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Isolation of polycyclic aromatic hydrocarbons (PAHs) degrading fungal strains from industrially polluted soils

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Abstract

Soil fungi play an important role in biodegradation of industrially polluted soils. In this study, we isolated the native fungal strains in industrial and city soils, assessed their diversity, and compared them with other fungal strains available in NCBI. Molecular identification of isolated strains had been performed by using 18S rRNA genes. Six strains, *Aspergillus flavus*, *A. niger*, *Talaromyces funiculosus*, *A. sublatus*, *A. nidulans*, and *A. ustus* were identified by molecular techniques, and phylogenetic analysis showed their divergent nature as they did not have any close relation to the other worldwide isolates. Possible reason of the genetic diversity lies in the impact of hot climatic conditions prevailing in Saudi Arabia. The concentration of total polycyclic aromatic hydrocarbons (PAHs) and heavy metals was determined to correlate the environment with other biodegradable strains. The native strains of soil fungi mainly depend on the exposure time and organic matter content. It was noted that areas with more plants showed the presence of more and effective fungal strains, and recorded low PAHs. This study, therefore, focused on the use of native strains and their potential for remediation of soils and the homogeneity of fungal strains, which are mainly evident of low organic matter and high salinity in the area. These results lay a strong foundation for providing comprehensive information about bioremediation of PAH-contaminated soils in the future.

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Introduction

The environmental contaminants are increasing every day due to the ever-growing population, industrialization, and urbanization. Among different pollutants, polycyclic aromatic hydrocarbons (PAHs) are semi-volatile organic compounds, mostly responsible for soil pollution. They are benzene ring-containing compounds; anthracene and phenanthrene are PAHs with three benzene rings, while other PAHs may contain four rings, such as chrysene and pyrene, and five rings, such as benzo (a) pyrene, which are considered to be more dangerous. The sources responsible for PAH emission could be the different industrial processes, such as burning of fossil fuels, production of gas and coal tar, polishing of wood furniture, and incineration of waste, especially from industrial areas (Cai *et al.*, 2007; Harvey, 1991). Due to these widespread sources, PAHs are among the most dominated contaminants in the environment. PAHs are non-polar, ubiquitous, and highly non-soluble in water. There are hundreds of PAHs present in the environment, but studies mostly focus on the 16 PAHs that are considered as priority pollutants by the US Environmental Protection Agency and the European Community (Chaineau *et al.*, 2005; Puglisi *et al.*, 2007). Seven of these 16 PAHs are considered to be carcinogenic or mutagenic (Adonis *et al.*, 2003).

Numerous treatment technologies, such as bioremediation, advanced oxidation, photo catalysis, phytoremediation, and thermal treatment, are being practiced for the remediation of PAH-contaminated soils (Cai *et al.*, 2007). Biodegradation has been the subject of active concern for the past 60 years and bioremediation is acknowledged as a capable, cost-effective, and multipurpose substitute to physicochemical treatment (Zhang *et al.*, 2011). A biological treatment of PAH-contaminated soil is more efficient, affordable, and adaptable than a physicochemical treatment is, because it has potential advantages, including degradation of total pollutants, less treatment costs, increased security, and less soil disturbance (HABE and OMORI, 2003). Metabolism or co-metabolism are processes most often used by fungi that degrade PAHs.

Research is now under progress to explore the microbial communities effective in remediating the PAH-contaminated soils. The Arabian Peninsula is illustrious with high salt and crude oil contaminations (Al-Mueini *et al.*, 2007).

In addition to bacteria, fungi are also used as bioremediations of organically contaminated soils. Basidiomycetes are widely distributed fungi and natural degraders of lignocellulose. White rot fungi (WRF) could be another choice of an appropriate bioremediation agent; however, hundreds of species of WRF need to be studied in this context (Crawford, 2006). Recently, Lee *et al.* (2014) found that *Eniophora incarnata* KUC8836 and *Phlebia brevispora* KUC9033 significantly degraded phenanthrene, anthracene, fluoranthene, and pyrene. For effective degradation of PAHs, fungi are used along with compost (Furuno *et al.*, 2012) as well as bioaugmentation with numerous fungal species (Pozdnyakova, 2012).

Moreover, fungal inoculum and bacterial communities can be efficaciously combined to degrade PAHs (Furuno *et al.*, 2012; Kohlmeier *et al.*, 2005; Šnajdr *et al.*, 2011); however, very few studies have been reported against it (Valentín *et al.*, 2010), (Nguyen *et al.*, 2013) revealed that mixed culture of bacteria and WRF in a fungus-augmented membrane bioreactor could achieve better degradation of organic compound traces than that by a system containing individual bacteria or fungi. Future research, therefore, is required to isolate and identify the most suitable biological agents to be used for the degradation of PAHs in the soil of a particular area. Most of the research has been done to expose PAH sources contaminating sediments, suspended matter, and forming aerosols. However, limited research has been done on soils contaminated with PAHs in industrial areas (Gan *et al.*, 2009). Industrial contaminated soil depicts heterogeneity in compounds and complexity of the environmental matrix making source identification difficult. Additionally, more than one source identification method is required to identify the origin of pollution in industrial soil.

Although the microbial communities have a potential to effectively degrade PAHs, the selection of appropriate microbial community is essential because of diversity in their mode of action. Currently, the microorganism-mediated mechanisms of PAH catalysis are well known and they help to improve bioremediation of PAH-contaminated soil (Peng *et al.*, 2008).

The fungi isolated from native soil had the advantage of having a better capability to survive in a particular soil environment. Moreover, the native fungal consortia can perform better under native environment, due to their specific metabolic pathways and their better adaptations to biodegradation mechanism and cellular resistance (Van Der Gast *et al.*, 2004). Recently, limited work has been done on isolation of native fungi, which could be helpful in degradation of PAHs.

Therefore, the current study focuses on the isolation and molecular identification of fungi so that they could be further utilized for bioremediation of polluted soils in an industrial area.

Materials and methods

Collection of Samples

Soil samples were obtained from different locations of Yanbu Industrial Area (Fig. 1). Total 41 soil samples were collected during the entire study.

The sampling area was divided into three parts—mainly Yanbu city area (CA), Light industrial area (LIA), and Heavy industrial area (HIA)—and the locations are shown in Table 1. The samples were divided into two parts, one for general soil analysis and the other for microbial population analysis, and were kept in ice boxes. GPS coordinates of each sampling location were recorded with the name of the industry. Standardized sampling protocols given by the Soil Science Department at King Saud University were followed (EL-Saeid *et al.*, 2015).

The samples were transported by air from Yanbu to Riyadh. Further, samples were dried, sieved, and preserved for further physicochemical analysis.



Fig. 1. The survey location of Yanbu city and industrial area.

Isolation, purification, DNA extraction and sequencing

Isolation of microorganisms from soil

Soil samples were collected (approximately 100g) in clean, dry, and sterile polyethylene bags using sterilized spatula and were stored in ice boxes. In the laboratory, microbes from the soil samples were isolated. Industrial soil samples contaminated with PAHs were serially diluted by ten-fold up to six dilutions. For assessing fungal growth, Martin medium was used.

Preparation of soil-borne microbial suspension

Ten grams of the soil sample was taken in a sterile 250-mL Erlenmeyer flask and 90mL distilled water was added to make a suspension. Further, the sample was incubated on a shaker at 160 rpm for 2h. The suspension was further serially diluted up to 10⁶. Then these dilutions were further used to grow microbes on specific media.

Assortment of microorganisms for PAH and heavy metal resistance

All media used in these studies were prepared in distilled water purified using a Milli-Q apparatus (Millipore) to a resistivity of 18.2M Ω .cm (at 25°C) and a TOC value below 5 ppb. For extraction and dilution of the fungus, pH was adjusted to 7.4. A fixed amount of 2.5mL heavy metal solution was added to Winogradsky-solution (W) (Holm & Jensen 1972) semi-solid media. Microorganisms used in this experiment were cultured on Potato dextrose agar (PDA) for further use. All growth media were purchased from Liofilchem (Teramo, Italy).

DNA extraction from microbial community

All fungal samples were subjected to total genomic DNA extraction. Aliquots (150 μ L) of fungal pellets were suspended in 400 μ L lysis buffer (100 mM Tris-HCl pH 8, 100 mM EDTA, 2% SDS). Lysozyme (1 mg ml^{-1}) was added and the suspensions were incubated for 2 h at 37°C. After the addition of proteinase K (0.1 mg ml^{-1}) the suspensions were further incubated for 2 h at 37°C. CTAB and NaCl were added at a final concentration of 1% and 1.5M, respectively, and the suspensions were incubated at 50°C overnight. After centrifugation, the supernatants were extracted using an equal volume of chloroform: isoamyl alcohol (24:1), the aqueous phases were added with 0.5 vol. of 5M ammonium acetate and incubated at 4°C for 1 h. After centrifugation, DNA in the supernatants was recovered by the addition of 0.55 vol. of isopropanol followed by centrifugation at 13,000 rpm for 15 min. The pellets were washed with 70% ethanol, dried, and suspended in 50 μ L sterile water.

PCR conditions

The selected strains obtained from specialized media were further subjected to molecular identification. For fungi, single-colony 18S r-DNA was used with primers NS1F (5'- GTAGTCATATGCTTGTCTC-3') with 19 base pairs and NS8 (5'- TCCGAGGTT CACCTACGGA-3') with 20 base pairs. The PCR amplification conditions were as follows: 94°C for 5 min; followed by 35 cycles at 94°C for 30 sec, variable temperature for 30 sec, 72°C for 40 sec; and 72°C for 7 min. PCR products were purified using Millipore plate MSNU030 (Millipore SAS, Molsheim, France). The purified PCR products were then Sanger-sequenced with the Big Dye terminator v3.1 sequencing kit and a 3730xl automated sequencer (Applied Biosystems, Foster City, CA). Nucleotide sequences were determined on both strands of PCR amplification products at the Macrogen sequencing facility (Macrogen Inc., Seoul, Korea). The obtained sequences were compared to database sequences using the BLAST system (<http://www.ncbi.nlm.nih.gov/BLAST>) and deposited in the Gen Bank® genetic sequence database (Nucleic Acids Research 2007 Jan. 35; Database issue D21-5), with the Accession Numbers from KY233188, 233189, KY233190, KY233191, KY233192, KY233193.

These Saudi Arabian isolates were compared phylogenetically with 18 selected isolates from NCBI to estimate their genetic diversity.

Pure culture of microorganisms

Single separate colonies on the agar plates were selected randomly according to the standard methods and streaked on the nutrient agar plates followed by incubation for 24h at $\pm$ 30°C. Code names were given to each of the isolated plates and stored at $\pm$ 40°C for characterization and identification by standard methods. Once colonies grew on the media, the sub-culturing was continued until a pure isolate was obtained. Identification of microbes was done with the help of standard literature. For isolation of fungi, PDA medium was prepared. Likewise, 1mL soil suspension was aseptically poured in media plates, prepared for the isolation of fungi. The plates were gently rotated to spread the suspension on medium. The plates were incubated at $\pm$ 30°C for 4–5 d.

Soil physicochemical characteristics

Soil physicochemical parameters are shown in Table 1. The pH of soil was determined using saturated soil paste and electrical conductivity (EC) was measured by soil saturated paste extract (Richard, 1954).

Soil texture was determined by hydrometer method (Bouyoucos, 1962). The contents of organic matter in the soil samples were determined by Walkley-Black method (Nelson and Sommers, 1982). Phosphorus in soil was determined by a previously described method (Olsen and Sommers 1982). DTPA (diethylene triamine penta acetic acid) extraction method was used to determine concentration of heavy metals in soil samples. First, samples were extracted for total heavy metals by EPA-3051 method, microwave digestion, and then analysis was done by ICP-OES (ICP-OES, PerkinElmer Optima 4300 DV, USA).

Results

Soil is an important source and a sink for different pollutants, but PAHs do not leach in soil and are usually found on the surface owing to their hydrophobic properties. The current study, therefore, was designed to isolate and identify the microbes,

which could be helpful in degrading PAHs in soil. For this purpose, physicochemical properties of 41 samples were analyzed, and results are shown in Table 1. The results reveal that pH of soil was generally alkaline in CA, LIA, and HIA. The pH range was 8.32–7.74 in CA with the mean value of 8.04, while pH of LIA was slightly higher than that of CA, but no significant difference was noted. The pH value of HIA was the lowest. A huge diversity in the electrical conductivity (EC) was recorded in CA.

The mean value was recorded as 7.87, while the range was quite broad (31.2–1.2 dS cm⁻¹). LIA and HIA showed mean EC values of 4.43 and 11.51, respectively.

The carbon content was also calculated and the mean values are 0.7, 0.43, and 0.86, in CA, LIA, and HIA, respectively. Organic matter content was higher in HIA than in LIA and CA.

Nitrogen and phosphorus content were almost similar in all the three sites. However, the calcium carbonate contents were high in LIA. Physicochemical characteristics are a general indicator of the location giving an overview of the situation. Soil from Yanbu industrial city (YIC) is usually alkaline (Hashem, 1993). EC was found to be the highest in HIA, which could be due to high cation content. Mean maximum EC value was recorded to be 11.51 dS cm⁻¹, which indicates that a large amount of soluble salts and ionic substances are present in soils.

High EC may cause toxicity to plants, hence majority of the soils were found without natural vegetation (Raju N.S., 2013). as compared to CA and HIA.

Table 1. Soil physicochemical properties of YIC (CA, LIA, HIA).

Parameter	City area (CA)		Light industrial Area (LIA)		Heavy industrial area (HIA)	
	Mean	Range	Mean	Range	Mean	Range
EC (dS cm ⁻¹)	7.87	1.2-31.2	4.43	0.59-6.23	11.51	4.45-38.9
pH	8.06	7.74-8.32	8.08	7.88-8.25	7.65	7.237-9.6
C (%)	0.70	0.28-0.97	0.43	0.35-0.51	0.86	0.64-1.12
OM (%)	1.08	0.68-1.24	0.84	0.64-1.02	1.56	0.99-2.21
N (%)	0.02	0.01-0.03	0.03	0.01-0.04	0.02	0.01-0.03
P (%)	0.01	0.002-0.012	0.01	0.004-0.021	0.01	0.004-0.019
CaCO ₃ (%)	15.18	9.9-19	25.61	12.9-5.9	7.92	3.89-14.5
Ca (mg/kg)	13733.5	1440-30250	14869.2	1194-24070	9431.8	4350-16160

Heavy metals

The concentration of heavy metals (Cadmium, Cobalt, Chromium, Nickel, Arsenic, and Lead) and trace elements (Zinc, Copper, Iron, and Manganese) was analyzed in YIC soils.

Arsenic and Cadmium were not detected as per the data shown in Table 2. Cobalt (Co) with the highest

mean value of 4.6 mg/kg was detected in LIA. Chromium with the highest mean value of 11.7 mg/kg, and Copper with the highest mean value was detected in CA. Manganese, Nickel, Lead, and Zinc with the highest mean value 297.2, 11.9, 10.1, and 79.8 mg/kg respectively, were detected in LIA. Data in Table 2 depicted that Iron was mainly dominant among the trace elements as noted in the analysis.

Table 1. Total concentration of heavy metals and selected properties of soil samples collected from the study area.

Parameter	City area (CA)		Light industrial Area (LIA)		Heavy industrial area HIA	
	Mean	Range	Mean	Range	Mean	Range
As (mg/kg)	ND	ND	ND	ND	ND	ND
Cd (297.2)	ND	ND	ND	ND	ND	ND
Co (mg/kg)	2.3	0-3.6	4.6	0-12.8	2.0	0-4.9
Cr (mg/kg)	11.7	3.4-16.4	19.7	1.4-42.1	14.3	6.4-27.3
Cu (mg/kg)	16.7	5.7-50.6	15.0	3.6-49.6	13.0	4.2-59
Fe (mg/kg)	8712.2	2896-12980	11489.5	2300-20550	8924.3	6554-12390
Mn (mg/kg)	149.1	103.9-197.5	297.2	50.6-649.0	188.1	116.4-282.1
Ni (mg/kg)	6.3	0.6-9.7	11.9	0.6-30.4	9.1	4.8-16.3

Parameter	City area (CA)		Light industrial Area (LIA)		Heavy industrial area HIA	
	Mean	Range	Mean	Range	Mean	Range
Pb (mg/kg)	5.9	0.5-11.2	10.1	0-23	8.8	1.4-29.2
Zn (mg/kg)	28.5	8.4-51.8	79.8	5.3-195.5	65.6	17.2-417.5

Total microbial count

The total microbial counts of YIC soils were determined by using the standard method and the results are shown in Table 3.

The mean total microbial count of CA samples was 20.8×10^6 CFU as counted by plate count method. The mean total microbial count for LIA and HIA were

9.6×10^6 and 6.39×10^6 CFU, respectively. The mean total count value was noted in the increasing order as follows: CA>LIA>HIA. Similarly, the highest value was recorded in CA for actinomycetes with a mean value of 50.7×10^3 CFU. Total fungi maximum mean value of 5×10^2 CFU was noted in case of LIA, while 0.8×10^2 and 0.2×10^2 CFU were observed in CA and HIA, respectively.

Table 2. Total mean microbial count and ranges in different regions of YIC (CA, LIA, HIA).

Parameter	City area (CA)		Light industrial area (LIA)		Heavy industrial area (HIA)	
	Mean	Range	Mean	Range	Mean	Range
Total Microbial Count (CFU)	20.8×10^6	$1-122 \times 10^6$	9.6×10^6	$1.4 \times 10^6 - 36 \times 10^6$	6.39×10^6	$0.1 \times 10^6 - 20.3$
Fungi (CFU)	0.8×10^2	$0-2 \times 10^2$	5×10^2	$0-20 \times 10^2$	0.3×10^2	$0-2 \times 10^2$

Soil PAHs

Twenty-three PAHs (Acenaphthylene, Acenaphthene, Naphthalene, Fluorene, Phenanthrene, Anthracene, Fluoranthene, Pyrene, Benz(a) anthracene, Chrysene,

Benzo (b + j) fluoranthene, Benzo (a) pyrene, Benzo (k) fluoranthene, 3-Methylcholanthrene, Dibenzo (a,h) acridine, Dibenzo (a,j) acridine, Indeno (1,2,3-cd) pyrene, Dibenzo (a,h) anthracene, 7H-Dibenzo (c,g) carbazole, Benzo (g,h,i) perylene, Dibenzo (a,e) pyrene, Dibenzo

(a,h) pyrene, and Dibenzo (a,i) pyrene) were analyzed and the mean and ranges of PAHs were calculated in the soil samples. The top 6 compounds with the highest values were Dibenzo (a,e) acridine > Dibenzo (a,h) acridine > Dibenzo (ah) pyrene > Dibenzo (ai) pyrene > Phenanthrene > Naphthalene. The microbial strains identified from these soil samples may have good potential as bioremediation agents against these top 6 compounds. The highest contamination by total PAHs was recorded in the following order: HIA>CA>LIA.

Table 4. Total and average concentrations of PAHs from soil samples collected from the study area

Parameter	City Area (CA)	Light Industrial Area (LIA)	Heavy Industrial Area (HIA)
	Mean	Mean	Mean
Total PAHs	$\Sigma=5599.2$	$\Sigma= 3784.8$	$\Sigma=7621.0$

Fungal isolation

Forty-one fungal isolates were obtained separately from a set of soil samples collected from YIC location, including CA, LIA, and HIA. The plates were inoculated with the fungi and were diluted (10^{-4}) and aliquoted for identification of fungi from soil. The isolates were further subculture as morphologically identical colonies on specific PAH-degrading media.

The soil was considerably root free but may have contained fine roots, and therefore, the particular source of the isolate was hard to delineate.

Submission to NCBI

The soil samples resulted in 6 quality sequences averaging 1653 sequences per sample. Initially, 11 samples were subjected to sequencing; among them, 5 failed sequencing.

The 6 sequences were deposited in NCBI under the accession numbers KY233188, KY233189, KY233190, KY233191, KY233192, and KY233193 for sample numbers FAB1, FAB5, FAB6, FAB8, FAB10, and FAB11, respectively. The microbes were identified as *Aspergillus flavus*, *A. niger*, *Talaromyces funiculosus*, *A. sublatus*, *A. nidulans*, and *A. ustus*.

Multiple alignment and phylogenetic analysis

The obtained fungal nucleotide sequence were processed, and aligned with other known fungal sequences obtained from the NCBI database, using the Clustal W program (Thompson *et al.*, 1997). The phylogenetic tree, based on fungal nucleotide sequences available on NCBI,

was constructed using the DNASTAR software. The results of phylogenetic analysis showed that isolates were divided into two major groups, Group I and II. Group I was further divided into Groups Ia and Ib which included all the isolates from NCBI and three Saudi Arabian isolates (one *Aspergillus ustus* one *Aspergillus* sp and one *Talaromyces funiculosus* isolate). All the local isolates showed a relatively higher level of genetic variations as they didn't share any clade. Whereas, FAB8 in group Ib and all three *Aspergillus* isolates belonging to three different species in group II showed greater genetic diversity as they are not closely related to each other however, not related to any other analyzed isolate.

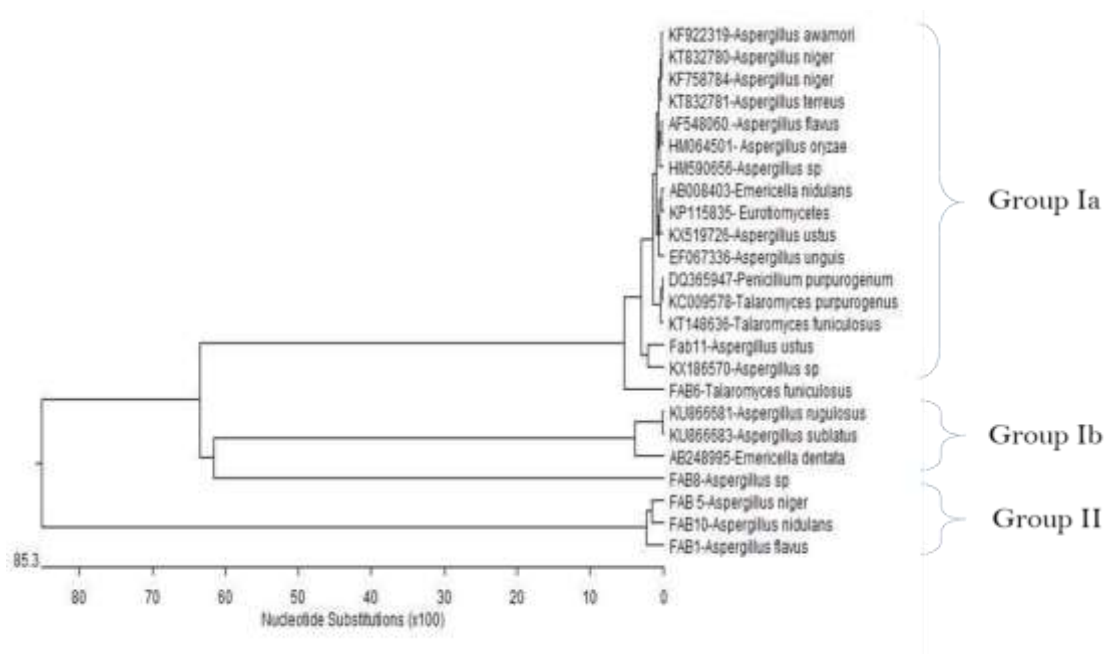


Fig. 2. Phylogenetic tree showing hierarchy of fungal distribution of different communities from the YIC samples at the genus level. Tree was constructed using DNASTAR software and nucleotide substations are mentioned at the baseline of the tree.

Discussion

Until now, emphasis was given on the overall industrial area in various studies. However, in our study, we divided study areas into three different parts—HIA, LIA, and CA. The native fungal species have been isolated and identified by molecular techniques. Different fungal communities and their diversity in the oil-contaminated soil from the three areas were analyzed.

The saline-alkali soils of the study area could be the main reason for high abundance of *Aspergillus*, which was also consistent with pH and EC values (Table 1). Hence, the foremost fungal phyla in our study were almost similar to those obtained in the study by Keshri *et al.* (2013) and Peng *et al.* (2015), (Keshri *et al.*, 2013; Peng *et al.*, 2015) and significantly different from those obtained in the study by Sutton *et al.* (2013) (Sutton *et al.*, 2013).

In our study we tried to develop a base for natural attenuation (NA) or bioattenuation, during which we used the indigenous fungal population that were isolated and identified by using 18S rRNA genes. The NA is widely used bioremediation method for degradation of PAHs in industrially polluted soil due to ability of microbes to do natural metabolic process. The NA helps to reduce toxicity and concentration of contaminants by using different physical, chemical and biological processes. We isolated *Aspergillus* sp. Which has the ability to grow and compete in alkaline, heavy metals soils for the degradation of PAHs (Pawar, 2015).

The results revealed that the growth media (Martin's Rose Bengal Agar medium) used in this study is more suitable for the growth of fungi only. The resultant fungal strains are the proof that this media is highly suitable for fungi isolation from industrially polluted soils ref. Moreover, it is evident that industrially polluted soils are rich source of microorganisms (Table 3) (Kidibule *et al.*, 2014).

The use of fungal 18S rRNA gene sequence is a well-known method by using primers NS1F (5'-GTAGTCATATGCTTGTCTC-3') with 19 base pairs and NS8 (5'-TCCGCAGGTTACCTACGGA-3') with 20 base pairs. Molecular identification of fungi has been entrenched more credible method for identification (Tanase *et al.*, 2015). Regarding fungi, Fig. 2 reveals that the 6 strains belong to genus *Aspergillus*, class Eurotiomycetes, and phylum Ascomycota. The rate of manifestation among the fungal isolates obtained from the soil samples is shown in Table 3, *Aspergillus* spp. are the dominant ones. *A. niger* among all fungi have better biodegradation ability against PAHs (Al-Nasrawi, 2012). Similar work involving *A. niger* was recorded by Simister *et al.* (2015) (Simister *et al.*, 2015) to demonstrate biodegradation of crude oil.

This study revealed that microorganism is regularly found in contaminated soils, and native microbes possess the better capability to degrade the polycyclic aromatic hydrocarbons, these results are also verified by (Al-Thani *et al.*, 2009; Keshri *et al.*, 2013).

Genetic diversity of the Saudi Arabian isolates refer to a possible adaptation to the local soils which ensures the ability of these fungi to get established and serve the purpose of biodegradation more efficiently as compared to introduction of any foreign isolates. *A. niger*, *A. nidulans* and *A. flavus* are of prime importance as they are not sharing any clade with other Saudi Arabian or worldwide isolates. Interestingly, ability to establish in local soils, having divergent genetic makeup and ability to efficiently degrade PAHs, are the attributes that make these Saudi Arabian isolates more worth studying.

Analysis of a larger portion of their genome could be a way to Fig. out the differences they have developed while making adaptations to the local environment. Fungal species, such as *Aspergillus* and WRF, have the potential to degrade the PAHs when one or more substitute carbon sources are available (Wu *et al.*, 2009). In our study, majority of fungal strains were isolated from LIA, the reason could be availability of alternate carbon source from the light industry. All the isolates of fungi in this study, as indicated in phylogenetic tree in (Fig. 2) have given an indication that fungal strain from YIC soils have the potential to degrade the hydrocarbons in soil.

Conclusion

This study revealed about the soil fungal diversity and variation in industrially polluted soils. Soil fungal community and diversity was delineated employing the phylogeny. The corollary depicted that PAHs polluted soils backed more diverse fungal communities than the less-polluted soils. Soil fungal community transformations were mainly accommodated by plantation and moisture. This exploration yield data to support our consideration for bioremediation of PAHs contaminated soil applying soil-degrading fungi.

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