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MOLECULAR STUDY TO SOME FUNGI ISOLATED FROM PHONE COVER AND IT'S USERS

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Abstract

60 samples were randomly isolated 30 samples from the cover of a mobile phone and 30 samples from the finger of its users for people from the city of Mosul - Iraq, most of them are pioneers of life sciences, College of Science, University of Mosul, with a ratio of 15 females and 15 males of different ages, occupation, region, type of device, number of hours of use, and the last date taken. Washing the hands and the user's hand, right or left. The results showed that the cover of the mobile device of a female student in the Department of Life Sciences, College of Science, University of Mosul, at the age of 27 years, was contaminated with the fungus Chaetomium globosum, which grew on PDA medium.it was also noticed that the finger of the mobile device was contaminated by a female student in the Department of life Sciences College of sciences, University of Mosul,28 years old with The yeast Meyerozyma caribbica, and these two samples were recorded in the Gen Bank of the National Center for Biotechnology Information NCBI, the fungus was recorded as Chaetomium globosum B-M1 and given an identification number LC723824.1, while the yeast Meyerozyma caribbica was recorded as Meyerozyma caribbica B-M2 and with definition number is LC723825, .By studying the genetic distance and affinity tree of the fungus Chaetomium globosum B-M1 it was observed that it was identical (2.283), while the affinity ratio with the Chinese one was (2.582) and it was genetically far from the Iranian isolate by (2.852). As for the American isolate, there was genetic divergence with the Iraqi local isolate by (3326.), while it was found from the tree of distance and genetic affinity for the yeast Meyerozyma caribbica B-M2 that it was identical by (0.001) with its Japanese counterpart and was genetically far from the Australian isolate by (2.086) . As for the Italian and Dutch isolates there was a genetic divergence with the Iraqi local isolate by (2.304).

Keywords: *Fungi Isolated*, The Mobile Device.

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Introduction

In recent times, the use of mobile phones has spread widely due to the ease of Using applications on them, which made people interested in them .Despite that, they have disadvantages,as the electromagnetic radiation emitted from them causes insomnia, headaches,and memory loss, despite their small size and ease of storing them in different places. They are dangerous because they contain of microbes that live in every part of the mobile phone, and these microbes that thrive on phones, are in contact with other parts of the phone .The human body is like the face,hands and ears,and it can stay on the surface of the phone for weeks[1]. Especially fungi that cause infections in the skin and airways [2]

There are many common fungi that contaminate mobile devices .There searcher [3] studied microbes contaminating mobile phones for,undergraduate students in Benin City, where 5genera of fungi were isolated including *Aspergillus niger*, *Penicillium sp.*, *Mucor* sp.,*Cladosporium sp.*,Isopropyl alcohol and ethanol were used at a concentration of 70%,and it was effective in killing contaminated fungi and getting grid of them by100%.As for their searcher [4], he conducted a similar study of fungi contaminated with mobile phones for 15samples,and the following fungi appeared *Aspergillus orchareus*(19%), *A.flavus*(6%),*A.afternaria*(1%), *A.nigar*(3%), *Penicillium sp.*(2%), *Cladosporium spp.*(10%), *Candida sp.*(2%),*A.fumigatus* (52%) and *Mucor sp.*(2%). There searcher [5] conducted a study on microbes contaminated with mobile phones among employees at the dental school, and the results showed the presence of (53%) Gram-positive bacteria,(2%) Gram-negative bacteria, and (3%)fungi .Environmental factors and hygiene have a significant impact on the number of microbes contaminated with phones .Researcher [6] collected 50 samples from personal and public mobile phones and the results showed the following fungi :*Aspergillus sp*,(32%),*Candida sp* (16%) *Mucor sp.*(43%) and (4%) *rhizopus* which isolation from public mobile phones and the following fungi (12%) *Candida sp.* and (40%).*Mucor sp.* isolating fungi from personal mobile phones,it was found that public mobile phones are more contaminated with fungi more than personal mobile phones. The researcher [7] conducted a study in which there search included the presence of bacteria,fungi and viruses contaminated with mobile phone devices and he found most of study that talked about bacteria and 16 studies on fungi, with a small percentage focused on viruses .The researcher [8] conducted a study on fungi that infect conducted a study in which samples were collected from the hands and rings of health care workers for 28 females and 12 males, and the result was the presence of (16.6%) *Candida sp.*, *Aspergillus flavus* (3.9%), *Aspergillus niger* (3.1%),*Rhodotoryla sp.*(3.9%),From this we infer that mobile phones carry different microbes on their fold sand surfaces that may be transmitted to users and vice versa,depending on the nature of their work,work place,age,gender and number of usage hours Thus,we decided to conduct this study to identify the extent of mobile phone contamination of selected people in the city of Mosul, most of whom are from the Department of life Sciences, College of Science, University of Mosul.

2. Materials and Methods

2.1. Preparation of culture media

2.1.1Potato Sucrose Agar(PSA)medium .PSA medium was used to isolate,diagnose

Preserve and regenerate fungi. Potato extract was prepared with a weight of 200gm of potatoes and boiled to obtain potato extract, and the volume was added to a litter after that,10gm of sucrose and10gm of agar were added to it the Ph of the

medium was adjusted at 5.6 and sterilized at 121°C for 20 minutes, and antibiotics were added and poured in to Petri dishes until use[9]

2.1.2 (Sabouraud Sucrose Agar(SSA) medium .was prepared by weighing 10gm of Pepton,10gm of sucrose and 10gm of agar in a litter of sterile distilled water and put it on the fire until boiling,and the pH of the medium was adjusted at 5.6.And Sterilize at 121°C for 20 minutes, add the antibiotic and pour it in to Petri dishes until use[10]

2.1.3Prepare Normal saline solution. Take the ready-made saline solution manufactured by the Indian company Brussels Laboratories .Pvt.Ltd, which consists of Sodium Chloride (0.9g) per 100ml of sterile distilled water.

2.2.Fungi isolation

collected 30 samples from the cover of the mobile phone and the30 samples from finger of its users these samples belong to 15 females and 15 males which different in(Ages, Region, The jobe especially the pioneers of the Department of Life Sciences /College of Science /University of Mosul, the quality of the device, the number of hours of use the mobile phone, the last time the hands were washed) the samples were taken by wearing sterile gloves and passing the cotton swab mixed with saline in a planned manner [11] on each of the mobile cover and the most used finger. The samples were planted in Petri dishes containing PDA and SDA medium and incubated at 28C° for 3 days, and then the results were taken at a rate of 7,5,3 days.

2.3.Fungal diagnosis.

2.3.1.Diagnosis of fungi externally and microscopically.

Fungi were diagnosed phenotypically based on the color and shape of the colony from the front and reverse sides in the dish and diagnosed microscopically by taking a small amount of the colony and placing it on a glass slideand examined under alight microscope at 40 x power.

2.3.2.Identification of fungi by polymerase chain reaction (PCR) According to the method of Munoz- [12], where the Lyticase enzyme was used to break down the cell wall of the fungus. And as follows:

2.2.2.1..DNA extraction from fungi under study .The ready-made Genomic DNA mini Kit from Geneaid company was used, included the following steps:

1 .Weigh 0.2 g of mushrooms, add liquid nitrogen to it in a ceramic mortar, and grind the mixture

for 3 seconds until it becomes a homogeneous powder.

2 .Transfer the powder to a 1.5ml tube and add 400 µL of GP1 and 5 µL of

of RNase and mixed using a mixing device (Vortex)

3 .Incubate the tube at a temperature of 60 °C for 10 minutes, turning the tube over this period every 3 minutes.

4. Add 100 microliters of GP Buffer solution, mix with a Vortex device, and incubate in

Ice for 3 minutes.

5. Transfer the mixture to a Filter Column and quickly centrifuge for 1 minute g1000 Then the filter tube is discarded and the leachate is transferred into a 1.5 ml tube.

6. Add 1.5 volts of GP3 solution and mix immediately for 5 seconds.

7. Transfer 700 microliters of the solution into a GD Column tube and centrifuge for 2 minutes at maximum speed.

8 .Discard the filtrate and re-install the GD Column to the collection tube.

9. Add 400 µL of solution W1 and centrifuge for 30 seconds at maximum speed.

10. Discard the filtrate and reinstall the GD Column to the collection tube.

11. Add 600 µL of Wash Buffer and centrifuge for 30 seconds

At maximum speed discard the filtrate and then centrifuge for 3 minutes at maximum speed

maximum.

12. Install a GD column in a 1.5ml tube and add 100 microliters of Elution solution to it. Leave for 3 minutes to allow it to bind with the DNA.

13. Centrifugation for 30 seconds at maximum speed discards the GD column and preserves the precipitate At a temperature of 20 C until use.

2.2.2.2DNA extraction from the gel . The bands resulting from the PCR reaction were extracted from the gel purified and sent for testing The sequence of nucleotides,depending on the analysis kit prepared by the company,a microliter of buffer solution DF and mixed using the Vortky device

Gene aid and according to the steps

1.Apacket of agarose gel is cut using a sterile scalpel removing the largest amount of the gel that surrounds the bundle

2.Transfer approximately 300mg of the gel piece to a 1.5ml Eppendorf tube and add 500mg microliters of DF buffer and mix using the Vorteky device.

3.The tube is incubated at a temperature of 550-1600C° for 15 minutes to ensure completeness of the piece of gel with the tube being turned every 3 minutes during the incubation period and the tube is left to cool to a degree room temperature.

4.Transfer 800 microliters of the sample mixture to the DF column installed in the collection tube then centrifuge at 16000g for 30 seconds and the filtrate is discarded.

5- The DF column is re-installed into the collection tube and 600 microliters of solution are added.

Wash and leave for one minute.

6- Perform a centrifuge with the same force, g16000, for 30 seconds and get rid of the filtrate.

7- The previous process is repeated.

8-Centrifugation for 3 minutes to ensure dryness of the DF column.

9- The collection tube is discarded and the DF column is transferred to a new 1.5 ml tube.

10- 50-200 microliters of ellution buffer are added to the center of the column .

11- Leave for two minutes to ensure absorption of the dissolving solution.

12- A g16000 centrifuge for two minutes to obtain the dissolved DNA.

*2.2.2.3.Preparationoftheacarosegelandtheprocessofelectrophoresisfor DNA.*To transfer and detect the DNA the agarose gel is prepared with a concentration of 1% and to obtain this concentration 0.5 g of agarose powder is dissolved in 50ml of X1TBE and 3 microliters of red safe dye are added This is done using a heat source with stirring Continue until boiling and leave to cool to a temperature of 50-60C° Then the gel solution is poured in to the tray of the relay device after installing the wells combat the edges of the gel taking in to account that the pouring is done quietly to avoid the formation of bubbles and if they are formed they are removed using a pipette,then the gel is left until it pours

Thenthetrayisplacedintheelectrophoresisbasincontaininganappropriate

amount of solution X1TBE after which the comb is gently lifted The migration samples are prepared by mixing 5 microliters of the DNA sample with microliters of the loading solution after that the migration device is operated by 3 passing an electric current with a voltage difference of 5 volts /cm and the process takes (1.5-2) hours .Gel Documentation to see the DNA bundles and also the product of the PCR reaction.

2.2.2.4.PCR reactions The concentration of DNA in all study samples is adjusted by dilution with TE Buffer solution to obtain the required concentration for conducting the PCR reactions. It was (50) ng / microliters per sample. As the Master Reaction mixture was prepared for each PCR reaction by mixing the DNA sample and the special initiator for each gene with the components of the Pre-mix inside a 0.2 ml eppendorf tube equipped by the English company Biolapse. The reaction volume was fixed to 20 ml. A microliter of distilled water, and the mixture was discarded in the Microfuge device for a period between (3-5) seconds to make sure that the reaction components were mixed, then the reaction tubes were inserted into the thermo cycler for the purpose of conducting the multiplication reaction using the special program for each reaction, after that the sample was loaded into gel pits The agarose prepared in advance with a concentration of 2%. Adding the evidence with the volumetric DNA ladder prepared by Biolaps in one of the pits, after that the samples are transferred by operating the electrophoresis device for a period ranging between (60-70) minutes, after that the gel is photographed using the Gel Documentation device.

1-Detection of the highly conserved ITS region in fungi using the PCR technique

The presence of the gene was detected in fungal samples (mold) when 4 microliters were added

(100ng) of template DNA and 1µl (10 picompl)of each specific primer gene to the contents of the master mix. As shown in Table (1)

Table (1) The sequence of primers used in the DNA sequence of the ITS gene

Primer	**Sequence**
Forward	TGAATCATCGACTCTTTGAACGC
Revers	TTTCTTTTCCTCCGCTTATTGATAT

After that there action tubes were inserted into the thermotorcycler to conduct the solidarity reaction using the special program for the reaction, as shown in Figure(2).

Figure (2) PCR reaction program for the ITS region of *Chaetomium globosum*.

NO.	Stage	Temperature	Time	Cycle number
1	Initial denaturation	95	5 min.	1
2	denaturation	95	45 sec.	35
3	Annealing	55	1 min.	
4	Extension	72	1 min.	
5	Final extension	72	7 min.	1

2.3.3.Diagnosis of yeasts by polymerase reaction(PCR) According to the method of [13], DNA was extracted from a yeast sample as follows

2.3.3.1.DNA extraction from yeast samples under study. The ready-made Genomic DNA mini Kit from Geneaid company was used included the following steps:

1. A precipitate of yeast grown in a liquid medium, equal to 101 cells, is taken into a tube eppendorf 1.5 ml
2. Add 400 µl of GP1 and 5 µl of RNase to it and mix using a device.

Confusion (Vortex).

3. Incubate the tube at a temperature of 60 °. m for 10 minutes, the tube is stirred during this period every 3 minutes.
4. Add 100 microliters of GP2 Buffer solution, mix with a Vortex device, and incubate in

Ice for 3 minutes.

5. Transfer the mixture to a Filter Column and quickly centrifuge for 1 minute

g1000 Then the filter tube is discarded and the leachate is transferred into a 1.5 ml tube.

6. Add 1.5 volts of GP3 solution and mix immediately for 5 seconds.
7. Transfer 700 microliters of the solution into a GD Column tube and centrifuge

for 2 minutes at maximum speed.

8. Discard the filtrate and re-install the GD Column to the collection tube.
9. Add 400 µL of solution W1 and centrifuge for 30 seconds at maximum speed.
10. Discard the filtrate and reinstall the GD Column to the collection tube.
11. Add 600 µL of Wash Buffer and centrifuge for 30 seconds
11. At maximum speed discard the filtrate and then centrifuge for 3 minutes at maximum speed

maximum.

12. Install a GD column in a 1.5 ml tube and add 100 µl of Elution solution to it.

Leave for 3 minutes to allow it to bind with the DNA.

2.3.3.2.DNA extraction from the gel . The bands resulting from the PCR reaction were extracted from the gel purified and sent for testing The sequence of

the nucleotide sequence, depending on the analysis kit prepared by the company (Geneaid) and according to the steps:

1- The package is cut from the agarose gel using a sterile scalpel, while removing the largest amount of the gel that surrounds the package.

2- Transfer approximately 300 mg of the gel piece to an Eppendorf tube of 5.1 ml and add 500 mg. 1 microliter of DF buffer and mixed using a vortex apparatus.
3 - Incubate the tube at a temperature of 55-60 degrees Celsius for 15 minutes to ensure a complete cut The gel was inverted every 3 minutes during the incubation period and the tube was left to cool down room temperature.
4- Transfer 800 microliters of the sample mixture to the DF column installed in the collection tube, then conduct Centrifuge at 16000 g for 30 seconds and discard the filtrate.
5- The DF column is fixed again to the collection tube and 600 microliters of solution are added.

Wash and leave for one minute.

6-Centrifuge with the same force g16000 for 30 seconds and get rid of the filtrate.
7- The previous process is repeated .

8 - Perform a centrifugation for 3 minutes to ensure the dryness of the DF column
9 - The collection tube is discarded and the DF column is transferred to a new 5.1 ml tube.

10- Add 20-50 microliters of buffer solution to the centre of the column.
11- Leave for two minutes to ensure absorption of the solute solution.
12- Centrifugation for two minutes at g16000 to obtain the dissolved DNA.

2.3.3.3Agarose gel preparation and DNA electrophoresis

To carry over the DNA and detect it, an agarose gel is prepared with a concentration of 1% to obtain this Concentration Dissolve 5.0 gm of agarose powder in (50 ml) of TBE X1 and add 3microliter of safe red dye This is done using a heat source with continuous stirring for a while Boil and leave to cool to a temperature (50-60C°). Then the gel solution is poured into the tray of the relay after the comb is installed For the formation of wells at the edges of the gel, taking into account that the casting be quietly to avoid Bubbles are formed, and if they are, they are removed using a pipette, then the gel is left until it solidifies. Then the tray is placed in the electrophoresis basin containing an appropriate amount of X1 solution TBE after which the metatarsal is gently lifted. Migration samples are prepared by mixing (5) microliters of the sample with (3) microliters of loading solution. After that, the relay device is operated by passing the electric current with a voltage difference (5) volts / cm and the process takes (2-5.1) hours. Then the gel is photographed under ultraviolet rays Ultraviolet rays using a Trans UV illumination gel imager to be able to see bands DNA and the product of the PCR reaction.

2.3.3.4.PCR reactions:

The concentration of DNA in all study samples is adjusted by dilution with TE Buffer solution To obtain the required concentration for PCR reactions, it was (50) ng / microliter per sample. The Reaction Master mixture was prepared for each PCR reaction By mixing the DNA sample and the specific primer for each gene with the components of the mix-master inside the tube of the pen drive Capacity of 2.0 ml and supplied by the English company Biolaps, the reaction volume was fixed to 20 microliter of distilled water, and the mixture is discarded in the Microfuge for a period of (3-5) seconds to make sure From mixing the reaction components, then the reaction tubes were inserted into the thermopolymer device Thermocycler for the purpose of performing the multiplication reaction using the

special program for each reaction, Then the sample was loaded into the pre-prepared agarose gel at a concentration of 2% with the addition of the guide volumetric DCA Ladder supplied by Biolaps company in one of the pits, after that it is transported Samples were cleaned by electrophoresis for a period ranging between (60-70) minutes Then the gel is photographed using a Trans UV illumination device.

1- Detection of the highly conserved ITS region in yeast using PCR technique The presence of the gene was detected in mutant bacteria samples, as 4 microliters were added (100 nanogram) of template DNA and 1 microliter (10 picompl) of each specific primer. Gene to the contents of the master mix As shown in Table (3)

Table (3) The sequence of primers used in the DNA sequence of the ITS gene

Primer	**Sequence**
Forward (ITS1)	TCCGTAGGTGAACCTGCGG
Revers (ITS4)	TCCTCCGCTTATTGATATGC

After that there action tubes were inserted into the thermotorcycler to conduct the solidarity reaction using the special program for the reaction, as shown in Figure(4).

Figure (4) PCR reaction program for the ITS region of *Meyerozyma caribbica*

NO.	**Stage**	**Temperature**	**Time**	**Cycle number**
1	Initial denaturation	95	6 min.	1
2	denaturation	95	45 sec.	35
3	Annealing	58	1 min.	
4	Extension	72	1 min.	
5	Final extension	72	5 min.	1

4. Results and discussion

the tow media (SSA) and(PSA) used for growth of fungi that werw isolated from the mobile phone and finger of its users, wher some fungi grow on (PSA) media as the fungi *Chaetomium globosum* was isolated from the cell phone cover of a female student in the Department of Life Sciences, College of Science, University of Mosul, and by age 27 years- old as shown in Figure (1).

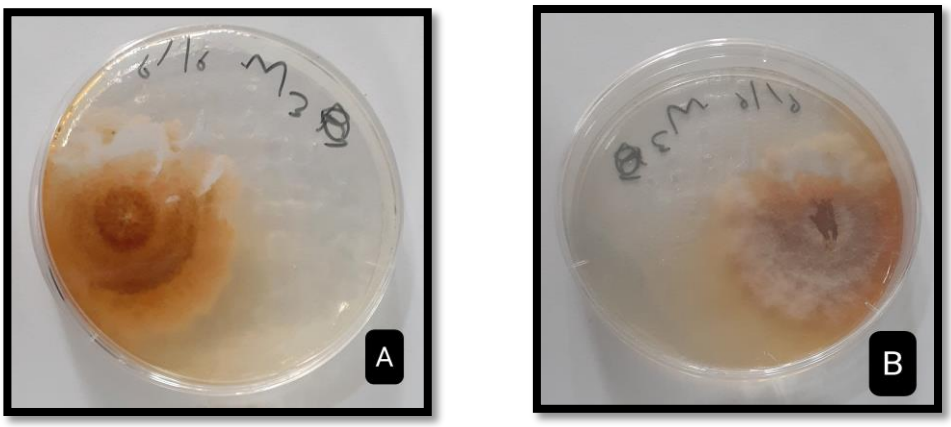

Figure (1) The fungus *Chaetomium globosum* isolated from the cell phone cover of a female student in the Department of Life Sciences, College of Science, University of Mosul, at the age of 27 years. A, the face of the colony, B, the reverse of the dish.

and som yeast was grown on (SSA) media as the yeast *Meyerozyma caribbica* isolated from the finger of a female student in the Department of Life Sciences, College of Science, University of Mosul, as shown in Figure (2).

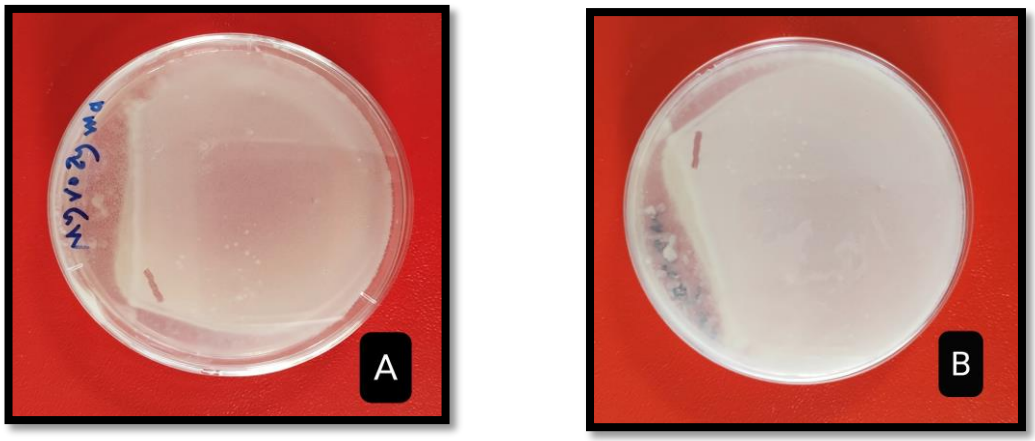

Figure (2) The yeast Meyerozyma caribbica isolated from the finger of a female student in the Department of Life Sciences, College of Science, University of Mosul, A - the face of the dish, B - the reverse of the dish

They were diagnosed externally and microscopically, and then DNA was extracted for both fungi to detect it by PCR method, where it was confirmed that the sample was pure and that the *Ghaetomium globosum* fungus belonged to molds, as shown in Figure (3), where one fluorescent package appeared, and this is evidence that the fungus *Ch. globosum* is pure

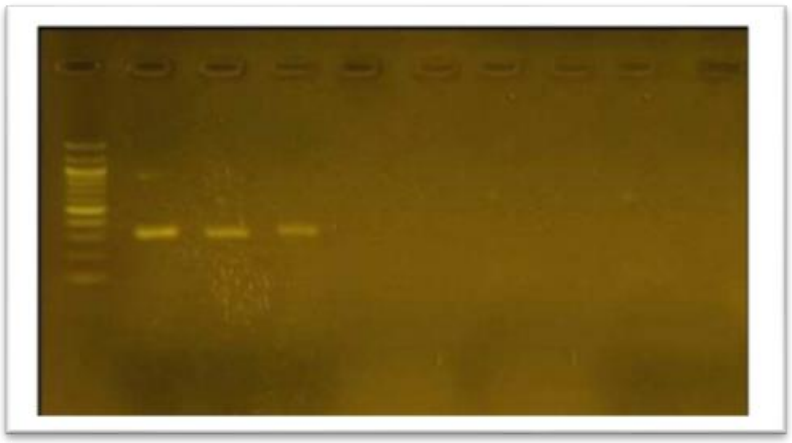

Figure (3) PCR reaction product of *Ghaetomium globosum* studied for the ITS region and a reaction product of 330bp, which was carried over by a 2% agarose gel

The purity of the yeast *Meyerozyma caribbica* was confirmed and that it belongs to the yeasts as shown in Figure (4) Where the figure shows the presence of one package, evidence that the yeast *M. caribbica* is pure.

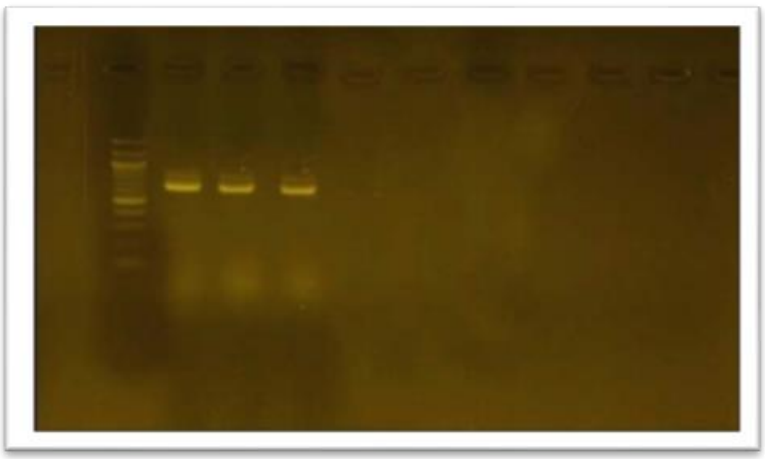

Figure (4) The product of the PCR reaction for a sample of the yeast Meyerozyma caribbica studied in the ITS region.700bp reaction yield which was migrated by 2% agarose gel

The two samples were sequenced to find out their genetic map, as shown in Figures (5) and (6) of the fungus *Chaetomium globosum*

TTCTGGCGGGCNTGCCTGTTCGAGCGTCATTTCA

CCATCAAGCCCCCGGGCTTGTGTTGGGGACCTGCGGCTGCCGCAGGGCCT

GAAAAGCAGTGGCGGGCTCGCTGTCGCACCGAGCGTATTATCATACATCT

CGCTCTGGTCGCGCCCCGGGTTCCGGCCGTTAAACCTCCTTTTTAACCCG

AGGTTGACCTCGGATCAGGTAGGAAGACCCGCTGAACTTAAGCATATCAA

TAAGCGGAGGAAAAGAAAA

Figure (5) ITS region sequences obtained from purified DNA Sequences

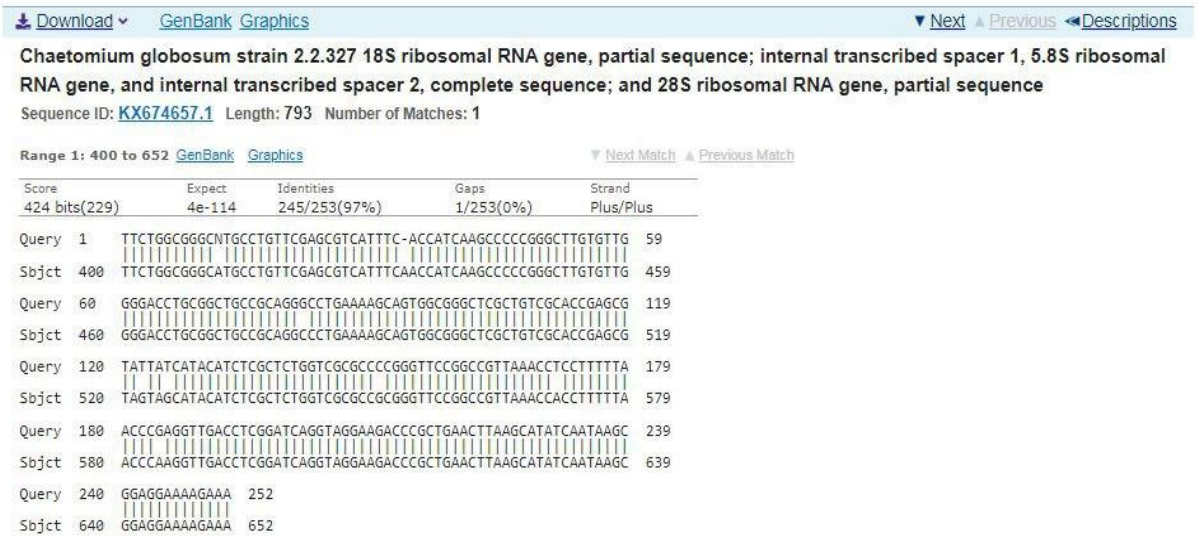

figure (6) Matching the nucleotides of the sample of the mushroom *Ghaetomium globosum* studied with Nucleotides sequenced with mushroom samples at the NCBI sit

Also, the genetic sequencing of the yeast Meyerozyma caribbica was carried out as shown in Figure (7) and (8).

TTCTTTTGCNGCGCTTAACTGCGCGGCGAAAAACCTT

ACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTAGAA

ATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTATTGA

TAGTCAAATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGG

TTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTG

CAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGT

ATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCCCGG

GTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAAAG

TATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAG

GTTTATCCAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGG

CCCGGCCTTACAACAACCAAACAAGTTTGACCTCAAATCAGGTAGGAATA

CCCGCTGAACTTAAGCATATNNNANNAGGNGNGAAGGAAACCCCCNTTTA

AGGGCGGGGGAAAAAAANCTTAAAAAAANGGGNTTTTTTNGGCNAAAATT

TTGCTTTTGTTTNGGCNNAAAAAANGGNGGNNNNNANNTTTNNCAAAACA

CCANTAAAAAAATTTTTTGGGGGGCAAATTTTGGAAAAAATTTNAAAATT

TTNAAACGGGNTTTTNGGTTTCCCCCCCCTTNAAAAACCCCCCNAAGGGG

GAGAANAAAAAAGGGAAATTTTTNGNAANACAAACTTTTAAAGAAATNNC

CCCCC

Figure (7) ITS region sequences obtained from purified DNA Sequences

Meyerozyma guilliermondii strain BEL44 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence

Sequence ID: MT355623.1 Length: 577 Number of Matches: 1

Range 1: 16 to 573 GenBank Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1020 bits(552)	0.0	556/558(99%)	1/558(0%)	Plus/Plus

```
Query  1    TTCTTTTG-CNGCGCTTAACTGCGCGGCGAAAAACCTTACACACAGTGTCTTTTTGATAC  59
            |||||||| | ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  16   TTCTTTTGCCAGCGCTTAACTGCGCGGCGAAAAACCTTACACACAGTGTCTTTTTGATAC  75

Query  60   AGAACTCTTGCTTTGGTTTGGCCTAGAAATAGGTTGGGCCAGAGGTTTAACAAAACACAA  119
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  76   AGAACTCTTGCTTTGGTTTGGCCTAGAAATAGGTTGGGCCAGAGGTTTAACAAAACACAA  135

Query  120  TTTAATTATTTTTATTGATAGTCAAATTTTGAATTAATCTTCAAAACTTTCAACAACGGA  179
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  136  TTTAATTATTTTTATTGATAGTCAAATTTTGAATTAATCTTCAAAACTTTCAACAACGGA  195

Query  180  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  239
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  196  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  255

Query  240  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGC  299
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  256  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGC  315

Query  300  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCCCGGGTTTGGTATTGAGTGATACTCT  359
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  316  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCCCGGGTTTGGTATTGAGTGATACTCT  375

Query  360  TAGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCATGGGTAGTACTGGATAGTGCTGTC  419
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  376  TAGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCATGGGTAGTACTGGATAGTGCTGTC  435

Query  420  GACCTCTCAATGTATTAGGTTTATCCAACTCGTTGAATGGTGTGGCGGGATATTTCTGGT  479
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Query  480  ATTGTTGGCCCGGCCTTACAACAACCAAACAAGTTTGACCTCAAATCAGGTAGGAATACC  539
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  496  ATTGTTGGCCCGGCCTTACAACAACCAAACAAGTTTGACCTCAAATCAGGTAGGAATACC  555

Query  540  CGCTGAACTTAAGCATAT  557
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Sbjct  556  CGCTGAACTTAAGCATAT  573
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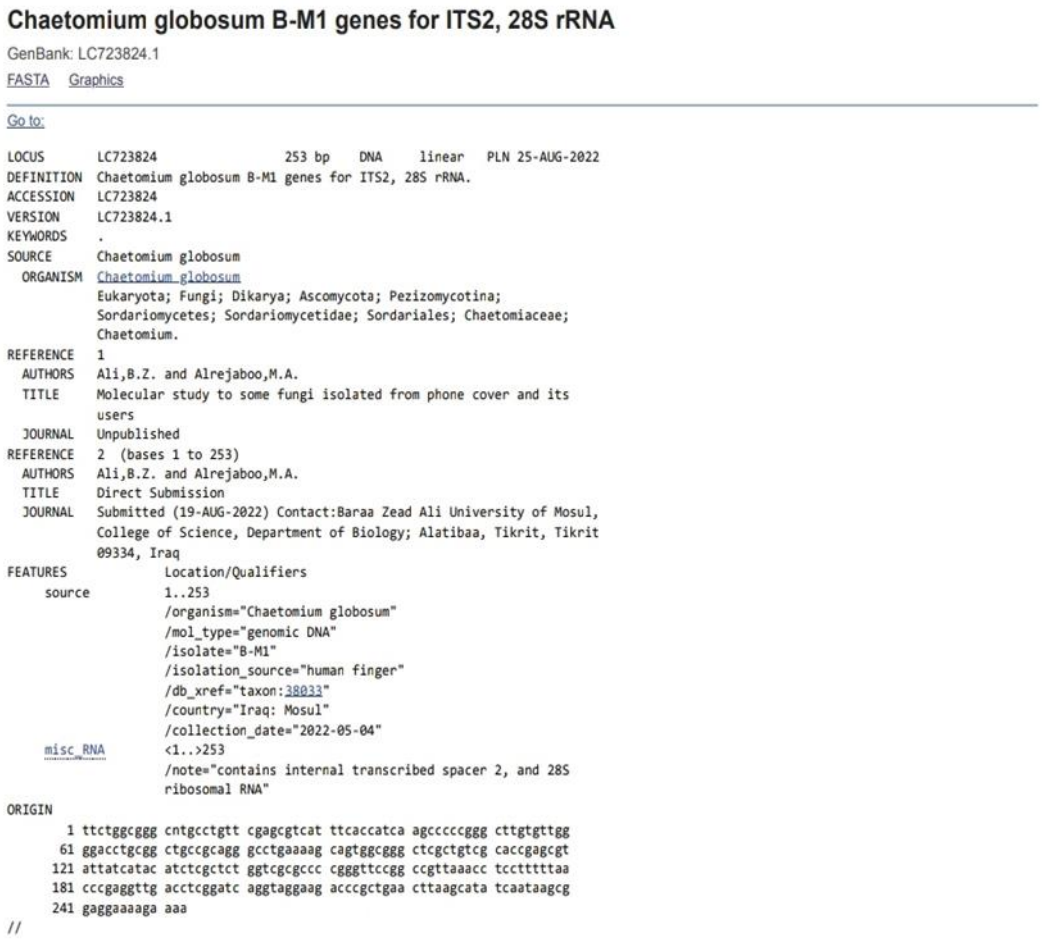
Figure (8) Matching the nucleotides of the yeast sample Meyerozyma caribbica studied with Nucleotides sequenced with yeast samples at the NCBI website.

The results showed that both fungi are genetically heterogeneous for their origins, as shown in the previous figures, and are considered a new record after they were sent to the gene bank at the National Information Center Biotechnology (NCBI) and proven on behalf of the researchers.

the fungus was recorded as *Chaetomium globosum* B-M1, and an identification number was given NCBI LC723824.1, as shown in Figure (9) and (10).



Chaetomium globosum B-M1 genes for ITS2, 28S rRNA

GenBank: LC723824.1

FASTA Graphics

Go to:

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ACCESSION   LC723824
VERSION     LC723824.1
KEYWORDS    .
SOURCE      Chaetomium globosum
  ORGANISM  Chaetomium globosum
            Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;
            Sordariomycetes; Sordariomycetidae; Sordariales; Chaetomiaceae;
            Chaetomium.
REFERENCE   1
  AUTHORS   Ali,B.Z. and Alrejaboo,M.A.
  TITLE     Molecular study to some fungi isolated from phone cover and its
            users
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 253)
  AUTHORS   Ali,B.Z. and Alrejaboo,M.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-AUG-2022) Contact:Baraa Zead Ali University of Mosul,
            College of Science, Department of Biology; Alatibaa, Tikrit, Tikrit
            09334, Iraq
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      181 cccgaggttg acctcggatc aggtaggaag acccgctgaa cttaagcata tcaataagcg
      241 gaggaaaaga aaa
//
```

Figure (9) Registration of a new type of fungus *Chaetomium globosum* B-M1 and an identification number was given NCBI LC723824.1

Chaetomium globosum B-M1 genes for ITS2, 28S rRNA

GenBank: LC723824.1

GenBank Graphics

>LC723824.1 Chaetomium globosum B-M1 genes for ITS2, 28S rRNA
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GGTCGCGCCCCGGGTTCCGGCCGTTAAACCTCCTTTTTAACCCGAGGTTGACCTCGGATCAGGTAGGAAG
ACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAAA

Figure (10) represents the sequence of prefixes recorded from the Fasta site

The yeast was recorded as *Meyerozyma Caribbica* B-M2 and giving an identification number NCBI LC723825.1, as shown in Figures (11) and (12).

Meyerozyma caribbica B-M2 genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2, 28S rRNA

GenBank: LC723825.1

FASTA Graphics

Go to:

```
LOCUS       LC723825               619 bp    DNA     linear   PLN 25-AUG-2022
DEFINITION  Meyerozyma caribbica B-M2 genes for 18S rRNA, ITS1, 5.8S rRNA,
            ITS2, 28S rRNA.
ACCESSION   LC723825
VERSION     LC723825.1
KEYWORDS    .
SOURCE      Meyerozyma caribbica (Candida fermentati)
  ORGANISM  Meyerozyma caribbica
            Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomycotina;
            Saccharomycetes; Saccharomycetales; Debaryomycetaceae; Meyerozyma.
REFERENCE   1
  AUTHORS   Ali,B.Z. and Alrejaboo,M.A.
  TITLE     Molecular study to some fungi isolated from phone cover and its
            users
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 619)
  AUTHORS   Ali,B.Z. and Alrejaboo,M.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-AUG-2022) Contact:Baraa Zead Ali University of Mosul,
            College of Science, Department of Biology; Alatibaa, Tikrit, Tikrit
            09334, Iraq
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                     /collection_date="2022-05-04"
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                     spacer 1, 5.8S ribosomal RNA, internal transcribed spacer
                     2, and 28S ribosomal RNA"
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       61 agcgcttaac tgcgcggcga aaaaccttac acacagtgtc tttttgatac agaactcttg
      121 ctttggtttg gcctagagat aggttgggcc agaggtttaa caaaacacaa tttaattatt
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      601 aagcatatca taaaagtcg
//
```

Figure (11) Recording a new type of yeast *Meyerozyma caribbica* B-M2 and giving an identification number NCBI LC723825.1

Meyerozyma caribbica B-M2 genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2, 28S rRNA

GenBank: LC723825.1

GenBank Graphics

>LC723825.1 Meyerozyma caribbica B-M2 genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2, 28S rRNA
AGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAAC
TGCGCGGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTAGAGAT
AGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTATTGATAGTCAAATTTTGAATTAATCT
TCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT
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AAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCATAAAAGTCG

Figure (12) represents the sequence of prefixes recorded from the Fasta website

The origins of the strain of the fungus Ghaetomium globosum B-M1 were confirmed by conducting a genealogy search for several neighboring countries, including India, China, Iran, and the United States of America, as in Figure (13)

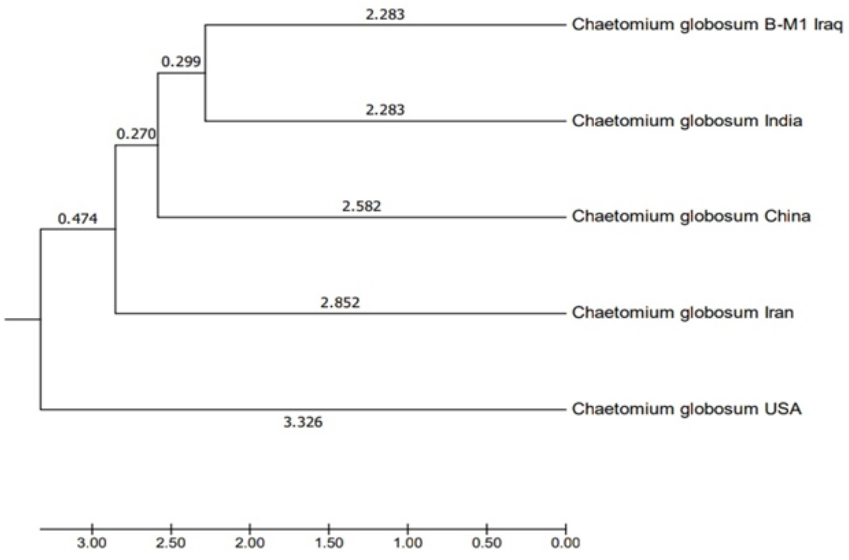

Figure (13) Genetic dimension and affinity tree for *Chaetomium globosum* B-M1 isolate Registered with NCBI.

It was observed that the fungus *Ghaetomium globosum* B-M1 It is identical by (2.283) with its Indian counterpart, while the affinity ratio with the Chinese was (2.582), and it was genetically far from the Iranian isolate by (2.852). As for the American isolate, there was a genetic divergence with the local isolate by (3.326).

The origins of the yeast *Meyerozyma caribbica* B-M2 were also confirmed by making lineages for several neighboring countries, including Japanese, Australian, Italian and Dutch, as shown in Figure (14).

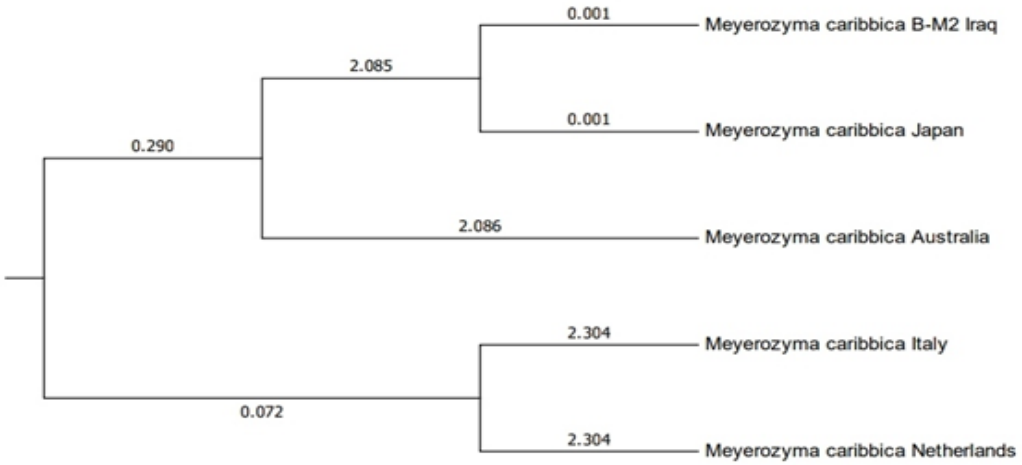

Figure (14) Genetic distance and affinity tree for the yeast isolate *Meyerozyma caribbica* B-M2 Registered with NCBI

It was observed that the yeast *M. caribbica* B-M2 was identical (0.001) with its Japanese counterpart, and was genetically distant from the Australian isolate (2.086). As for the Italian and Dutch isolates, there was a genetic divergence with the local isolate (2.304).

4. Conclusion

1. Clean mobile phones continuously because they are considered a source of pollution, especially after leaving contaminated areas

2. Washing hands after using a mobile phone and after touching objects exposed to microbial contamination

3. Increasing interest in studying fungi contaminated with mobile phones to see the extent of their colonization

5. Reference

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