlights phenotypic contrasts across four differentiation zones: central (aging), fruiting, productive, and peripheral (expansion).

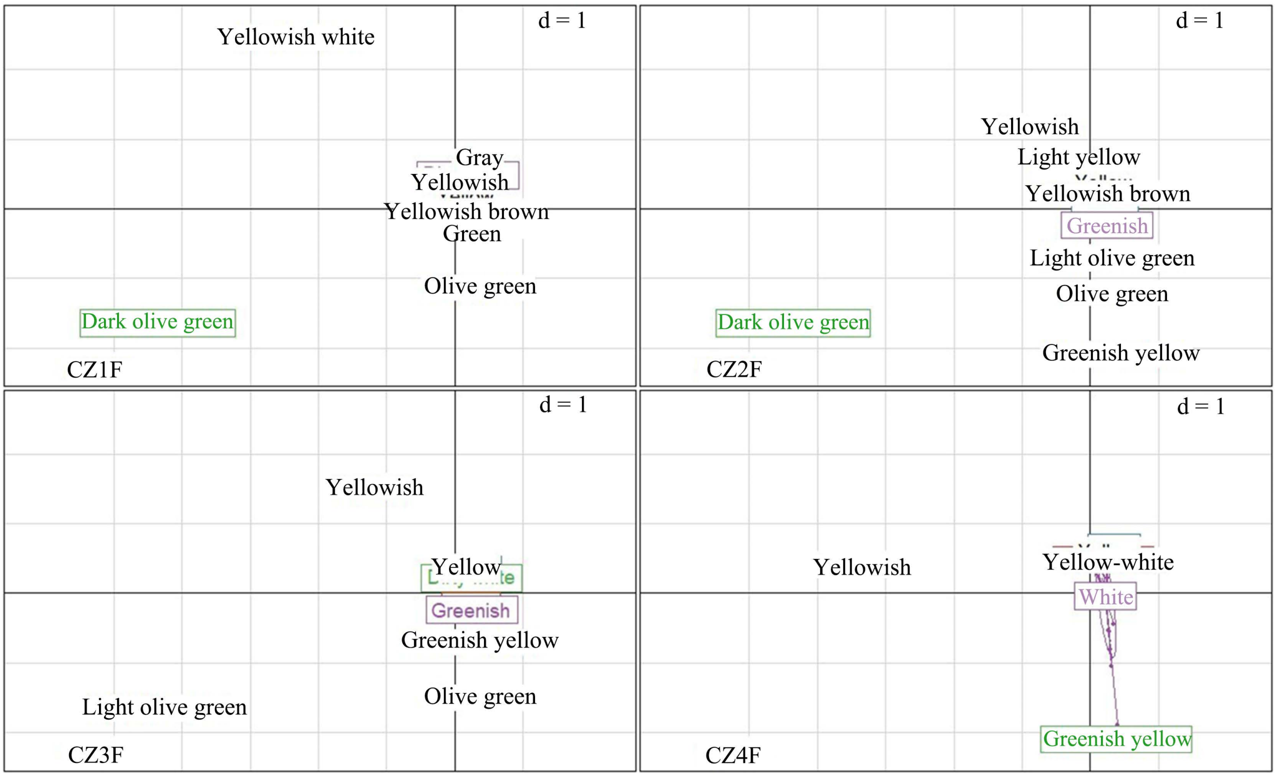

Figure 3. Phenotypic diversity of pigmentation patterns of 31 mold colonies, front view, based on differentiation zones.

Colony coloration varied according to the isolate, the observation side (surface or reverse), the differentiation zone, and the incubation time. From the upper surface, 13% of the isolates (F, H, L, N) exhibited a uniform white pigmentation across all zones. In contrast, the remaining 87% displayed at least two distinct shades, with perceptible variations between differentiation zones. Remarkably, isolates Q and EE showed striking pigmentation features: isolate Q developed an intense black coloration, while isolate EE produced a vivid yellow hue. In both cases, the dominant pigment covered approximately 90% of the Petri dish surface.

The clustering and dispersion of color descriptors reveal distinct phenotypic profiles, with certain hues consistently associated with specific zones, darker tones predominating in aging centers and lighter or greenish shades appearing more frequently in peripheral expansion zones. The observed pigments included white, off-white, yellow, yellowish, brown, green, olive green, greenish, dark brown, gray, grayish, and black (**Figure 3**).

The reverse side of the mold colonies also exhibited notable chromatic diversity. Observation from underneath revealed that in 12 colonies, a uniform coloration dominated by pigments such as white, yellow, or grayish was observed. In contrast, the remaining 19 isolates displayed more complex pigmentation patterns, characterized by at least two distinct hues depending on the differentiation zones. These variations are illustrated in **Figure 4** (CZ1V to CZ4V), where the differentiated zones are clearly visible.

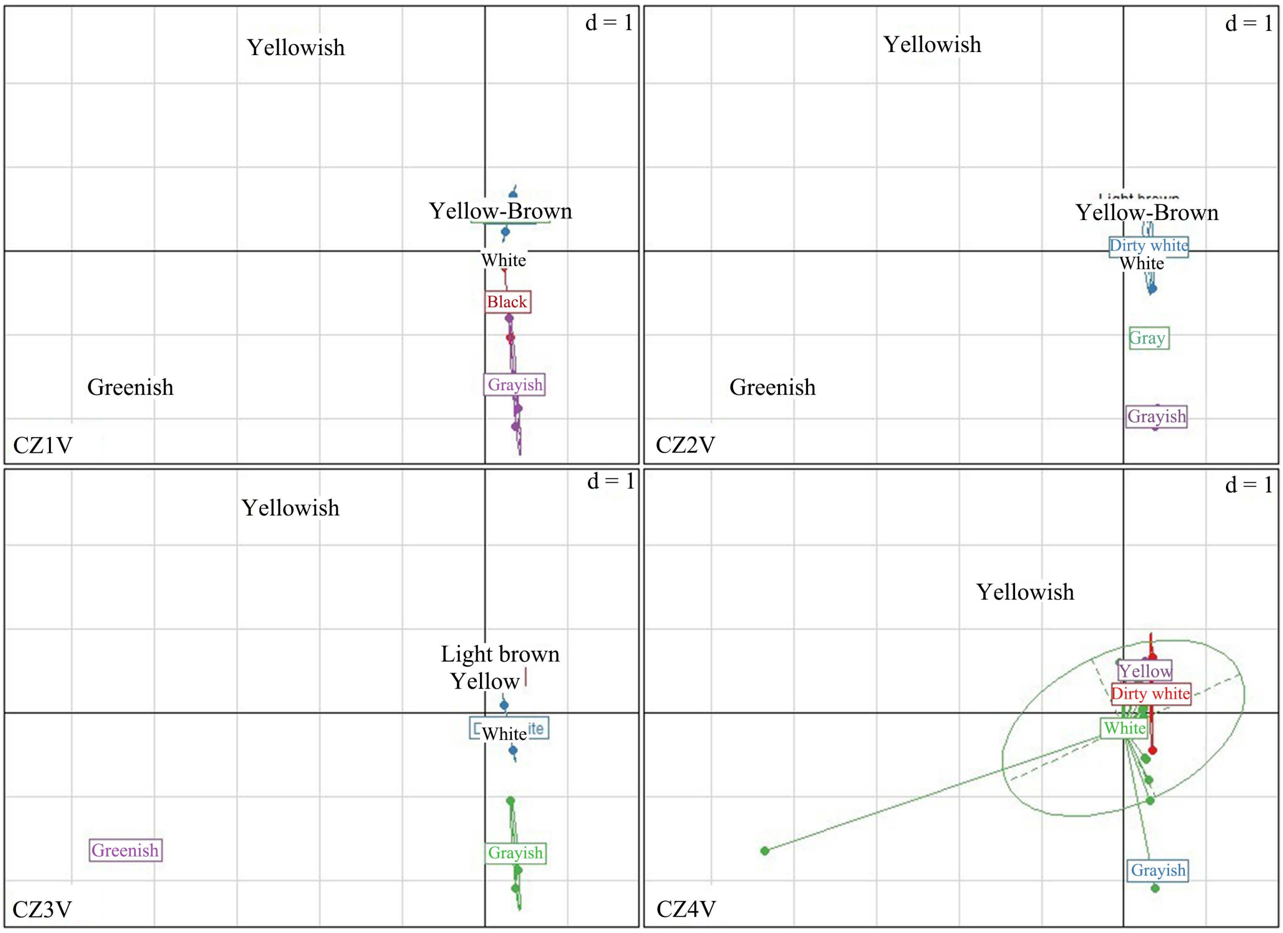

Figure 4. Phenotypic characterization of pigmentation patterns of 31 mold colonies, reverse view, based on differentiation zones.

This figure presents a comparative visualization of the chromatic profiles of the reverse view across four differentiation zones (CZ1V to CZ4V). The scatter plots display the spatial distribution of color categories—such as yellowish, greenish, black, white, grayish, yellow-brown, light brown, and dirty white—within a color space.

In CZ1V, CZ2V, and CZ3V, color trends appear widely dispersed, indicating a high degree of chromatic variability among the isolates. In CZ4V, the grouping is more pronounced, with an ellipse and directional arrows highlighting a concentrated cluster around yellow, dirty white, and white tones (**Figure 4**).

A distinctive feature was observed for mold isolate P, which secreted a diffusible pigment that modified the coloration of the surrounding agar without reducing its transparency. This isolate was the only one to induce a color change in Sabouraud agar, within a radius of approximately 0.7 cm, shifting from translucent white to translucent brown. On the reverse side, pigmentation was clearly zonal, with dark brown in CZ1V, light brown in CZ2V and CZ3V, and off-white in CZ4V.

3.2.2. Microscopic Characteristics

The assessment of the microscopic characteristics of the isolates revealed distinct vegetative and reproductive structures. All mold isolates displayed either conidia or sporangia, associated with a vegetative network of hyphae forming the mycelium (**Figure 5(a)**).

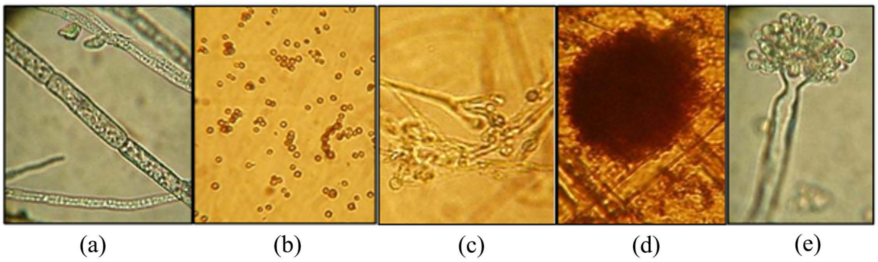

Figure 5. Spores (b), mold hyphae (a), a conidiophore ending in brush-like structures (c), and conidiophores ending in vesicles (d), (e), observed under a light microscope at 400× magnification.

Among them, 23 isolates exhibited septate hyphae. Within this group, conidiophores either terminated in a vesicle bearing conidia (A, B, E, I, M, O, Q, R, W, Y, Z, BB, EE, CC, DD) or branched into brush-like structures forming visible chains of conidia (C, D, J, K, L, S, T, V) (**Figures 5(c)-(e)**).

Additionally, seven isolates (G, F, N, P, U, X, AA) produced fusiform macroconidia or kidney-shaped microconidia, while a single isolate (H) revealed rectangular arthroconidia (irregular tubular elements, arthrospores) formed by hyphal fragmentation.

All macroscopic and microscopic characteristics of the mold isolates, summarized in **Figures 6-9** of the supplementary material, were used for preliminary taxonomic affiliation. Based on these criteria, 48% of the isolates were affiliated with the *Aspergillus* spp. (A, B, E, I, M, O, Q, R, W, Y, Z, BB, EE, CC, DD), 26% with

Penicillium spp. (C, D, J, K, L, S, T, V), 23% with *Fusarium* spp. (G, F, N, P, U, X, AA), and 3% with *Geotrichum* spp. (H). The *Aspergillus* and *Penicillium* genera were distinguished by the morphology of the conidiophore head—vesicular in *Aspergillus* and brush-like in *Penicillium*.

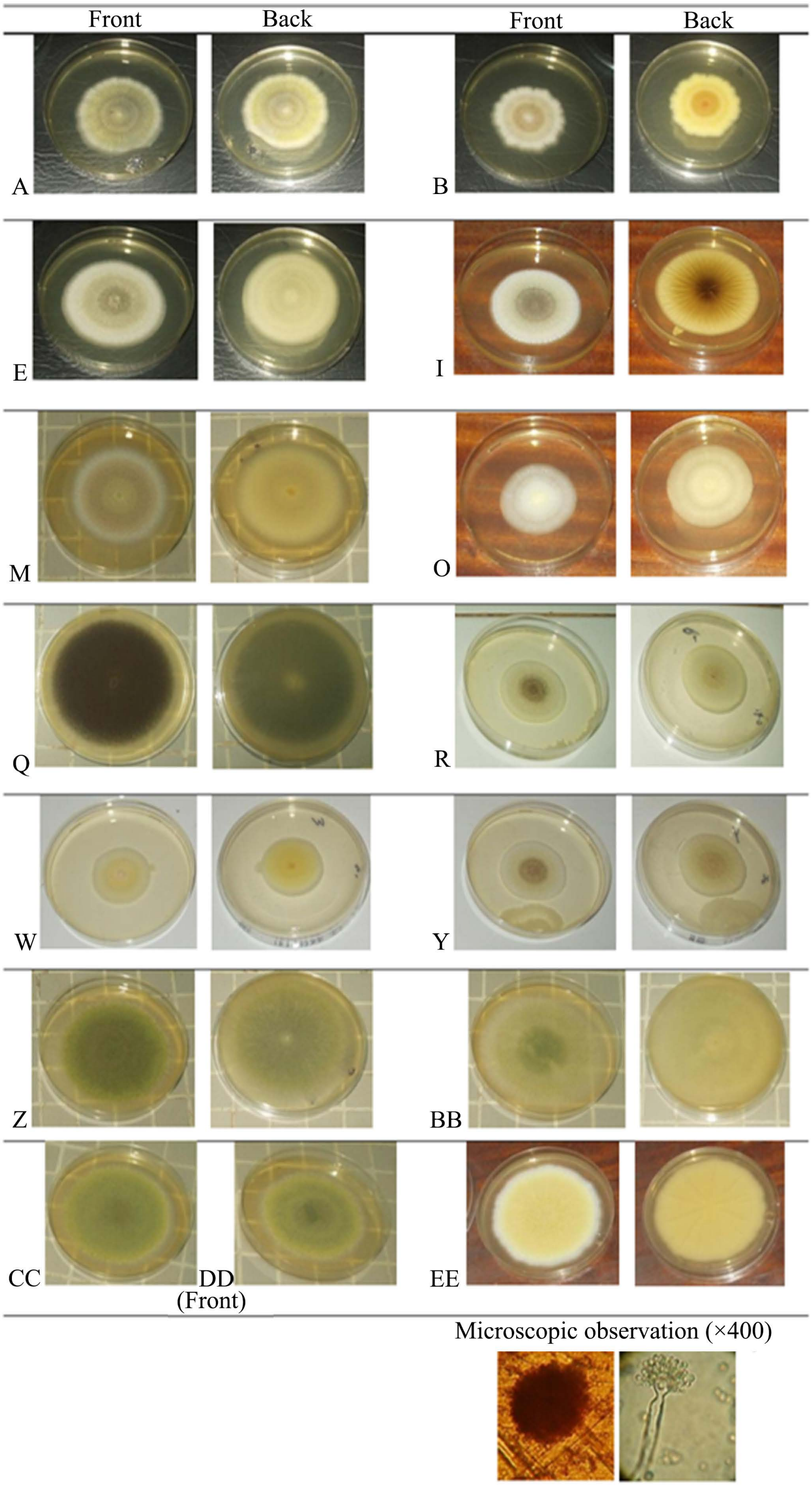

Figure 6. Macroscopic and microscopic characteristics of *Apergillus* spp.

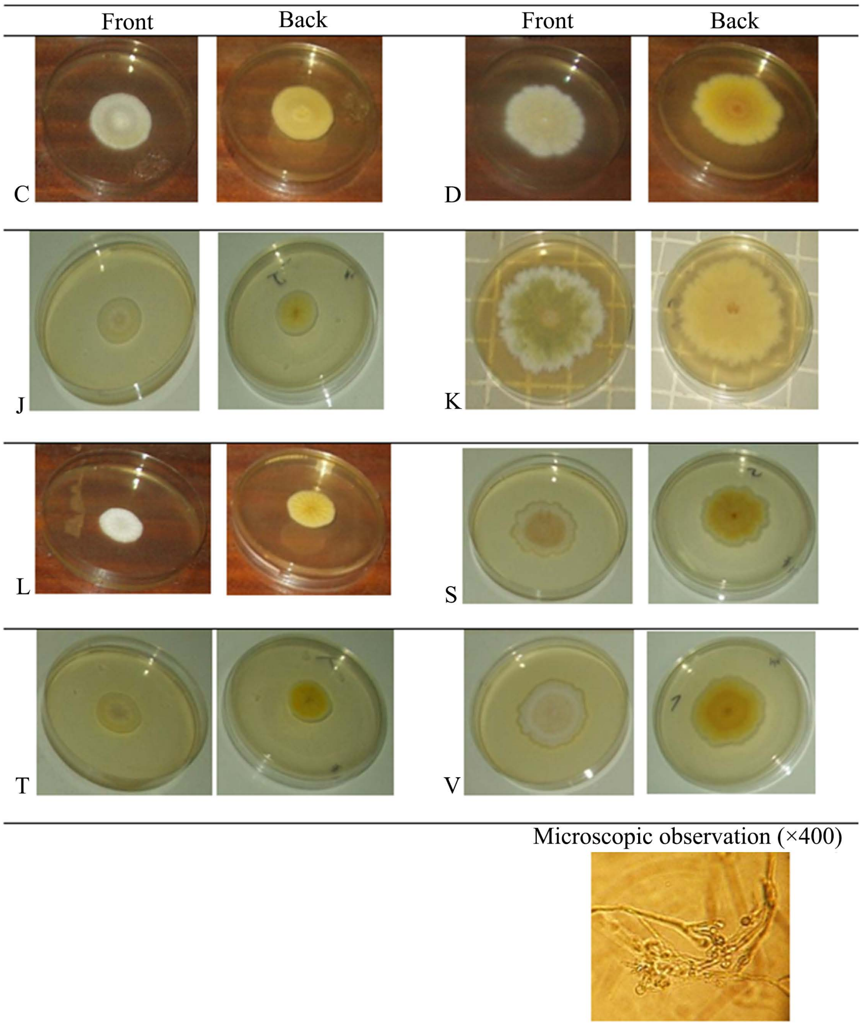

Figure 7. Macroscopic and microscopic characteristics of *Penicillium* spp.

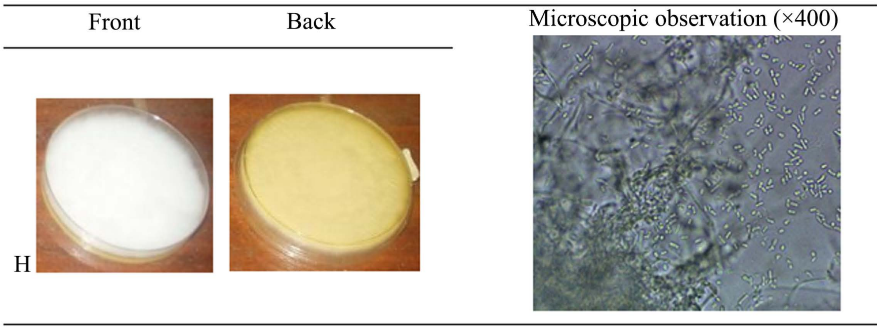

Figure 8. Macroscopic and microscopic characteristics of *Geotrichum* spp.

3.3. Effect of DDO on Mold Isolate Diameter

The colonies exhibited macroscopic characteristics (color and diameter) that varied depending on the isolate, incubation time, and enrichment of the medium with 5% DDO. All mold colonies showed a reduction in their diameter by at least 1.2-fold in the presence of DDO (**Figure 10**).

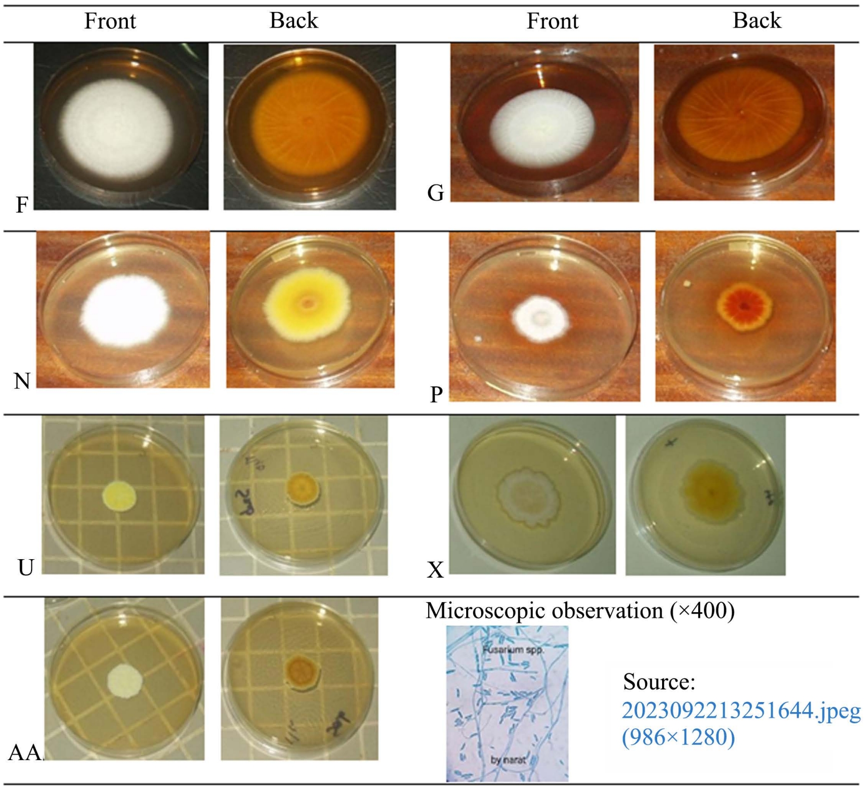

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Figure 9. Macroscopic and microscopic characteristics of *Fusarium* spp.

The isolates were grouped into three main growth patterns on the culture medium. Firstly, 78% of the isolates (A, B, C, D, G, I, J, K, L, M, N, O, P, Q, R, S, T, U, V, W, X, Y, AA, EE) produced small colonies (<3 cm) on DDO-enriched Sabouraud, compared to only 19% (P, L, J, T, AA, U) on the control medium. Secondly, 19% of the isolates (E, F, Z, BB, CC, DD) developed colonies of medium size (3 - 5 cm), while 32% (B, EE, O, Y, R, V, X, C, S, W) reached this size on the control medium. Finally, 3% of the isolates, composed of H mold only, formed large colonies (>5 cm) with a diameter of 6.5 cm, while 49% of the isolates (A, D, E, F, G, H, I, K, M, N, Q, Z, BB, CC, DD) reached or exceeded this size on the control medium (Figure 10).

In terms of growth inhibition, isolates K and Q showed the greatest sensitivity in the presence of 5% DDO, with reductions in colony diameter of 77% and 87%, respectively. Nineteen isolates revealed a reduction of about 50%, while ten isolates (C, E, L, R, S, X, AA, BB, CC, EE) were less affected, with a reduction below 50%. Isolate C demonstrated the highest tolerance, with only 19% inhibition (Figure 10).

Growth dynamics also differed in the absence of DDO. Isolates Q and H were highly invasive, filling the Petri dish in less than 96 h: Q reached 8 cm within 72 h and fully occupied the dish at 96 h, while H reached 8 cm within 48 h and completely covered the dish by 72 h. Conversely, isolate U consistently exhibited the smallest colony diameters under all conditions, whereas isolate H remained the most invasive (Figure 10).

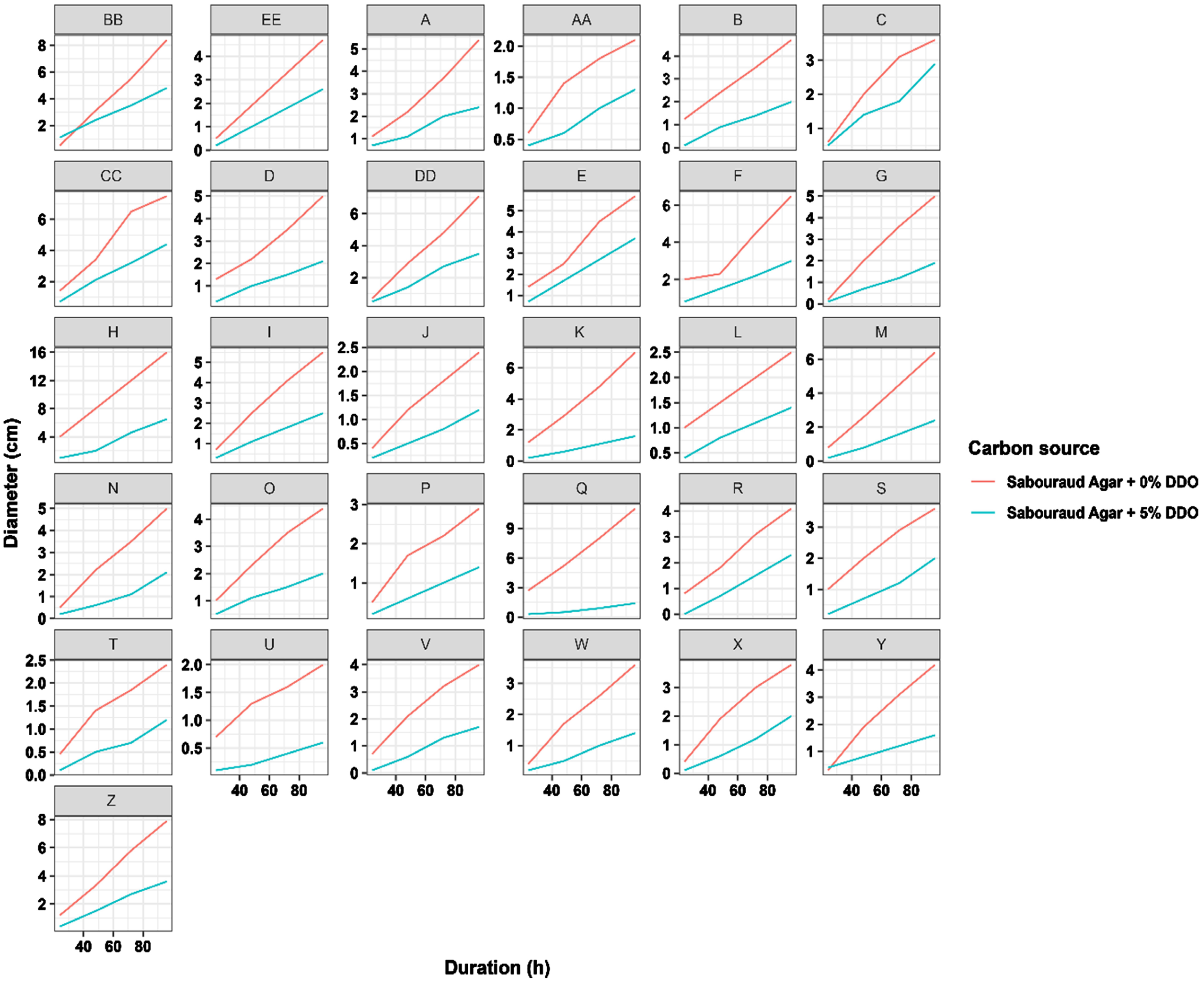

Figure 10. Changes in colony diameter over time during incubation on Sabouraud agar, with and without the addition of Distillate Diesel Oil (DDO).

Overall, the addition of 5% DDO inhibited the growth of all isolates to varying degrees, but none were completely suppressed, indicating survival and metabolic tolerance under hydrocarbon stress.

3.4. Effect of DDO on Mold Isolates' Growth Kinetics

Analysis of the growth kinetics revealed a difference in colony growth rates depending on the presence or absence of DDO in the media (Figure 11).

In the absence of DDO, the growth rate (cm/h) increased progressively over time. Some isolates, such as C, N, Y, W, and EE, exhibited faster growth than others (Figure 11). Under these conditions, 68% of the isolates showed a consistent increase in growth rate every 24 hours, while 22% (isolates B, D, E, F, L, Q, U) displayed a decrease, and 10% (isolates A, H, S) maintained a constant rate. After 48 hours of incubation, the growth rates varied depending on the isolate and the incubation duration.

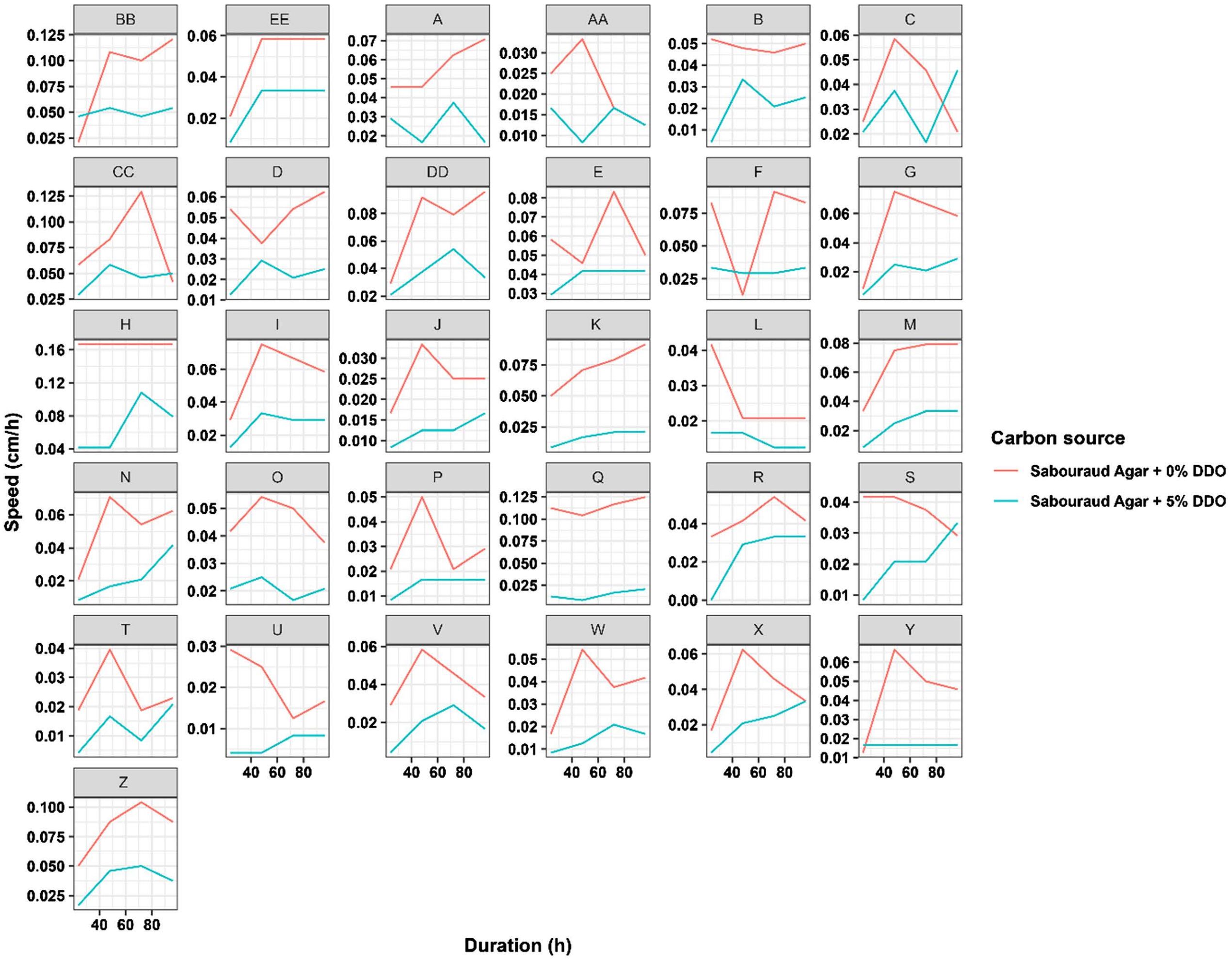

Figure 11. Mold growth kinetics according to period and media used.

During the study, the mold isolates showed average growth rates ranging from 0.021 to 0.088 cm/h, except for the isolates H and Q, which were invasive. Indeed, the isolates H and Q exhibited higher rates of growth, with averages of 0.167 cm/h and 0.111 cm/h, respectively.

It was further observed that the average colony growth rate decreased by more than 1.3-fold when the growth medium was supplemented with DDO. In this condition, the growth rates ranged from 0.006 to 0.068 cm/h, compared to 0.021 to 0.167 cm/h on the standard medium. Indeed, the lowest rate of growth was recorded for isolate U, whereas the highest was observed for isolate H.

4. Discussion

4.1. Mold Isolation

During the study, 31 mold isolates were obtained based on macroscopic characteristics. This preliminary screening provides a crucial foundation for identifying fungal isolates with potential applications in hydrocarbon degradation. Although only macroscopic identification was conducted at this stage, each isolate may represent a unique biological entity capable of contributing to hydrocarbon biodegradation in polluted soils. Such diversity holds promising implications for selecting effective mold isolates for bioremediation and ecosystem restoration [8] [13] [29]-[33].

The diversity observed among these isolates highlights the richness and adaptability of the fungal microbiota in petroleum-contaminated environments undergoing bioremediation. Previous studies have shown that microbial diversity during bioremediation is influenced by factors such as the nature of the initial substrate, prevailing environmental conditions, and the availability of organic compounds that favor the selective proliferation of specific fungal taxa [15] [25] [34]-[36].

These isolates may contribute significantly to the degradation of persistent organic pollutants, particularly polycyclic aromatic hydrocarbons (PAHs), which are commonly found in petroleum-contaminated environments [10] [37]-[39]. Thus, further research should be performed to evaluate the ability of these mold isolates to degrade a wide range of petroleum substrates.

4.2. Preliminary Identification of Molds

The results obtained allowed for an initial classification of the isolates according to their morphological and structural characteristics [25] [34]-[36].

4.2.1. Macroscopic Identification

Macroscopic characteristics of the mold isolates revealed a large phenotypic diversity among the mold strains isolated. Colonies exhibited concentric or radiating morphologies with centrifugal development, typical of filamentous fungi.

Color variations across colony zones (center, fruiting, expansion) reflected metabolic dynamics and intra-strain heterogeneity [40]. In addition, the pigmentation on the reverse side of the Petri dish highlighted differences in growth and metabolic activity, potentially linked to asymmetric pigment production or distinct structural organization within the mycelium [25]. During the study, an isolate (P) produced a diffusible pigment. This characteristic is linked to the enzymatic activity of this isolate, illustrating the biodegradability of the substrate by the isolate [41].

These macroscopic data have allowed the classification of the mold isolates into the genera *Aspergillus*, *Penicillium*, *Fusarium*, and *Geotrichum*. Many studies have shown that mold isolates belonging to those genera are frequently encountered in contaminated soils [22] [23] [25]-[27] [34]-[36].

4.2.2. Microscopic Identification

Microscopic examination of the 31 mold isolates revealed a wide range of morphological traits, underscoring the ecological adaptability and taxonomic diversity of molds inhabiting hydrocarbon-polluted soils. The presence of septate hyphae, non-septate hyphae, and reproductive structures (such as conidiophores terminating in vesicles or brush-like formations) corresponds to classical descriptions of filamentous fungi typically involved in biodegradation processes [24].

A clear morphological distinction between *Aspergillus* and *Penicillium* was observed based on conidiophore head type: vesicular in *Aspergillus* and brush-like in *Penicillium*, serving as a reliable preliminary taxonomic marker [42]. The predominance of *Aspergillus* spp. (48%) and *Penicillium* spp. (26%) reflects their ubiquity in organic-rich environments and their well-documented resilience and metabolic versatility in contaminated ecosystems. Both genera are known to produce extracellular enzymes that catalyze the breakdown of complex hydrocarbon compounds [10] [12] [25] [37]-[39].

The detection of *Fusarium* spp. (23%) and *Geotrichum* spp. (3%) further broadens the functional spectrum of the mold community. *Fusarium* species are frequently associated with petroleum hydrocarbon degradation [31] [33], while *Geotrichum*, characterized by rapid growth and a cottony appearance, is recognized for its capacity to enhance substrate colonization and biomass production [13].

All mold isolates presented invasive mycelial growth, which increases the volume of soil explored and the surface area in contact with pollutants, thereby facilitating hydrocarbon degradation [13] [43]. The identified genera are recognized for their enzymatic capacities to degrade hydrocarbons, a finding consistent with previous studies. Lotfinasabasl *et al.* [38] reported degradation efficiency in hydrocarbon-contaminated soil ranked as follows: *Aspergillus niger* > *Rhizopus* sp. > *Aspergillus terreus* > *Penicillium* sp. Likewise, *Aspergillus niger* isolated from petroleum-polluted soils demonstrated strong degradation potential [31] [44]. Additional studies further confirmed the biodegradation capacity of *Penicillium*, *Geotrichum*, *Fusarium*, and *Cladosporium* [13] [37] [43] [45].

4.3. Effect of DDO on Mold Isolate Growth Parameters

Analysis of the growth parameters demonstrated that DDO reduced mold growth in all isolates, with inhibition rates varying across isolates. Nevertheless, the ability of the isolates to grow on DDO-enriched medium confirmed their tolerance to hydrocarbons and indicated an enzymatic potential for the degradation of persistent petroleum-derived compounds, supporting their biotechnological relevance for hydrocarbon bioremediation [40].

Growth dynamics fluctuated over time, likely influenced by the metabolic state of the isolates, the nutrient composition of the medium, and competition for resources. Similar patterns were reported by Lotfinasabasl *et al.* [38] who observed that *Aspergillus niger* may grow rapidly during the first 2 - 3 days, followed by a slowdown as colonies expand and nutrient availability declines.

Among the 31 isolates, ten (C, E, AA, BB, CC, R, L, S, EE, and X) revealed the highest tolerance to DDO, making them promising candidates for the bioremediation of soils contaminated with hydrocarbons. Moreover, all isolates maintained apical mycelial growth in the presence of DDO, confirming the persistence of vegetative activity and their ability to proliferate. This observation also indicates that hydrocarbons, at certain concentrations, do not fully inhibit the reproductive processes of these molds [40].

In addition, some mold isolates could produce pigments, develop dense mycelia, or sporulate abundantly. These isolates could play critical roles in hydrocarbon degradation and soil restoration processes [10] [15] [30] [37] [41].

The process of hydrocarbon degradation is a synergistic process involving other soil microorganisms such as bacteria, yeast [9] [11] [20] [45] as demonstrated in large-scale biotreatments, leading to a decrease in hydrocarbon concentration in the soil of up to 67.92% after eight months of biotreatment [9].

5. Conclusions

This study isolated and characterized 31 mold isolates from soils contaminated by hydrocarbons and demonstrated their ability to grow on media enriched with Distilled Diesel (DDO). The results showed that the isolates could tolerate 5% hydrocarbons, although their growth was partially inhibited. Despite this inhibition, all isolates maintained vegetative activity, indicating metabolic tolerance and potential for hydrocarbon biodegradation.

The isolates were identified as belonging mainly to the genera *Aspergillus*, *Penicillium*, *Fusarium*, and *Geotrichum.* These taxa appear particularly promising, combining notable growth capacity with morphological diversity, thus illustrating their suitability for biotechnological applications in soil bioremediation. It should be emphasized, however, that this identification is preliminary and based on morphological traits, and definitive confirmation will require molecular characterization.

Overall, the results provide a basis for the targeted use of indigenous mold in large-scale soil decontamination programs in Burkina Faso. Nevertheless, further studies are needed to assess their ability to degrade a broader range of hydrocarbons, to achieve molecular-level identification, and to conduct field trials using these isolates as inoculants. Such studies would help elucidate the enzyme pathways involved and identify the most effective isolates for large-scale application.

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Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

References

[1] Emenike, E.C., Adeleke, J., Iwuozor, K.O., Ogunniyi, S., Adeyanju, C.A., Amusa, V.T., *et al.* (2022) Adsorption of Crude Oil from Aqueous Solution: A Review. *Journal of Water Process Engineering*, **50**, Article 103330. https://doi.org/10.1016/j.jwpe.2022.103330

[2] Zongo, S.A., Ouédraogo, J.P. and Zongo, P. (2025) Assessment of Greenhouse Gas

Emissions from the Kossodo Thermal Power Plant Using the Carbon Balance Method: Financial Year 2022. *Smart Grid and Renewable Energy*, **16**, 13-33. https://doi.org/10.4236/sgre.2025.161002

[3] Das, N. and Chandran, P. (2011) Microbial Degradation of Petroleum Hydrocarbon Contaminants: An Overview. *Biotechnology Research International*, **2011**, 1-13. https://doi.org/10.4061/2011/941810

[4] Varjani, S.J. (2017) Microbial Degradation of Petroleum Hydrocarbons. *Bioresource Technology*, **223**, 277-286. https://doi.org/10.1016/j.biortech.2016.10.037

[5] Atuanyan, E. and Tudararo Aherobo, L. (2015) Ecotoxicological Effects of Discharge of Nigerian Petroleum Refinery Oily Sludge on Biological Sentinels. *African Journal of Environmental Science and Technology*, **9**, 95-103. https://doi.org/10.5897/ajest2014.1717

[6] Nwadibe, E.C., Jude, O.U. and Kenneth, O.C. (2019) Effects of Lead and Mercury on Crude Oil Utilization by *Pseudomonas aeruginosa. Applied Research Journal of Biotechnology*, **2**, 1-9.

[7] Hassand, M.H., Omirbekova, A., Baseer, A.Q., Monib, A.W., Sediqi, S. and Niazi, P. (2024) Petroleum Hydrocarbons Biodegradation Uncovering the Variety and Capabilities of Oil-Oxidizing Microbes. *European Journal of Theoretical and Applied Sciences*, **2**, 319-333. https://doi.org/10.59324/ejtas.2024.2(2).28

[8] Nunes Serralha, M.F. and De Sousa Coelho, A.C. (2024) Eco-Insights on Hydrocarbon Bioremediation. *Progress in Petrochemical Science*, **6**, 644-650.

[9] Ouédraogo, W.P., Otoidobiga, C.H., Tidiane, C.A., Ouattara, A.S. and Traoré, A.S. (2020) Pilot Bioremediation of Contaminated Soils by Hydrocarbons, from an Electricity Production and Distribution Site in Ouagadougou, Burkina Faso. *Scientific Research and Essays*, **15**, 69-77.

[10] Vanishree, M., Thatheyus, A.J. and Ramya, D. (2014) Biodegradation of Petrol Using the Fungus *Penicillium sp*. *Science International*, **2**, 26-31. https://doi.org/10.17311/sciintl.2014.26.31

[11] Orji, F.A., Ibiene, A.A. and Okerentugba, P.O. (2013) Bioremediation of Petroleum Hydrocarbon-Polluted Mangrove Swamps Using Nutrient Formula Produced from Water Hyacint (*Eicchornia crassipes*). *American Journal of Environmental Sciences*, **9**, 348-366.

[12] Vandermeer, K.D. and Daugulis, A.J. (2007) Enhanced Degradation of a Mixture of Polycyclic Aromatic Hydrocarbons by a Defined Microbial Consortium in a Two-Phase Partitioning Bioreactor. *Biodegradation*, **18**, 211-221. https://doi.org/10.1007/s10532-006-9056-8

[13] Rafin, C., Veignie, E., Woisel, P. and Cazier, F. (2004) Intérêt des champignons telluriques dans des processus de bioremédiation de sols pollués par des hydrocarbures aromatiques polycycliques. *Environnement, Ingénierie & Développement*, **33**, 1-5. https://doi.org/10.4267/dechets-sciences-techniques.2055

[14] Feitkenhauer, H., Müller, R. and Märkl, H. (2003) Degradation of Polycyclic Aromatic Hydrocarbons and Long Chain Alkanes at 60-70˚C by *Thermus* and *Bacillus spp*. *Biodegradation*, **14**, 367-372.

[15] Okrasińska, A., Decewicz, P., Majchrowska, M., Dziewit, L., Muszewska, A., Dolatabadi, S., *et al.* (2022) Marginal Lands and Fungi—Linking the Type of Soil Contamination with Fungal Community Composition. *Environmental Microbiology*, **24**, 3809-3825. https://doi.org/10.1111/1462-2920.16007

[16] Sawadogo, A., Cissé, H., Otoidobiga, H.C., Odetokun, I.A., Zongo, C., Dianou, D., *et*

al. (2024) Characterization of Two Bacterial Strains Isolated from Wastewater and Exhibiting *In- Vitro* Degradation of Diesel and Used Oils. *Scientific African*, **25**, e02289. https://doi.org/10.1016/j.sciaf.2024.e02289

[17] Kaboré-Ouédraogo, W.P., Ouattara, C.A.T., Savadogo, W.P., Ouattara, A.S. and Traoré, A.S. (2018) Impact of Pollution by the Hydrocarbons on the Biological Activity of Soils in Ouagadougou, Burkina Faso. *Journal of Soil Science and Environmental Management*, **9**, 180-188.

[18] Sawadogo, A., Otoidobiga, H.C., Nitiema, L.W., Traoré, A.S. and Dianou, D. (2016) Optimization of Hydrocarbons Biodegradation by Bacterial Strains Isolated from Wastewaters in Ouagadougou, Burkina Faso: Case Study of SAE 40/50 Used Oils and Diesel. *Journal of Agricultural Chemistry and Environment*, **5**, 1-11. https://doi.org/10.4236/jacen.2016.51001

[19] Sawadogo, A., Harmonie, O.C., Sawadogo, J.B., Kaboré, A., Traoré, A.S. and Dianou, D. (2014) Isolation and Characterization of Hydrocarbon-Degrading Bacteria from Wastewaters in Ouagadougou, Burkina Faso. *Journal of Environmental Protection*, **5**, 1183-1196. https://doi.org/10.4236/jep.2014.512115

[20] Kaboré-Ouédraogo, P.W., Savadogo, P.W., Ouattara, C.A.T., Savadogo, A. and Traoré, A.S. (2010) Etude de la Bio-dépollution de Sols contaminés par les Hydrocarbures au Burkina Faso. *Journal de la Société Ouest-Africaine de Chimie*, **30**, 19-28.

[21] SONABEL (2023) Rapport d'activités 2023. https://www.sonabel.bf/nos-rapports/

[22] Botton, B., Breton, A., Févre, M., Gauthier, S., *et al.* (1990) Moisissures utiles et nuisibles: Importance industrielle. 2nd Edition, Masson.

[23] Samson, R.A. (2000) Introduction to Food- and Airborne Fungi. Centraalbureau voor Schimmelcultures, Utrecht.

[24] Carlile, M.J., Watkinson, S.C. and Gooday, G.W. (2001) The Fungi. Gulf Professional Publishing.

[25] Diba, K., Kordbacheh, P., Mirhendi, S., Rezaie, S. and Mahmoudi, M. (2007) Identification of *Aspergillus* Species Using Morphological Characteristics. *Pakistan Journal of Medical Sciences*, **23**, 867-872.

[26] Samson, R.A., Noonim, P., Meijer, M., Houbraken, J., Frisvad, J.C. and Varga, J. (2007) Diagnostic Tools to Identify Black Aspergilli. *Studies in Mycology*, **59**, 129-145. https://doi.org/10.3114/sim.2007.59.13

[27] Samson, R.A., Hong, S., Peterson, S.W., Frisvad, J.C. and Varga, J. (2007) Polyphasic Taxonomy of Aspergillus Section Fumigati and Its Teleomorph Neosartorya. *Studies in Mycology*, **59**, 147-203. https://doi.org/10.3114/sim.2007.59.14

[28] Campbell, C.K., Johnson, E.M., and Warnock, D.W. (2013) Identification of Pathogenic Fungi. 2nd Edition, Wiley-Blackwell.

[29] Gadd, G.M. (2001) Fungi in Bioremediation. Cambridge University Press.

[30] Adenipekun, C.O. and Fasidi, I.O. (2005) Bioremediation of Oil-Polluted Soil by *Lentinus subnudus*, a Nigerian White-Rot Fungus. *African Journal of Biotechnology*, **4**, 796-798.

[31] Burghal, A.A., Abu-Mejdad, N.M.J.A. and Al-Tamimi, W.H. (2016) Mycodegradation of Crude Oil by Fungal Species Isolated from Petroleum Contaminated Soil. *International Journal of Innovative Research in Science, Engineering and Technology*, **5**, 1517-1524.

[32] Clarkson, M.A. and Abubakar, S.I. (2015) Bioremediation and Biodegradation of Hydrocarbon Contaminated Soils: A Review. *IOSR Journal of Environmental Science*,

Toxicology and Food Technology, **9**, 38-45.

[33] Al-Dhabaan, F.A. (2021) Mycoremediation of Crude Oil Contaminated Soil by Specific Fungi Isolated from Dhahran in Saudi Arabia. *Saudi Journal of Biological Sciences*, **28**, 73-77. https://doi.org/10.1016/j.sjbs.2020.08.033

[34] Zain, M.E., Razak, A.A., El-Sheikh, H.H., Soliman, H.G. and Khalil, A.M. (2009) Influence of Growth Medium on Diagnostic Characters of *Aspergillus* and *Penicillium* Species. *African Journal of Microbiology Research*, **3**, 280-286.

[35] Sharma, G. and Pandey, R.R. (2010) Influence of Culture Media on Growth, Colony Character and Sporulation of Fungi Isolated from Decaying Vegetable Wastes. *Journal of Yeast and Fungal Research*, **1**, 157-164.

[36] Devi, K.S., Misra, D.K., Saha, J., Devi, P.S. and Sinha, B. (2018) Screening of Suitable Culture Media for Growth, Cultural and Morphological Characters of Pycnidia Forming Fungi. *International Journal of Current Microbiology and Applied Sciences*, **7**, 4207-4214. https://doi.org/10.20546/ijcmas.2018.708.440

[37] Pérez-Armendáriz, B., Martínez-Carrera, D., Calixto-Mosqueda, M., Alba, J. and Rodríguez-Vázquez, R. (2010) Filamentous Fungi Remove Weathered Hydrocarbons from Polluted Soil of Tropical México. *Revista Internacional de Contaminación Ambiental*, **26**, 193-199.

[38] Lotfinasabasl, S., Gunale, V.R. and Rajurkar, N.S. (2012) Assessment of Petroleum Hydrocarbon Degradation from Soil and Tarball by Fungi. *Bioscience Discovery*, **3**, 186-192.

[39] Al-Saeedi, S.S., Mandeel, T.A.J. and Al-Ani, B.M. (2014) Biodegradation of Gasoil by Fungal Isolates from Petroleum Contaminated Soils. *Journal of Environment and Earth Science*, **4**, 1-8.

[40] Deshmukh, R., Khardenavis, A.A. and Purohit, H.J. (2016) Diverse Metabolic Capacities of Fungi for Bioremediation. *Indian Journal of Microbiology*, **56**, 247-264. https://doi.org/10.1007/s12088-016-0584-6

[41] Bagy, M., Nafady, N., Hassan, E. and Reyad, M. (2023) Isolation and Characterization of Pigment Producing Fungi. *Assiut University Journal of Multidisciplinary Scientific Research*, **52**, 152-176. https://doi.org/10.21608/aunj.2022.176419.1040

[42] Harris, S.D. (2012) Evolution of Modular Conidiophore Development in the Aspergilli. *Annals of the New York Academy of Sciences*, **1273**, 1-6. https://doi.org/10.1111/j.1749-6632.2012.06760.x

[43] Solanki, P., Kumar, A. and Laura, J.S. (2014) Isolation and Assessment of Biodegradation Potential of Fungal Species Isolated from Sludge Contaminated Soil. *International Journal of Current Microbiology and Applied Sciences*, **3**, 197-204.

[44] Damisa, D., Oyegoke, T.S., Ijah, U.J.J., Adabara, N.U., Bala, J.D. and Abdulsalam, R. (2013) Biodegradation of Petroleum by Fungi Isolated from Unpolluted Tropical. *International Journal of Applied Biology and Pharmaceutical Technology*, **4**, 285-292.

[45] Okerentugba, P.O. and Ezeronye, O.U. (2003) Petroleum Degrading Potentials of Single and Mixed Microbial Cultures Isolated from Rivers and Refinery Effluent in Nigeria. *African Journal of Biotechnology*, **2**, 288-292.