

## Abiotic Factors and Microbial Communities Fouling Anion Exchange

### Resin Causing Performance Deficiency in Electric Power Plants

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**D**EMINERALIZATION using ion exchange resin is an important step required for production of ultra-pure water used in high pressure steam generation systems. This resin may get fouled in different ways resulting in loss of its efficiency. Such problem was investigated in Shoubra El-khiema and Damietta power plants in Egypt. Physicochemical analysis of the resin showed decrease in total exchange capacity of the used resin in the two plants. Chemical and microscopical examination revealed fouling by organic matter and iron. Resin scanning using electron microscope showed growth of bacilli bacteria adsorbed on its surface. Epifluorescence stains showed the presence of living microflora on the new resin, as well as living and dead ones on the used resin. Culture on different media revealed the growth of bacteria on nutrient and blood agar, but not on MacConkey's Agar. Fungal growth was observed on Sabouraud dextrose agar and Czapek's dox agar. Eight gram positive bacterial isolates were isolated from the used resin of the two plants, all of them were bacilli. Sequence analysis followed by phylogenetic investigation showed that seven isolates belonged to *Bacillus* sp., whereas one isolate was identified as *Brevibacterium frigoritolerans* CMG M5. The fungal isolates differed in the two plants, and included *Penicillium* sp, *Fusarium* sp, *Aspergillus flavus*, *Aspergillus niger* and *Alternaria* sp.

In conclusion, adequate storage conditions of new resins and efficient water treatment system are needed to maintain the performance of electric power plants.

**Keywords:** Power plants, Water treatment, Anion exchange resin, Fouling, Steam generation.

#### Introduction

Electricity generation using fossil fuel needs almost 150 billion gallons of water/day for steam production and cooling purposes. Water sources with their unique characteristics vary in microbial load, dissolved and suspended solids, and contamination which can cause some difficulties in performance of the power plants. Hence, it is obligatory to use high quality water in order to avoid any potential scaling, fouling, silting and corrosion to keep the efficient performance of these plants. Therefore, water pretreatment- also known as water makeup- became a vital step in order to remove the inherent contaminants in source water (Bagchi et al., 2014).

Ionic impurities can seriously affect the reliability and operating efficiency of a boiler or process system. Overheating caused by the buildup of scale

or deposits formed by these impurities can lead to catastrophic tube failures, costly production losses and unscheduled downtime. Hardness ions such as calcium and magnesium must be removed from the water supply before its use as boiler feed water. For high-pressure boilers, feed water systems and many processes are needed for complete removal of all ions including carbon dioxide and silica. Ion exchange systems are used for efficient removal of dissolved ions from water (Flemming et al., 2007 and Bagchi et al., 2014). Using polymeric organic ion exchange resins for the deionization of water is now a fully mature and developed technology. Modern ion exchange resins are stable high quality products which have made ion exchange a highly reliable process capable of producing high purity deionized water (Xu et al., 2010).

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Ion exchange resins may get fouled in different ways resulting in loss of its efficiency to deliver pure water (Anupkumar *et al.*, 2001). This fouling may be due to iron fouling, organic contaminants or biological fouling (Murthy & Venkatesan, 2009).

Ion exchange resins have a limited capacity for storage of ions on its skeleton (called its exchange capacity). Eventually, it becomes depleted from its desirable ions, and saturated with unwanted ions. It is then washed with a strong regenerating solution containing the desirable species of ions to replace the accumulated undesirable ions. Thus, returning the exchange material to a usable condition (Tchobanglous *et al.*, 2003). Fouling causes short cycle length loading with low exchange capacity. Hence, the resin needs to be regenerated continuously with consumption of chemicals and time as well as loss of electricity.

The present study aimed to investigate fouling of an anion exchange resin used in Damietta and Shoubra El-khiema power plants, where River Nile water is used as water source for steam generation, and to identify the contaminating culturable microbial populations.

## **Materials and Methods**

### *Resin sampling*

One kilogram from each of new and used anion exchange resin were collected at different bed depths in clean sterile bag, remixed and transferred to laboratory at 4°C in ice cold box. Bacteriological analyses were performed within 2-24 h of collection.

### *Physicochemical analysis of resin*

Physicochemical analyses were performed according to the American Society for Testing and Materials (ASTM, 2009) and water treatment hand book (Degrémont, 1973).

*Total moisture holding %:* Each resin has a characteristic water content associated with the functional groups and adhering to the outer surface of the resin particles. This moisture content referred to as moisture holding capacity. Differentiation between wet and dry resins was performed according to the following equations:

Percent solids = Weight of oven dried resin / Weight of resin before drying X100, and percent moisture = 100 - % Solids (ASTM, 2009).

*Total exchange capacity (meq/ml):* The total capacity of a resin sample was calculated according to ASTM (2009).

*Iron fouling:* One hundred grams of the exchange resin were left for 24 h in one liter of 10% HCl at 40°C. The concentration of iron in the aqueous phase was measured using 5-sulfosalicylic acid as an indicator and EDTA as titrate (Degrémont, 1973).

*Organic matter fouling:* One hundred grams of the resin were left in 1L of 10% NaCl and 5% NaOH at 40°C for 24 h. The concentration of organic material in the aqueous phase was measured using KMnO<sub>4</sub> and oxalic acid, and titrated against KMnO<sub>4</sub>. (Degrémont, 1973 and ASTM, 2009).

### *Microscopic examination*

*Anion resin beads* were washed thoroughly with sterilized double distilled water. Two kinds of microscopic examinations were used to show formation of microbial biofilm as follow:

*Epifluorescence microscope:* The new and used resin beads were stained with acridine orange (0.1% solution for 5 min). Photomicrographs were taken according to Anupkumar *et al.* (2001) from both of the crushed resin beads and fouled resin using Zeiss AxioStar Plus model: HBO50 /AC Germany.

*Scanning electron microscope (SEM):* Resin samples were fixed in ice – cold solution of glutaraldehyde (2.5% v/v) in phosphate buffer and refrigerated overnight. The air-dried specimen was then mounted on a copper stub with conducted silver paint. The stubs containing resin sample were coated with a film (about 200 Å) of gold and palladium (60:40) using a vacuum-coating device (Jeol model: JFC-1100 ion sputtering device) and observed in a Jeol model: JSM 5400 scanning electron microscope. (Anupkumar *et al.*, 2001).

### *Microbial analysis*

*Isolation of microorganisms:* Microorganisms in the biofilm found on the surface of an anion exchange resin were isolated according to Katsunori *et al.* (2009). Twenty grams of the resin were mixed with 50 ml sterile saline. After vigorous vortexing for 30 min and overnight incubation (4°C), the mixture was centrifuged (1000 rpm for 5 min), and the resulting supernatant was collected and used as the sample.

One ml from stock saline resin solution was inoculated into different media plates. The plates were incubated at 22°C and 37°C. For culture of bacteria, plate count agar, blood agar, and MacConkey agar were used applying the pour plate method (Vasanthi et al., 2014). The plates were incubated at 22°C for 24- 48 h and at 37°C for 3-5days. Meanwhile, Czapek- dox agar and Sabouraud dextrose agar were used to culture fungi using spread plate method. The plates were incubated at the mentioned temperatures for 3-5days.

#### *Identification and characterization of isolated bacterial and fungal strains from fouled resin*

*Phyotypic identification:* Isolated bacteria (8 isolates that differ in their cultural characteristics) were stained by Gram stain and examined under light microscope (Leica Galen III Germany) to determine their morphology and staining reaction. Isolated fungi (5 isolates) were identified based on cultural and microscopical characteristics according to Watanabe (2002).

*Molecular identification of isolated bacteria:* Since microscopic and staining techniques were insufficient to reveal the taxonomic details of the isolated bacterial strains, sequencing of gene encoding 16S rRNA was applied (Janda et al., 2007).

*Genomic DNA extraction:* Genomic DNA extraction was performed using a pure cultivated bacterium culture by applying InstaGene Matrix (Bio-Rad USA) following the manufacturer.

*PCR- amplification of 16S rRNA gene:* The gene encoding 16s rRNA was amplified by using 2 consensus universal primers set: forward primer 518F (5'- CCAGCAGCCGCGTAATACG-3') and reverse primer 800R (5'- TACCAGGGTATCTAATCC-3') using AmpliTaq® DNA polymerase. Amplification of DNA was carried out under the following conditions: denaturation at 94°C (5 min), followed by 30 cycles. Each cycle consists of 94°C (45 sec), 55°C (60 sec), 72°C (60 sec), and final extension at 72°C (10 min). *E.coli* genomic DNA was used as positive control. The reaction mix without DNA was considered as negative control. The PCR product was purified using Motage PCR Clean up kit (Millipore, USA) following the manufacturer instructions.

*Sequencing:* The purified PCR products (approximately 1500 bp) were sequenced by the Big Dye terminator cycle sequencing kit (Applied BioSystems USA). The products were resolved on an Applied Biosystems model 3730XL automated DNA sequencing system (Applied BioSystems, USA).

*Sequence analysis:* The deduced sequences were subjected to basic local alignment search tool (BLAST) algorithm from the National Centre of Biotechnology Bethesda MD, USA (<http://www.ncbi.nlm.nih.gov>) to retrieve homologous sequences from GenBank.

Sequences that gave high query coverage and maximum identities were selected and aligned. Phylogenetic tree was constructed using ClustalW in MEGA sequence analysis software program version 7.0 (Kumar et al., 2016).

## **Results**

### *Physicochemical analysis of resin*

Results shown in Table 1

#### *Total moisture holding %*

All values of total moisture % for the new and used resins from two plants were within permission limits.

#### *Total exchange capacity (meq/ml)*

The total exchange capacity values of the new resin at the two plants were within the permission range, while the values of used resin at Shoubra plant was at the border and less than the limits at Damietta plant.

#### *Iron fouling*

Whereas iron fouling was absent in the new anion resin, it was unacceptable at the two electric power plants. It was 0.0056 g Fe /kilo anion resin, and 0.224 g Fe /kilo anion resin in Shoubra El-Khiema and Damietta plants, respectively.

#### *Organic matter fouling*

Fouling with organic matter was only detected in the used resin in the two electric power plants. In Shoubra El-Khiema resin, it was 0.553g as KMnO<sub>4</sub>/kilogram anion resin, whereas in Damietta resin it was 17.6 g as KMnO<sub>4</sub>/kilogram anion resin.

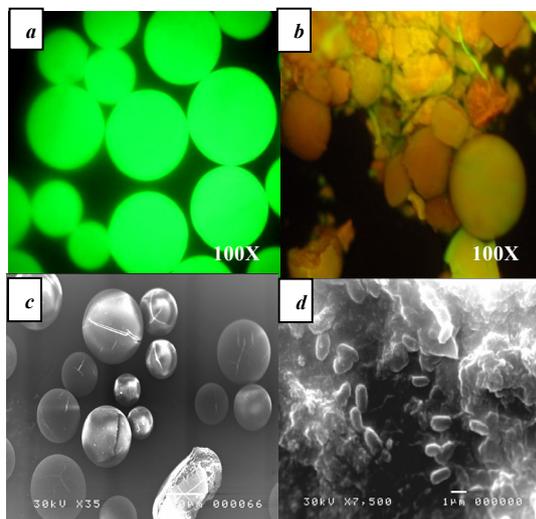
**TABLE 1. Properties of the new and used ion exchange resins in Shoubra El-Khiema and Damitta electric power plants.**

| Description  | Shoubra El-Khiema plant                    |  |  | Damitta plant                                  |  |  |
|--|--|--|--|--|--|--|
|  | Standard specification                     | New resin                                  | Used resin                                     | Standard specification                         | New resin                                      | Used resin                                     |
| Physical form  | Pale yellow translucent spherical beads    | Pale yellow translucent spherical beads    | Brownish spherical beads                       | Cream coloured opaque beads                    | Cream coloured opaque beads                    | Brown coloured opaque beads                    |
| Matrix   | Styrene divinylbenzene copolymer clear gel | Styrene divinylbenzene copolymer clear gel | Styrene divinylbenzene copolymer Brownish gel  | Polystyrene homoporous / microporous structure | Polystyrene homoporous / microporous structure | Polystyrene homoporous / microporous structure |
| Total moisture holding % (Cl <sup>-</sup> form)      | 49 -55                                     | 50%  | 49%  | 50-55%   | 54%  | 51.9%  |
| Total exchange capacity meq/ml(Cl <sup>-</sup> form) | >1.3                                       | 2.13                                       | 1.3  | >1.3   | 1.4  | 0.98   |
| Iron fouling   | Not present                                | 0.0  | 0.0056g Fe / kilo anion resin                  | Not present                                    | 0.0  | 0.224 g Fe / kilo anion resin                  |
| Organic matter fouling                               | Not present                                | 0.0  | 0.553g as KMnO <sub>4</sub> / kilo anion resin | Not present                                    | 0.0  | 17.6 g as KMnO <sub>4</sub> /kilo anion resin  |

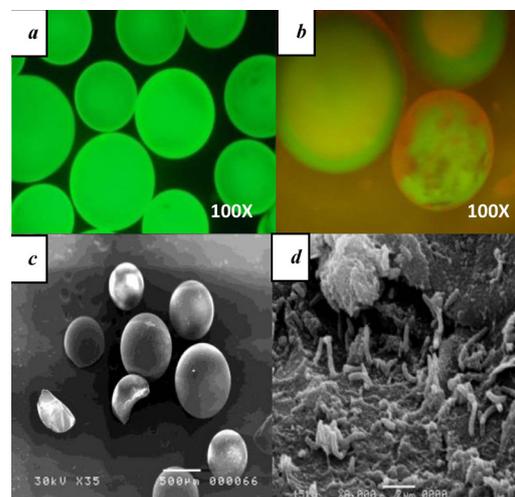
Resin used in Shubra plant (AMBER LITE IRA 402Cl, with recommended flow rate 8-40 BV/h).

Resin used in Damitta plant (DUOLITE A101 D, with recommended flow rate 5-40 BV/h).

1BV (bead volume)= 1m<sup>3</sup> solution/m<sup>2</sup> resin.



**Fig. 1.** Microscopical examination of anion exchange resin from Damitta power plant Epifluorescence photomicrographs of a; the new anion resin b; of the fouled anion resin showed green color due to viable microorganisms and orange color due to dead ones. SEM photographs of: c; the fouled anion resin sample showed cracks, d; Bacilli bacteria presented inside the matrix and appeared on the surface after enrichment.



**Fig. 2.** Microscopical examination of anion exchange resin from Shoubra El khiema power plant Epifluorescence photomicrographs of a; the new anion resin b; of the fouled anion resin showed green color due to viable microorganisms and orange color due to dead microorganisms SEM photographs of c;the fouled anion resin sample showed fractures of the resin beads; d; Bacilli bacteria presence inside the matrix and appeared in the pits surface after enrichment.

*Microscopic examination**Epifluorescence microscope*

Whereas staining with acridine orange showed green color with the new anion resin, it showed deep green and orange colors in the used resins from the two plants (Fig. 1 and 2).

*Scanning electron microscope (SEM)*

The SEM photographs of used resin of Shoubra El-Khiema and Damietta showed entangled resin bead with fractured pitted rough surface. Moreover, growth of bacilli bacteria was observed at two plants (Fig. 1 and 2).

*Microbial analysis**Isolation of microorganisms*

The microbial counts of new resin were significantly higher than that of used resin at two electric power plants except for Czapek's dox agar the case is inverted (Table 2). The microbial count of used resin of Damietta electric power plants was higher than that of Shoubra El-Khiema. The counts of bacteria and fungi at 22°C were higher than those at 37°C at two electric power plants anion resin. No growth was found on MacConkey's Agar at the two electric power plants anion resin. The counts of bacteria in plate counts agar were almost higher than at blood agar at two electric power plants anion resin.

*Identification and characterization of isolated bacterial and fungal strains from fouled resin*

*Phyotypic identification:* Eight bacterial strains (aerobic Gram positive bacilli) were isolated from fouled resin. Using Sabouraud Dextrose agar, two fungal isolates (*Penicillium* sp, *Fusarium* sp) were isolated from anion resin of Shoubra El-Khiema. Moreover, four fungal isolates (*Aspergillus flavus*, *Aspergillus niger*, *Alternaria* sp. and *Penicillium* sp.) were isolated from Damietta plant (Fig. 3 and 4).

*Molecular identification of isolated bacteria:* The PCR products (~1500 bp) were purified and sequenced. All positions containing gaps and missing data were eliminated from the data sets. A BLASTN analysis was carried out through GenBank (<http://www.ncbi.nlm.nih.gov>), followed by phylogenetic analysis.

TABLE 2. Count of isolated organisms from anion exchange resin in the two plants using different media (CFU/ml±SD).

|                         | Shoubra El-khiema plant |            |           |           |        |           | Damietta plant |          |           |        |          |           |
|-------------------------|-------------------------|------------|-----------|-----------|--------|-----------|----------------|----------|-----------|--------|----------|-----------|
|                         | 22°C                    |            | 37°C      |           | P      |           | 22°C           |          | 37°C      |        | P        |           |
|                         | new                     | used       | new       | used      |        | new       | used           | new      | used      |        | new      | used      |
| Blood agar              | 19.33±2.62              | 1.48±0.45  | 3.19±0.31 | 0.26±0.04 | 0.001* | 42.0±2.5  | 1.82±0.25      | 8.8±3.35 | 1.20.79   | 0.000* | 8.8±3.35 | 1.20.79   |
| Plate count agar        | 35.52±4.46              | 3.06±1.51  | 38.4±2.04 | 0.21±0.05 | 0.000* | 24.0±1.82 | 12.0±4.37      | 14.8±1.8 | 1.86±0.57 | 0.012* | 14.8±1.8 | 1.86±0.57 |
| Mac-Ckonky agar         | NG                      | NG         | NG        | NG        | NA     | NG        | NG             | NG       | NG        | NA     | NG       | NG        |
| Sabouraud Dextrose agar | 28.0±4.85               | 7.57±29.1  | NG        | NG        | 0.007* | 3.34±0.73 | 6±1.66         | NG       | NG        | 0.128  | NG       | NG        |
| Starch Nitrate agar     | NG                      | NG         | NG        | NG        | NA     | NG        | NG             | NG       | NG        | NA     | NG       | NG        |
| Czapek's dox agar       | 1.28±0.94               | 14.61±3.33 | NG        | NG        | 0.002* | 40±13.67  | 69.0±8.16      | NG       | NG        | 0.034* | NG       | NG        |

NG= no growth, \* = p < 0.05, NA= not applicable

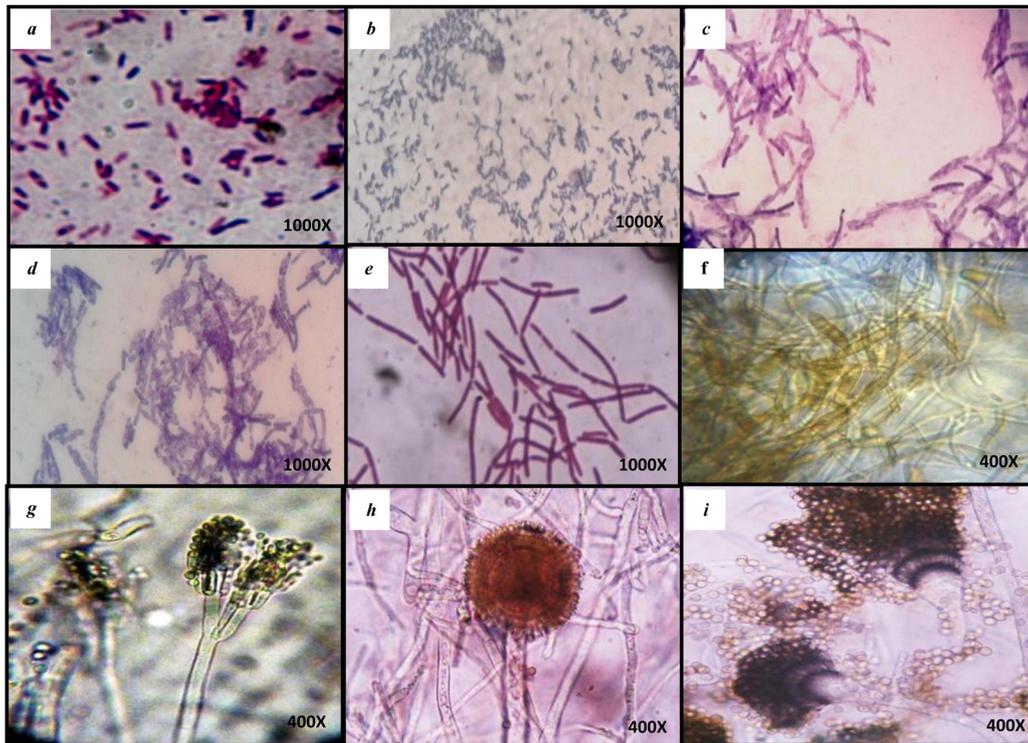


Fig. 3. Microscopic micrograph of the microbial isolates isolated from Damietta fouled anion exchange resin (Bacterial isolates a; BaDB24, b; SH12, c; SH16, d; SH42 and e; SH43. Fungal isolates f; *Alternaria* sp.; g; *Penicillium* sp. h; *Aspergillus niger* and i; *Aspergillus flavus*).

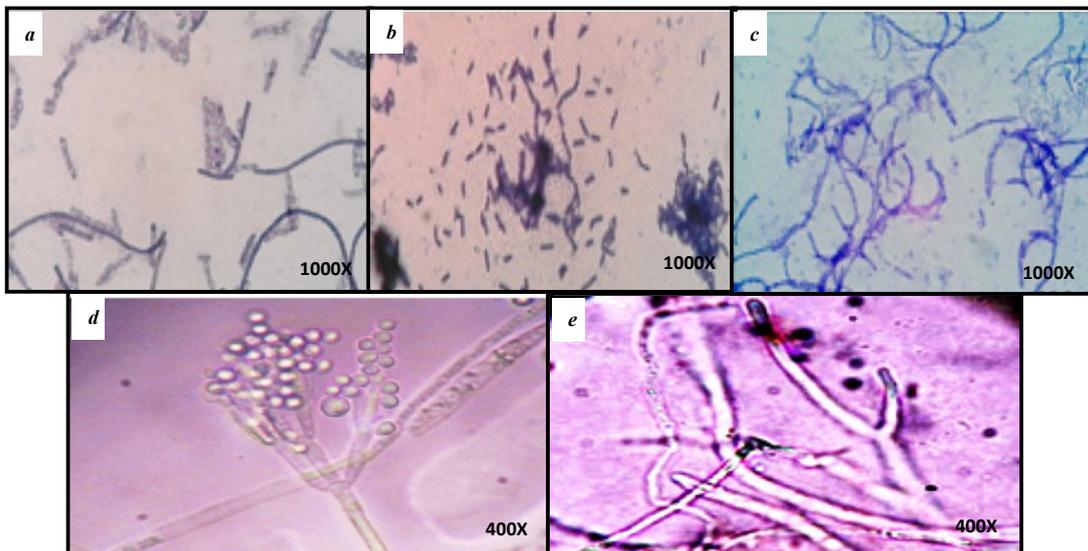
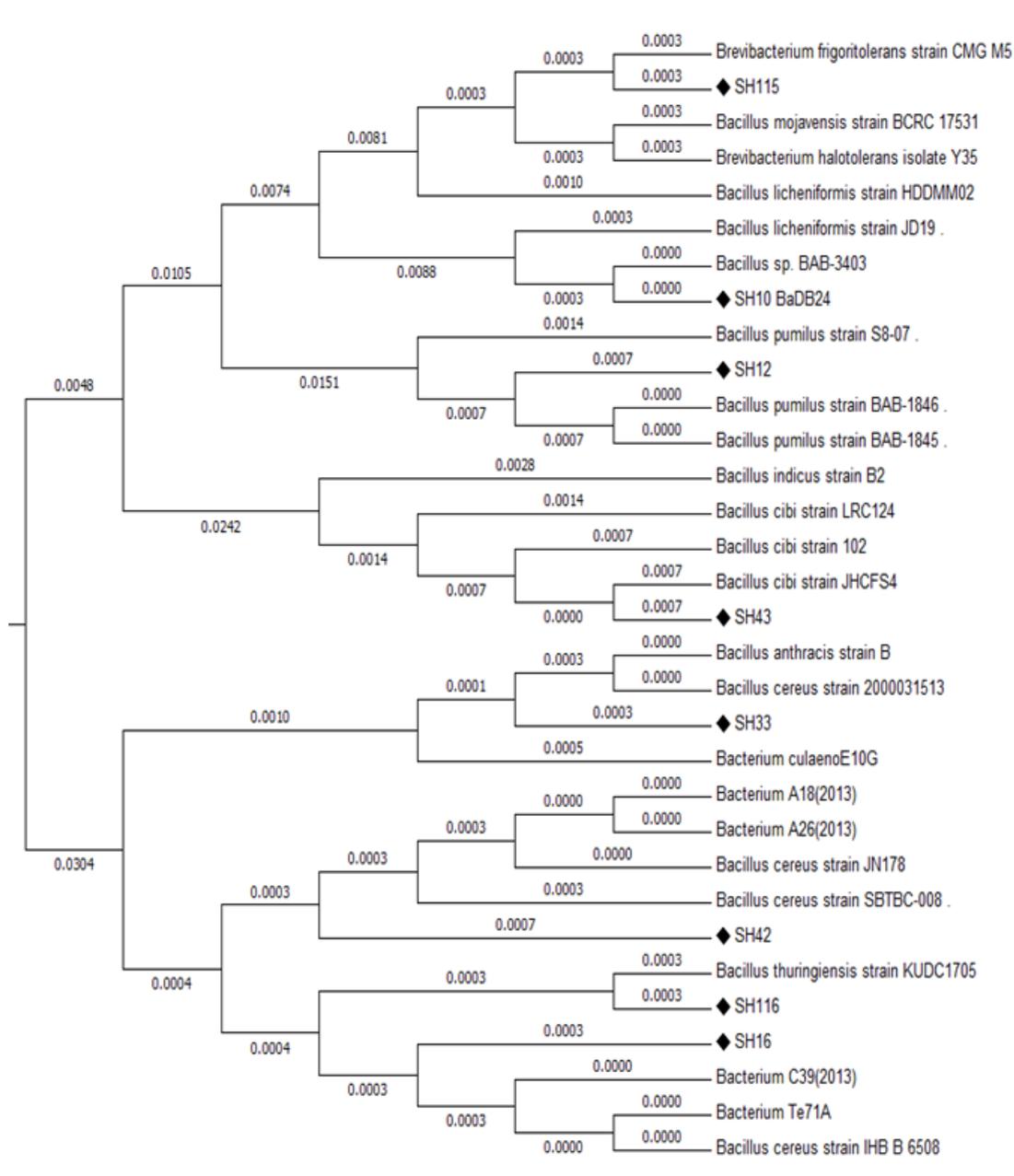


Fig. 4. Microscopic micrograph of the microbial isolates isolated from Shoubra fouled anion exchange resin (Bacterial isolates a; SH33, b; SH115, c; SH116. Fungal isolates d; *Penicillium* sp. e; *Fusarium*).



**Fig. 5. Phylogenetic analysis of eight bacterial isolates (SH10-BaDB24, SH12, SH16, SH33, SH42, SH43, SH115 and SH116) using ClustalW in MEGA 7 program.**

All isolates were related to two different genera. Seven bacterial isolates belonged to the *Bacillus* group and one isolate belonged to *Brevibacterium* (Fig. 5). Sequences of isolated strains were submitted to National Centre for Biotechnology Information (NCBI) with accession numbers indicated in Table 3.

### **Discussion**

Depending on the water quality, ion exchange resins may get fouled in different ways with loss of their efficiency, hence lead to undesirable periods of operational shutdown (Bagchi et al., 2014).

TABLE 3. Accession numbers and Gene bank IDs used to identify bacterial isolates fouling the plants' resins.

| Isolate code (nt)<br>Source<br>Accession no. | Gene Bank ID                                   | Gene Bank Accession no. | Query cover | Identity |
|--|--|-------------------------|-------------|----------|
| BaDB24(1550 )                                | <i>Bacillus sp.</i>                            | KF917134.1              | 97%         | 99%      |
| Damitta                                      | * <i>Bacillus licheniformis s JD19</i>         | JX237858.1              | 96%         | 99%      |
| KJ754933                                     | <i>Bacillus licheniformis</i>                  | JX068661.1              | 96%         | 99%      |
| SH12(1576)                                   | * <i>Bacillus pumilus s BaB-1846</i>           | KF535137.1              | 93%         | 99%      |
| Damitta                                      | <i>Bacillus pumilus strain BaB-1845</i>        | KF535136.1              | 93%         | 99%      |
| KM248380                                     | <i>Bacillus pumilus S8-07</i>                  | EU620415.1              | 93%         | 99%      |
| SH16(1546)                                   | * <i>Bacillus cereus sIHB B6508</i>            | KF601957.1              | 97%         | 99%      |
| Damitta                                      | <i>Bacterium C39(2013)</i>                     | KF114462.1              | 96%         | 99%      |
| KM248381                                     | <i>Bacterium Te71A</i>                         | AY587795.1              | 96%         | 99%      |
| SH33(1553)                                   | <i>Bacillus cereus SBTBC-008</i>               | KF601957.1              | 97%         | 99%      |
| Shoubra                                      | <i>Bacillus anthracis sB</i>                   | HQ200405.1              | 95%         | 99%      |
| KM248375                                     | * <i>Bacillus cereus 2000031513</i>            | AY138279.1              | 95%         | 99%      |
|  | <i>Bacterium culaeno E10G</i>                  | KC484954.1              | 95%         | 99%      |
| SH42(1572)                                   | * <i>Bacillus cereus SBTBC</i>                 | KF601957.1              | 97%         | 99%      |
| Damitta                                      | <i>Bacillus cereus sJN178</i>                  | KF150419.1              | 94%         | 99%      |
| KM248376                                     | <i>Bacterium A18 (2013)</i>                    | KF114414.1              | 94%         | 99%      |
|  | <i>Bacterium A26 (2013)</i>                    | KF114419.1              | 94%         | 99%      |
| 43 SH43(1542)                                | <i>Bacillus cibi s102</i>                      | FJ607434.1              | 95%         | 99%      |
| Damitta                                      | * <i>Bacillus cibi sJHCFS4</i>                 | FJ458438.1              | 95%         | 99%      |
| KM248377                                     | <i>Bacillus indicus sB2</i>                    | GQ304783.1              | 95%         | 99%      |
|  | <i>Bacillus cibi LRC124</i>                    | JF772067.1              | 95%         | 99%      |
| SH115(1558)                                  | * <i>Brevibacterium frigoritolerans CMG M5</i> | EU081510.1              | 95%         | 99%      |
| Shoubra                                      | <i>Brevibacterium halotolerans isolate Y35</i> | KF730751.1              | 94%         | 99%      |
| KM248378                                     | <i>Bacillus mojavensis sBCRC17531</i>          | KF054921.1              | 94%         | 99%      |
|  | <i>Bacillus licheniformis</i>                  | EU723824.1              | 94%         | 99%      |
| SH116(1566)                                  | <i>Bacillus cereus SBTBC</i>                   | KF601957.1              | 97%         | 99%      |
| Shoubra                                      | * <i>Bacillus thuringiensis KUDC1705</i>       | KC414685.1              | 95%         | 99%      |
| KM248379                                     | <i>Bacillus cereus IHBB6508</i>                | KF475854.1              | 95%         | 99%      |

\*Gene bank Isolates that give the most identities with isolate under study.

Physical and chemical analyses of anion exchange resin showed decrease of total exchange capacity of Shoubra El-Khiema and Damietta used anion resin than new resin. Such decrease was beyond the limits, and was greater at Damietta anion resin. In addition to the physical degradation of resin as obtained in our study and as mentioned by Ning (2002), it may be due to fouling of anion resin by organic matter, iron, and/ or microorganisms.

The current study revealed organic fouling at the used anion resin in the two electric power plants which may be due to escaping of coals from carbon filter to columns' resin, as well as humic and fulvic acids came from humic substances found in

soil (humus), hence, indicates an improper water treatment.

The hydrophobic nature of the contaminating surface organics and their strong adsorptive forces, as well as, presence of soluble organics with their relatively high molecular weight can readily block the exchange sites and lead to irreversible loss of exchange capacity as mentioned by Ning (2002) and Ramzan *et al.* (2012).

The current study revealed iron fouling in the used anion exchange resins. Chattopadhyay (2000) found that iron may find its way to the resin bed either as insoluble ( $Fe^{3+}$ ) or soluble forms ( $Fe^{2+}$ ).

The soluble ferrous ions can migrate into the body of the resin beads and become oxidized during the service cycle with conversion to insoluble ferric hydroxide which occupy a large volume that result into internal stress followed by resin cracking. The nutrient rich resin surface due to organic and iron fouling- iron concentration is a limiting factor for microbial growth-increases the opportunity of microbial fouling.

Ultra-pure water accompanied by microbial contamination causes biofouling (Bohus et al., 2010). The presence of microflora on the new resins, as indicated by our results, may be due to bad storage. The need for relatively long period (~ 72 h) for bacteria to grow may indicate its presence in a spore form. Furthermore, the lower microbial counts on used resin can be explained by its intolerance to the demineralization and regeneration conditions. Rokicki (2013) indicated that bacteria, particularly gram-positive, can adhere to resin structure. Besides, the negatively charged nature of the bacterial peptidoglycan layer allowed its accumulation on the used resins with decrease of their the exchange capacity (Sarkar & SenGupta, 2010). The low bacterial counts on the nutrient rich blood agar may reflect its presence in a starved state as reported by Forbes et al. (2007).

In spite of the efficiency of heterotrophic plate count as an indicator for hygienic conditions and the disinfection of any surface, most cells particularly those present in the depth of biofilms, can't multiply on the commonly employed nutrient agars (Yamaguchi et al., 2007). Consequently, the actual biomass can be determined using epifluorescence microscopic analysis (Flemming, 2011 and Simoes et al., 2015).

In several microorganisms "acridine orange" will fluoresce green when they are viable and orange for dead ones due to their leaky membranes (Adams & Moss, 2008). Epifluorescence photomicrographs of Shoubra El-Khiema and Damietta resins indicated microbial contamination. The new anion resins showed green color, whereas the used resins showed deep green and orange colors which mean fouling with viable and dead microorganisms, respectively (Fig. 1 and 2).

In the present study, eight Gram positive bacteria could be isolated (Table 3 and Fig. 3,4). Seven of the isolates found in our study were found to belong to *Bacillus* sp., whereas one isolate was

identified as *Brevibacterium frigiditolerans* (Fig. 5). All isolates were previously identified as biofilm-forming bacteria (Minglu et al., 2011).

*Bacillus* spp. are often detected in drinking water supplies which have been treated and disinfected due to the resistance of its spores to disinfection processes and enhancement of complex colony formation by iron fouling (Pelchovich et al., 2013).

*B. cereus* spores are both highly resistant to a large number of stresses and very hydrophobic molecules and allow them to adhere easily to food processing equipment (Faille et al., 2002). Moreover, they can form biofilms on several substrata (Ryu & Beuchat, 2005). *B. thuringiensis* was known to form biofilms in a low nutrition medium and to be highly resistant to cleaning procedures (Rustan, 2010). The presence of *B. pumilus* among our isolates came in harmony with the reports of Dusane et al. (2010) who isolated the same strain from the surface of titanium coupons immersed in seawater. This bacterium can form extensive biofilms as compared to other species such as *Bacillus licheniformis*, *Pseudomonas* PAO1 and *Pseudomonas aureofaciens*.

One isolate was identified as *Brevibacterium frigiditolerans* which was considered a chlorination resistant organism (Roi et al., 2015), and a biofilm associated organism on metal plates immersed in metal working fluids (Langbein, 2016).

The absence of Gram negative bacteria (no growth was observed on MacConkey agar) in our study may be due to the antagonistic effect of *B. cereus* and/ or the improper pH of the regeneration process.

The ability of fungi to attach to a surface and/ or to one another and to be enclosed within an exo-polymeric substance (EPS) is sufficient to fit the basic criteria of a microbial biofilm (Ramag et al., 2011). The isolation of five genera of fungi in our study supported their role in biofilm formation (Fig. 3, 4). Many species in *Fusarium* genus have been reported to grow as biofilms and considered not only a biofilm forming organisms but also pathogenic factors (Peiqian et al., 2014). *Aspergillus* sp. and *Penicillium* sp. were found to be the most frequent molds in treated water in many studies (Yamaguchi et al., 2007 and Virginia & Nelson, 2013). Siqueira & Lima (2012) found that water biofilms of *Penicillium* sp. have specific

hydrophobic hyphae which may be involved in fungal ecological functions.

The hydrophobic nature of *Aspergillus niger* spores leads to surfaces adhesion followed by the initial growth and maturation. Subsequently, the formation of dense well developed biomass with internal channels (Gutierrez-Correa & Villena, 2003). This could explain its role in biofilm initiation and development.

In conclusion, our study revealed that resin fouling is a problem that affects water quality in power plants, and lead to corrosion during steam generation. Regular and more accurate aquatic control measures as well as storage of the unused resin in more adequate conditions may help reduction of resin fouling and increasing efficiency of electric power generation.

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## العوامل الغير حية و المجتمعات الميكروبية الملوثة لوحدة المبادل الأيوني الراتنجي والمؤدية إلى نقص كفاءة محطات توليد الطاقة الكهربائية

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تعد إزالة المعادن باستخدام راتنج التبادل الأيوني خطوة مهمة و مطلوبة لإنتاج المياه عالية النقاوة المستخدمة في أنظمة توليد البخار ذات الضغط المرتفع. و قد يتسبب هذا الراتنج بطرق مختلفة مما يؤدي إلى فقدان كفاءته. وقد تم فحص هذه المشكلة في محطتي شبرا الخيمة ودمياط لتوليد الكهرباء في مصر.

أظهر التحليل الفيزيوكيميائي للراتنج المستخدم في المحطتين انخفاضا في قدرته الكلية على التبادل الألكتروني. كما كشف الفحص الكيميائي والمجهري له وجود تجمع من المواد العضوية والحديد. وعند مسح الراتنج باستخدام المجهر الإلكتروني ظهر وجود تجمعات من بكتريا عسوية و عسوية قصيرة نامية على سطحه. كما أظهر الفحص باستخدام الميكروسكوب فوق الفلوريسنتي وجود ميكروبات حية على الراتنج الجديد وأخرى حية و ميتة على الراتنج المستخدم. وقد كشف عدد البكتريا الحية على المستنبتات المختلفة وجود نمو بكتيري على بيئة الأجار المغذي وبيئة آجار الدم، ولم يلاحظ أي نمو على بيئة ماكونكي. وأخيرا تم ملاحظة نمو فطري على بيئات سبارود وزابكس دوكس. وقد تم عزل ثمانى عزلات بكتيرية متنوعة من كلتا المحطتين جميعهم بكتريا عسوية موجبة لصبغة جرام. و أظهر فحص التتابع النيكلوتيدي لـ (16S rRNA) الحصول على عدد سبع عزلات تنتمي لجنس *Bacillus* و عزلة واحدة تنتمي لجنس بريفي باكتريم (*Breve-bacterium*). اختلفت العزلات الفطرية في المحطتين، وشملت عزلات من جنس البنسليوم ، فيوزاريوم ، أسبرجيلوس ، و ألترناريا.

وخلصت الدراسة إلى أن تخزين الراتنج الجديد في ظروف أكثر إحكاما و زيادة كفاءة نظام معالجة المياه الداخلة لوحدة التبادل الأيوني، قد يؤدي إلى الحفاظ على كفاءة أداء محطات الطاقة الكهربائية و خفض فترات توقفها عن العمل .