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Effectiveness of pesticides and their derivatives on soil fungal Biota and role of these fungi in bioremediation of pesticides residues

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ABSTRACT

Pesticides that are used to control mold, grass, and pests on agricultural land are highly toxic pesticides. *In vitro* Study of biodegradation was performed to monitor the biodegradability of fungicides, herbicides, and pesticides using native taxa of Egyptian fungi isolated from sandy loam agricultural soils. Supplemented with Esfenvalerate, Tribenuro-methyl, and Actamiprid 20% SP 3 times and irrigated for 45 days. The effectiveness of organophosphate pesticides was evaluated on soil fungal populations. The results showed a clear difference in the number of fungi between no treatment (control) and pesticide treatment. When treating the soil; fungicides, herbicides, and pesticides; Fungicides revealed 19334 colonies, herbicides 19130, and pesticides 40572 total colonies. Control soil (untreated) showed a total of 16666 colonies.

Three types of fungi (*Fusarium oxysporum*, *Aspergillus terreus*, and *Penicillium chrysogenum*) isolated from soil treated with various pesticides were selected to evaluate their ability to degrade tested pesticides in laboratory conditions. Data show that (*Aspergillus terreus*) and (*Fusarium oxysporum*.) accelerated the decomposition rate of all pesticides mentioned in this study and had the greatest effect by comparing with *Penicillium chrysogenum*. Present study, help to develop suitable environmental strategy to remove pesticides from polluted environments.

Keywords:

Mycoremediation, Pesticides, Soil-borne fungi, Organophosphorus, Mycotaxa.

1. INTRODUCTION

Pesticides play an important role in the success of modern agriculture and food production. However, one of the major environmental concerns is that pesticides are released into the environment, causing air, soil, and groundwater pollution. The environmental issues associated with the accumulation of pesticides in the environment and food necessitate the development of safe, convenient, and cost-effective pesticide cleaning methods [1]. The scale of this problem, which has become a huge problem facing the world today, has led to the development of several biological methods involving the biodegradation of organic compounds by microorganisms [2]. An important group of organisms that naturally aid in the purification of ecosystems, fungi have multiple environmental and industrial uses for the removal of pollutants and for the production of

various industrially important enzymes, dyes, and secondary metabolites. Biodegradation Abilities of Microorganisms.

Bacteria, actinomycetes, and fungi have the greatest ability to break down pesticides. The bacteria and soil fungi most active in degrading pesticides are bacteria of the genera *Arthobacter, Flavobacterium, Bacillus, Pseudomonas, and Corynebacterium*. *Actinomycetes* of the genera *Streptomyces and Nocardia* and the fungi *Aspergillus, Penicillium, Trichoderma, and Fusarium* [3], [4], [5], [6], [7]. [8] [9], and [7] in their study, the greatest biodegradability potential was Pseudomonas sp. and *Nocardioides spp*.

Fungi like *Pleurotus ostreatus* [10], [7], *Daedalea dickinsii, Fomitopsis pinicola, Gloeophyllum trabeum* [11], *Fomitopsis pinicola* [12], [13], [7], *Trichoderma hamatum, Rhizopus arrhizus* [14], [7], were reported for the degradation of DDT. *Fusarium sp*. [15], [7], *Aspergillus terreus* [16], [7], and *Mortierella sp*. [17], [7] were reported degrading pesticides.

The use of naturally occurring or introduced microorganisms (fungi or bacteria) to break down contaminants is called bioremediation [18]. Bioremediation is a fast, not expensive, efficient, and environmentally friendly method that began as a method of cleaning environmental components. Bioremediation is based on the fact that the degradation of microorganisms that obtain C, N, or energy from pesticide molecules convert long-term pollutants into carbon dioxide. Ecologically point of view, such a complete conversion is desirable as it represents complete detoxification [19].

Bioremediation by fungi, also named mycoremediation, is considered a willing process in the field decontamination of the environment because many fungi of different genera and species were shown to be able to degrade variant types of organic pollutants, including pesticides. Although converted to non-toxic compounds, this method is currently under investigation and not widely used [20], [21]. Most pesticides are very toxic substances used to control pests and herbs of agricultural soil. Many types of pesticides with high persistence characterization and toxicity are used to control different types of pests in a wide range of ornamentals and crops [22]. The present investigation has been made to characterize fungal biota of untreated and pesticides treated (amended) soils and the role of isolated fungal biota in bioremediation of pesticides residues. Three widely distributed fungal strains were isolated, purified, and identified in pesticide-treated soils and then, it used in in vitro tests to assess their impact on the rate of biodegradation of the pesticides tested, providing key indications for pesticide mycodegradation and micro calcification in soil.

2. MATERIALS AND METHODS

2.1. Pesticides.

Three pesticides that belongs to 3 groups of organophosphate have been used as shown in table (1).

Table 1. : Common name, chemical formula and rate of uses of tested organophosphate pesticides.

Type of pesticide	Common name	Trade name	Chemical name	Rate/ feddan
Fungicide	Esfenvalerate.	Sumi Eight 5% EC	[(S)-cyano-(3-phenoxyphenyl)methyl] (2S)-2-(4-chlorophenyl)-3-methylbutanoate.	200 ml / 500 liter water.
Herbicide	Tribenuro–methyl.	Granstar 75% DF	[Methyl 2(((N-(4-methoxy-6-methyl1, 3, 5-triazin-2-Y) methylamine carbonyl) amino) sulphul) benzoate].	8.0 gm
Pesticide	Actamiprid 20% SP.	Mospilan.	(E)-N^1-[(6-chloro-3-pyridyl)methyl]-N^2-cyano-N^1-methylacetamidine.	50-80 gm

2.2. Field experiments.

A cultivated soil within the Botanical Garden of the Faculty of Science campus, Port Said University at Port Said, has been selected where open field experiments were carried out. The selected soil part (Fig. 1) has been divided into four plots (1.5 x 2.5 meters each). Three plots were amended with three different

pesticides; fungicide, herbicide, and pesticide at the rate of 20ml /50L water, 1g /50L water, and 12,5g /50L water respectively; while the fourth plot was kept un-amended (control).

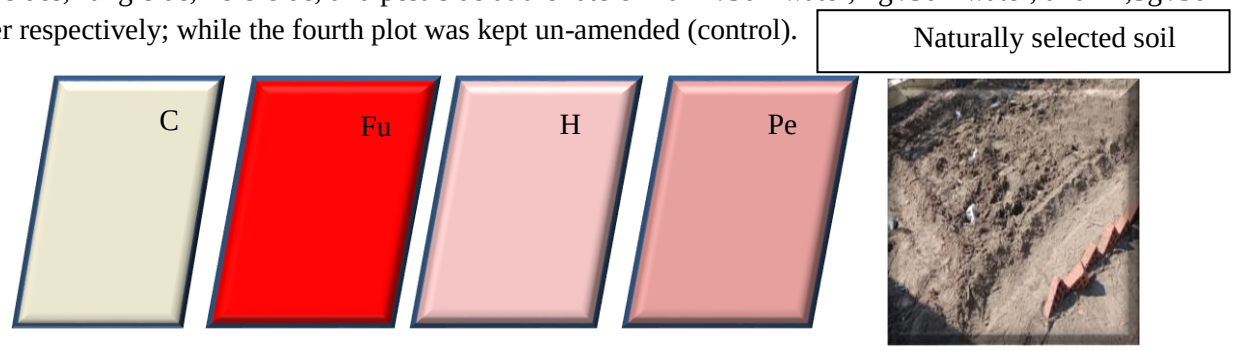

Figure. 1: Selected soil divided into four plots.

2.2. Sampling.

Soil samples were taken from the topsoil layer (3-20 cm deep) from untreated and treated (fertile) soil. Thirty soil samples (500 g each) were taken from healthy, contaminated soil (15 samples each). Samples were delivered to the laboratory in sealed, sterile polyethylene bags and stored at low temperature until inoculation.

2.3 Isolating and identification.

Fungi were isolated from the basement (approximately 3 x 15 cm) using the petri dish method [23] (Johnson et al., 1960), in which 6 dishes were used for isolation/sampling. Czapek agar supplemented with 0.5% yeast extract (CYA) and potato dextrose agar (PDA) supplemented with rose Bengal (1/15000) and chloramphenicol (50 ppm) were used for primary isolation. Plates were incubated at 28 °C for 5 days and the number of developing fungi was counted. For culture maintenance and proper identification, pure cultures of isolated fungi are grown on standard media such as plant agar (V8), oatmeal agar (OA), Czapek yeast extract agar (CYA), malt extract agar (MEA), potato dextrose has been agar (PDA) and potato carrot agar (PCA). Taxonomic identification by the morphology of the isolated fungus was mainly based on the following identification keys: for *Penicillium* [23], [24], [7]; [25], [7] for *Aspergillus*; [26], [27], [7] in cases of necrotic hyphomycetes; [28], [7] for *Fusarium*; [29], [30], [7] about other mushrooms.

2.4. Isolation and identification of soil-borne fungi for pesticides utilization.

The method of dilution plate was used [31]. For fungal isolation, Czapek-Dox agar medium (g/l: sodium nitrate 3.0, magnesium sulfate 0.5, potassium chloride 0.5, agar 15.0) media was used. Potassium dihydrogen phosphate (5 mmol/L) was used as the phosphorus source and sucrose (50 mmol/L) was used as the carbon source. Organophosphates were used as the sole source of phosphorus, inorganic phosphates were replaced with pesticides in concentrations of 0.5, 1, 3, and 5 mmol/l. As the sole carbon source, pesticides were used, 5 mmol/L of glucose was used as a control and substituted with 0.5, 1, 3 and 5 mmol/L of pesticides. Rose Bengal was added as a bacteriostatic agent to the medium. For each concentration, five plates were used. Plates were incubated at 28 °C for 15 weeks and grown according to [25] for *Aspergillus*, [28] for *Fusadum*, [32] for *Emericella*, and [33] for *Penicillium spp*. counted and identified. To obtain the number of colonies per g/m of dry soil, the average number of colonies per plate was multiplied by the dilution factor.

2.5. Screening of fungal isolates for the ability to pesticides utilization.

The culture medium (Czapek`sDox broth) including (g/L): sucrose 30, NaNO3 3, MgSO4 0.5 and KCl 0.5. KH2PO4; was omitted from the medium and replaced by the organophosphate pesticides in a final concentration of 0.5 mmol/L. The pH of the media was adjusted to 7. 250mL Eden Meyer flasks containing 50 mL of a sterilized medium were inoculated with I mL of spore suspension of *A. terreus, F. oxysporum and P. chrysogenum.* Ammonium sulfate was used in the culture media of *P. chrysogenum* due to the NaNO3 toxicity. The flasks were then incubated at 28 ~ on a shaking platform at a frequency of 1.7 Hz. After 5 d, the cultures were filtered and dry mycelial mass was determined.

2.6. Parameters used for comparing mycobiota isolated from pesticides amended and un-amended soils.

Count: the colony number formed units (CFU) per gram dried soil.

Diversity: (= Spectrum) a number of genera and species was isolated from each soil.

Species richness: number of species belonging to each genus.

Species density: average number of colony-forming units of each species out of three samples.

Species frequency: percentage number of each isolated species cases out of three samples.

2.7. Phylogenetic tree analysis.

To draw the phylogenetic tree, deduced amino acid sequences of *Fusarium oxysporum* DNA (cytosine-5)-methyltransferase PliMCI has been alignment through the usage of (L-INS-i) of MAFFT version 7 (http://mafft.cbrc.jp/alignment/server/), then the resulted alignments have been taken to Gblocks (http://molevol.cmima.csic.es/castresana/Gblocks_server.html) to cast off gaps and predict homologous genes relying on conserved amino acids, then ultimately phylogenetic tree changed into drawn the usage of the Neighbouring-Joining technique through Mega7 software [34, 35, 36,37].

3. RESULTS AND DISCUSSION

3.1. Diversity of soil mycobiota:

Fungal biota of untreated and pesticides treated soils were surveyed by the dilution plate technique and Czapek's-yeast extract ager medium. A total of 12 composite soil samples of control and three different pesticides amended soils (three each) were investigated.

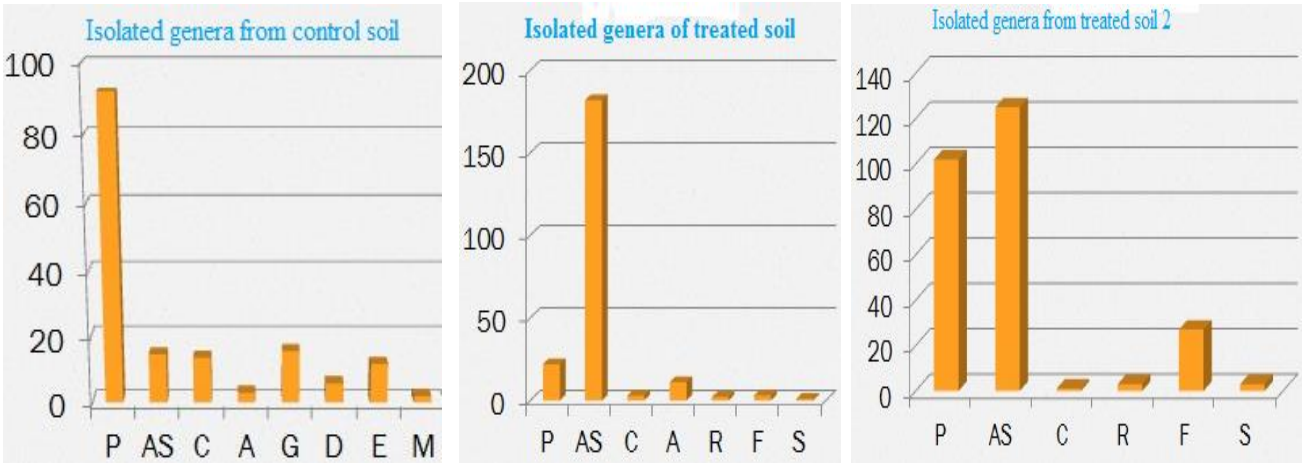

Figure. 2: Isolated fungal taxa from untreated (control) and treaded soils P: *Penicillium sp*., AS: *Aspergillus sp*., .C: *Cladosporium sp*., A: *Alternaria sp*., G : *Geotrichum sp*., D : *Drechslera sp*., E : *Eurotium sp*., M : *Mucor sp*., R : *Rhizopus sp*., F : *Fusarium sp*., S : *Scopulariopsis sp.*

Table 2: Fungal biota isolated from pesticides amended and control soils.

Organisms	Control			Fungicide			Herbicide			Pesticide		
	count (N)	D	freq. (%)	count (N)	D	freq. (%)	count (N)	D	freq. (%)	count (N)	D	freq. (%)
Absidia corymbifera	-	-	-	3	500.0	50.0	-	-	-	-	-	-
Aspergillus carnus	-	-	-	-	-	-	-	-	-	4	666.6	50
Aspergillus flavus	2	333.3	16.6	-	-	-	-	-	-	3	500	50
Aspergillus candidus	-	-	-	-	-	-	-	-	-	3	500	50
Aspergillus glaucus	2	333.3	33.3	-	-	-	-	-	-			
Aspergillus niger	-	-	-	-	-	-	5	833.3	83.3	33	5500	100.0
Aspergillus sydowii	-	-	-	2	3 33.3	33.3	-	-	-	60	10000	100.0
Aspergillus terreus	2	333.3	33.3	5	833.3	83.3	28	4630	83.3	100	18800	100.0
Aspergillus nidulans	-	-	-	-	-	-	-	-	-	4	666.6	66.6
Aspergillus versicolor	-	-	-	7	1333.3	83.3	-	-	-	-	-	-
Aspergillus wentii	-	-	-	-	-	-	2	333.3	33.3	3	500.0	33.3
Alternaria chlamydospora	-	-	-	-	-	-	3	500	33.3	-	-	-
Cladosporium sp.	2	333.3	33.3	3	500	50.0						
Cladosporium cladosporioides	5	833.3	33.3	-	-	-	-		-	-	-	-
Eurotium rubrum	12	2000	100.0	-	-	-	-	-	-	-	-	-
Fusarium oxysporum	8	1333.3	66.7	-	-	-	-	-	-	-	-	-
Fusarium solani	-	-	-	3	500	50.0	-	-	-	3	500	50.0
Fusarium culmorum	-	-	-	24	4000	50.0	-	-	-	11	1888.8	66.6
Drechslera halodes	5	833.3	50.5		-	-		-	-	-	-	-
Geotrichum candidum	16	2666.6	100.0	-	-	-		-	-	-	-	-
Mucor racemosus	4	666.6	50.0	-	-	-	-	-	-	-	-	-
Myrothecium verrucaria	7	1333.3	83.3	-	-	-	-	-	-	-	-	-
Penicillium canescens	30	5000	50.0	-	-	-	0	3333.3	83.3	3	500	50.5
Penicillium cyclopium	5	833.3	66.7	-	-	-	-	-	-	-	-	-
Penicillium variable	19	3333.3	83.3	24	4000	50.5	-	-	-	-	-	-
Penicillium chrysogenum	-	-	-	43	7000.3	66.6				25	4000.3	50.0
Penicillium jenseni	-	-	-	-	-	-	7	1166.67	50.0	-	-	-
Penicillium funiculosum	4	666.6	33.3	3	500	50.0		-	-	-	-	-
Rhizopus stolonifer	-	-	-	-	-	-	5	833.3	50.0	4	666.7	66.7
Scopulariopsis brevicaulis	-	-	-	-	-	-	-	-	-	3	500	33.3
Scopulariopsis brumptii	2	333.3	33.3		-	-	-	-	-	-	-	-
Talaromyces flavus	-	-	-	-	-	-	-	-	-	2	333.3	33.3
Yeast	-	-	-	2	333.3	33.3	-	-	50.0	-	-	-
Total	135	16666.0	-	116	19834	-	60	19130	-	261	40572	-

Out of 12 soil samples, it was possible to isolate 32 fungal species and only one yeast species (Table 2). Fungi belonging to Hyphomycetes accounted for the major part of taxa by being represented by 25 species (accounting for 78% of all taxa).

3.2. Total fungal count:

The effect of pesticides soil amendments on fungal count have been followed in three plots (Fig.1). Each plot was represented by three composite soil samples. Counts were showed as total numbers of colony formed units per gram dry soil (cfu /g).

The data of table 1 show very clear difference in fungal counts between untreated (control) and pesticides treated plots. While treated soil by; fungicide, herbicide, and pesticide; revealed a total colony count of 19334 for fungicide, 19130 for herbicide, and 40572 for pesticide respectively; control soil (untreated) showed a total colony count of 16666.

Data clearly indicated that pesticides increasing the total counts of isolated taxa. It has been also, treatment favours some taxa and leads to disappear another one.

3.3. Species frequency:

It is expressed as percentage cases number isolated out of 12 soil samples. According to the frequency value, three groups are recognized:

High occurrence group: including species showing a frequency of 75 % or more (represented by 12 species).

Moderate occurrence group: comprising taxa having frequency of 50 % - 74 % (represented by 20 species).

Low occurrence group: contains species of frequency less than 50 % (represented by 14 species).

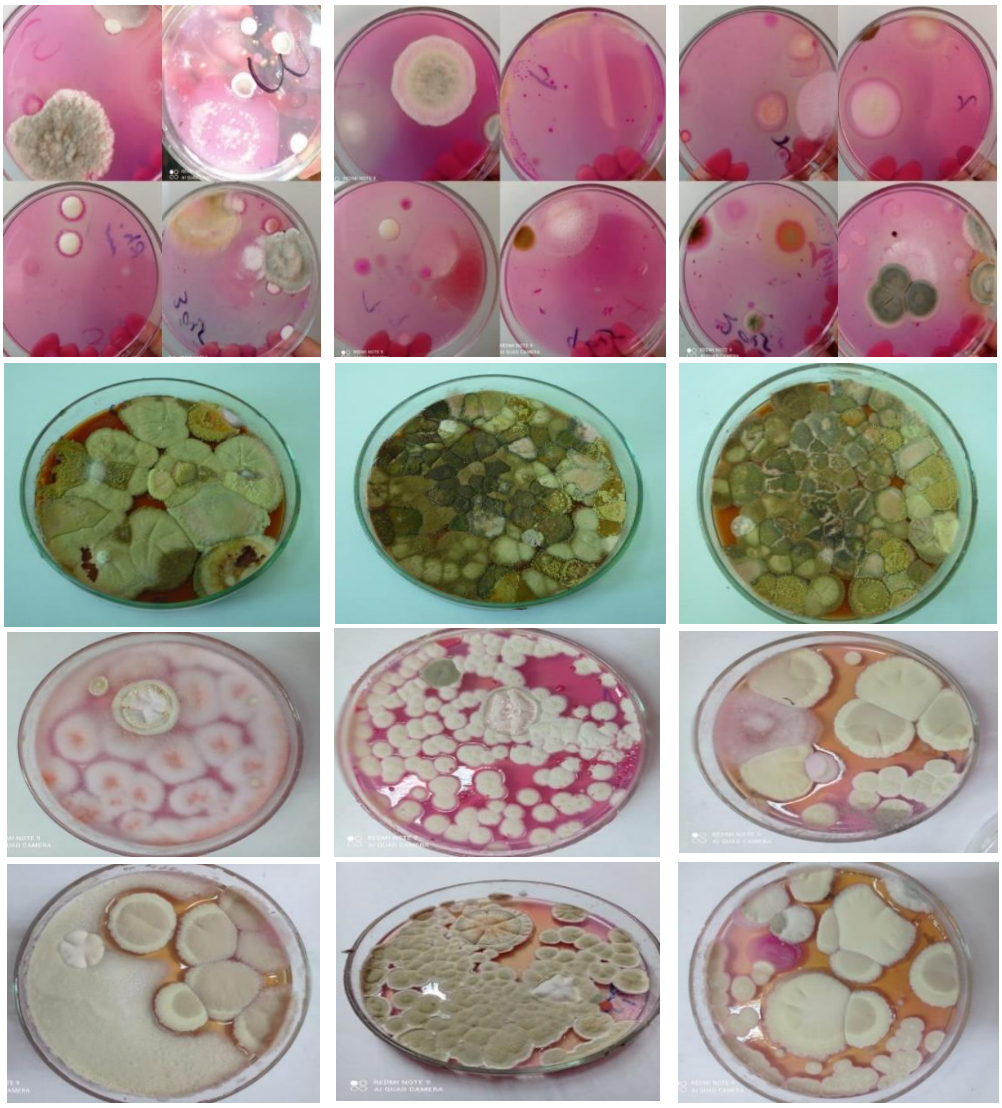

Figure. 3: Rose Bengal yeast extract ager showing developing colonies.

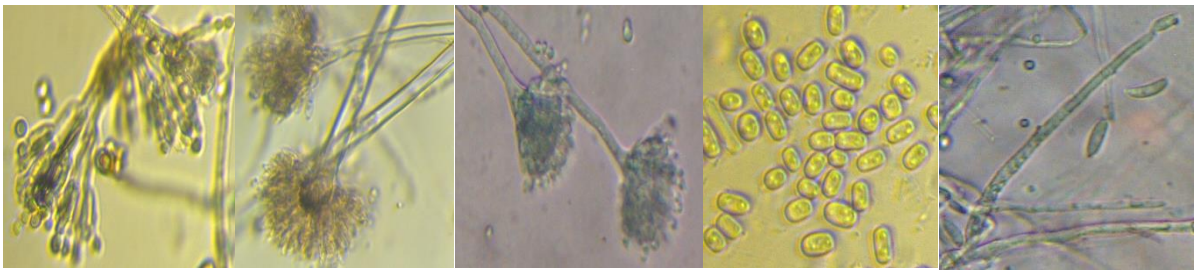

Figure. 4: Micro-morphology of some isolated fungal taxa.

3. 4. Efficacy of fungal biota in bioremediation of pesticide.

The ability of candidates fungal taxa (*A. terreus, F. oxysporum and P. chrysogenum*) to utilize different pesticides; fungicide, herbicide, and pesticide, were carried out by amendment of Czapek's broth medium with the tested pesticides at the rate of 0.2, o.4, 0.8, for each pesticide (Fig. 4, 5, 6). Obtained data showed that *A. terreus, P. chrysogenum* strongly used different pesticides as carbon source; while *F. oxysporum* weakly or moderately utilizing pesticides (Fig. 7).

Figure. 5: Rate of growth of *Penicillium chrysogenum* in different concentration of fungicide, herbicide, and pesticide.

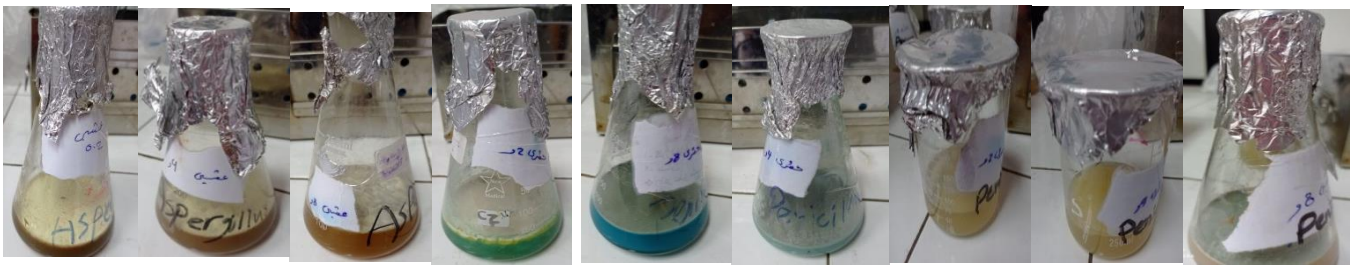

Figure. 6: Rate of growth of *Aspergillus terreus* in different concentration of fungicide, herbicide, and pesticide.

Figure. 7: Growth rate of *Fusarium oxysporum* in different concentration of fungicide, herbicide, and pesticide.

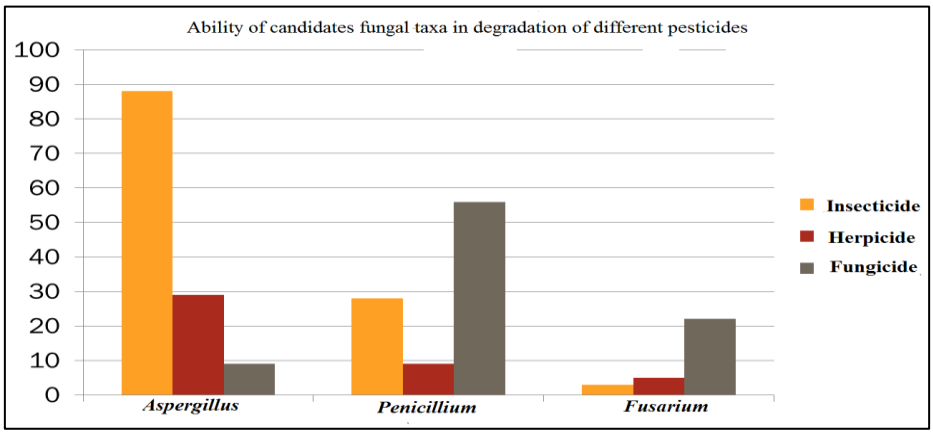

Figure. 8: Ability of candidate's fungal taxa in degradation of different pesticides.

3.5. Phylogenetic tree analysis.

The phylogenetic tree of sequence data of the selected fungal genes isolates shows that all isolates have at least 99% to 100% similarity to those previously deposited with GenBank. Read sequences were deposited with NCBI GenBank and assigned accession numbers (Table 3). A phylogenetic tree analysis of the identified fungal species confirmed the affiliation of that species (Fig. 9). The neighbor-joining method [34] was used to determine the evolutionary history. In the bootstrap test (1000 iterations), the proportion of duplicate trees is displayed next to the branch where the related taxa are grouped together [35]. Trees are drawn to scale with branch lengths in the same units of evolutionary distance used to derive phylogenetic trees. Using the JTT matrix method, evolutionary distances were calculated in units of the number of amino acid substitutions per site [36]. The analysis included a sequence of 15 amino acids. All locations with spaces and missing data have been removed. The final data set has a total of 474 locations. Evolutionary analysis was performed on MEGA7. [37]. Many organisms and eukaryotic cell membranes produce compounds that play role in inhibition of sphingolipid metabolism. Some inhibitors are similar structurally to the sphingolipid biosynthesis intermediate sphinganine and are called sphinganine-like metabolites (SAMs). For food and feed safety reasons, fumonisin biosynthesis has recently been investigated, including the fumonisin biosynthesis characterized genes in some important agricultural fungi *Fusarium and Aspergillus* [38].

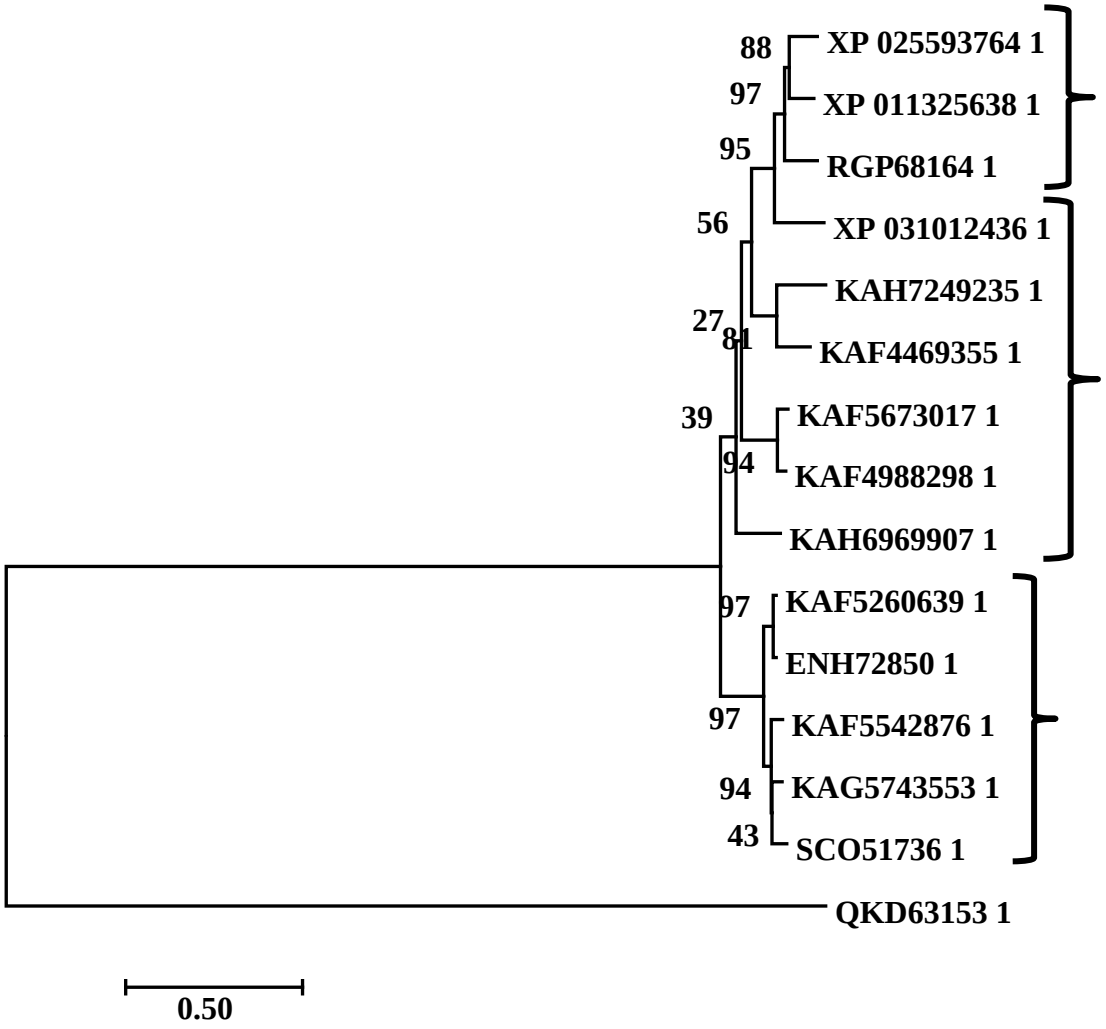

Figure. 9: Phylogenetic tree analysis construction for *Fusarium oxysporum* identified in the present study.

Table 3. Show accession number of selected protein sequences with the full name and organism name for each protein.

Accession number	Protein name	Organism (Fungus)
XP_025593764	**UNCHARACTERIZED PROTEIN FVRRES_10127**	*Fusarium venenatum*
XP_011325638	**HYPOTHETICAL PROTEIN FGSG_10766**	*Fusarium graminearum PH-1*
RGP68164	**DNA CYTOSINE-5-METHYLTRANSFERASE**	*Fusarium longipes*
XP_031012436	**UNCHARACTERIZED PROTEIN FIESC28_09377**	*Fusarium coffeatum*
KAH7249235	**HYPOTHETICAL PROTEIN B0J15DRAFT_527155**	*Fusarium solani*
KAF4469355	**DNA (CYTOSINE-5-)-METHYLTRANSFERASE**	*Fusarium albosuccineum*
KAF5673017	**DNA (CYTOSINE-5-)-METHYLTRANSFERASE**	*Fusarium heterosporum*
KAF4988298	**HYPOTHETICAL PROTEIN FGRMN_9849**	*Fusarium graminum*
KAH6969907	**HYPOTHETICAL PROTEIN DER45DRAFT_601162**	*Fusarium tricinctum*
KAF5260639	**HYPOTHETICAL PROTEIN FOXYS1_8703**	*Fusarium oxysporum*
ENH72850	**DNA(CYTOSINE-5)-METHYLTRANSFERASE PLIMCI**	*Fusarium oxysporum f. sp. cubense race 1*
KAF5542876	**DNA (CYTOSINE-5-)-METHYLTRANSFERASE**	*Fusarium mexicanum*
KAG5743553	**HYPOTHETICAL PROTEIN H9Q70_013737**	*Fusarium xylarioides*
SCO51736	**RELATED TO CYTOSINE C5-DNA-METHYLTRANSFERASE**	*Fusarium fujikuroi*
QKD63153	**HYPOTHETICAL PROTEIN FOBC_17427**	*Fusarium oxysporum* Fo47

Continued use of pesticides can lead to the formation of pesticide residues combinations in plants or soil, which can lead to pre maturation of pesticide inactivation, damage of crops, or forming new complex residues. Therefore, biodegradation is highly desirable of soil residues.

Bioremediation is taken into consideration greater environmentally pleasant than traditional remediation strategies and taken into consideration an inexperienced generation because it most effective relies upon processes and organic organisms. It is now require no longer any chemical addition or heating remedy however, it's miles nonetheless now no longer unfold extensively and has now no longer continually yielded pleasant results, nevertheless, bioremediation could be very promising biotechnology [39]. It additionally has a few obstacles while a few chemical compounds aren't with no trouble prone to organic degradation because of their chemical homes or robust sorption to the environmental matrix, or microbial degradation of a few compounds can also additionally yield metabolites which might be greater poisonous than the determine compound, or the long time clinical research required to find out the exceptional microorganisms for the job [40]. Fungi utilization in bioremediation until the instant remains beneath neath exam and untapped extensively [41].

Our results indicated that Egyptian native fungal biota is a promising organism in biodegradation of different pesticides residues which used routinely in planting soil.

Data showed that generally increasing fungal counts and frequency in pesticides amended soils as compared with unamended soil (control), this result agree with [4]; [5]; [6]; [42]; [43].

[44] Apparently, the use of pesticides; it also causes mild changes in the structure of the bacterial and fungal communities either directly on the leaves or through the soil. They conclude that further research will focus on isolating and characterizing fungal strains stimulated by pesticide use and determining their ecological roles and interactions with the pesticides under study. [45] Can isolate *Aspergillus terreus, Penicillium citrinum, Trichoderma harzianum,* and *Aspergillus fumigatus* in aquatic habitats, but these strains grow and degrade pesticides very efficiently.

Results [46] clearly show that applying single pesticides and/or pesticide mixtures to tomato cultivation at field application rates (2.5–5.0 kg/ha) improved bacterial and fungal populations in soil 1 and soil 2 significantly. However, an increase in pesticide use (7.5 to 10 kg/ha) resulted in a sharp decrease in fungal and bacterial populations. On the other hand, a negative effect on the fungal population was shoed when pesticides combined with fungicides.

However, data [47] show that pesticides have a significant effect on the soil microbiome, changing the response from high resistance to high sensitivity. The most noticeable decreasing in the number of nitrifying microorganisms and fungi in the soil like (*fusarium, penicillium, trichoderma, humicola, mucor*) is under the influence of pesticides. Bacteria like (*Pseudomonas, Corynebacterium, Flavobacterium*) and *actinomycetes* are less stressed, especially with related to the rhizosphere.

One study [48] showed a negative effect of pesticides on the presence of antagonist fungi due to decreased abundance, diversity, and uniformity of antagonist fungi. The most remarkable of these effects is Fusarium sp. As pathogenic fungi at all frequencies of pesticide use. However, the appearance of Trichoderma spp. In all fields treated with various pesticides, the endogenous *A. niger* was very important in this study. Because fungi have resilient properties with various pesticide residues, their presence can turn into a biological agent.

3. 4. The efficiency of fungal biota in bioremediation of pesticides.

The ability of candidate fungal taxa (*A. terreus, F. oxysporum and P. chrysogenum*) to use various pesticides; Fungicides, herbicides, and pesticides were performed by introducing the tested pesticides into Czapek medium at the ratio of 0.02, 0.04, 0.08 ml/50 ml of the medium for each pesticide (Fig. 5, 6, 7).

According to the data obtained, *A. terreus, P. chrysogenum* intensively used various pesticides as carbon sources. *F. oxysporum* uses pesticides sparingly or moderately (Fig. 8).

Considering the ability of fungal biota in degradation of pesticides, data revealed that the efficacy of candidates Egyptian native fungal taxa in degradation tested organophosphorus. While *A. terreus* and *P. chrysogenum* strongly degrade different used pesticides, *Fusarium oxysporum* comes next by showing weak and moderately degradation.

Our finding is in constant with the data obtained by many researchers in Egypt and other country all over the world. [49] Obviously, five types of fungi have been isolated and identified from agricultural soils. Of these, *Aspergillus flavus* and *Fusarium oxysporum* clear their ability to degrade some organophosphate nematicides such as *triazophos, etoprofos,* and *fenamiphos* [50]. It has been reported that inoculation with a consortium of high-potency microorganisms isolated from in situ contaminated soil yields the most effective bioremediation consortium, which can significantly remove phosphate residues from the soil. [45] Many fungi that are resistant to and capable of degrading chlorfenvinphos have been isolated. They concluded that the fungus should show an important role in the breakdown of fungicide and other pollutants present in the aquatic environment. Fusarium species produce a variety of toxic metabolites that cause plant disease and plant and soil fungal toxicity. A thorough understanding of the potential for mycotoxins in the biological removal of pesticides from soil is important for assessing the toxicological risks associated with *Fusarium* disease. [51]

In any case, [52] reported that the herbicides tested at various concentrations of 0.5 μg/ml, 1.0 μg/ml, 2.0 µg/ml, 5.0 µg/ml and 10.0 µg/ml inhibited the growing mycelium of the isolated rhizome fungi. Growth inhibition of rhizome fungi increased with increasing concentration of each herbicide.

4. CONCLUSION

Environmental pollution caused by pesticides affects the ecosystem services of soil, water resources, and the health of plants, microorganisms, animals, and humans. Therefore, there is a need to develop suitable environmentally friendly strategies to remove pesticides from polluted environments. A review of the data presented in this article, as well as data from around the world, highlights the role and importance of fungi in the biodegradation of various pesticides.

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