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Special Issue for Proceeding of 3rd National (1st international conference of biology) (ICBSUM 2021) 5, 6 July College of Education for Pure Science, University of Mosul, Mosul, Iraq.

Molecular Identification of Local Isolated *Streptomyces* Species from North Region soil in Iraq

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Abstract

In this study *Streptomyces* were isolated from 50 bacterial isolates taken from 30 soil samples, these samples were collected from various locations in Iraq's various regions. The species of *Streptomyces* were isolated using starch casein agar and diagnosed microscopically and morphologically by Gram staining and glass slide. The sequence analysis 16S rRNA is used to report 11 *Streptomyces*. 10 bands of DNA gene, a result of specific polymerase chain reaction PCR, are elected from bacterial local isolates where 1000 base pairs within one volume, The PCR products of DNA samples were chosen from 11 local isolates based on nitrogenous base sequences. These organisms are revealed as a result of the study and by using DNA Blast NCBI as fellows; *Streptomyces gancidicus, S. werraensis, S. griseorubens, S. hawaiiensis, S. thermocarboxydus, S. cyaneus, S. misionensis, S. bellus, S. parvulus, S. labedae,*

Keywords: Streptomyces. specific PCR, Sequencing analysis

التشخيص الجزيئي لأنواع Streptomyces المعزولة محلياً من ترب المنطقة الشمالية في العراق

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الخلاصة

تم في هذه الدراسة ، الحصول على 50 عزلة بكتريا من جنس Streptomyces اخذت من 30 عينة تربة، جمعت من مواقع مختلفة من شمال العراق. عزلت العينات باستخدام اكار كازائين – النشأ وشخصت مايكروسكوبياً ومورفولوجياً بواسطة صبغة كرام والشريحة الزجاجية. تحليل التتابع 16 srRNA استخدام اكار كازائين – النشأ وشخصت مايكروسكوبياً ومورفولوجياً بواسطة صبغة كرام والشريحة الزجاجية. تحليل التتابع 16 srRNA استخدام اكار كازائين – النشأ وشخصت مايكروسكوبياً ومورفولوجياً بواسطة صبغة كرام والشريحة الزجاجية. تحليل التتابع 16 srRNA استخدام اكار كازائين – النشأ وشخصت مايكروسكوبياً ومورفولوجياً بواسطة صبغة كرام والشريحة الزجاجية. تحليل التتابع 16 srRNA استخدام الكشف عن 11 عزلة من جنس Streptomyces تم اختيار 10 حزم من المحليمة الزجاجية للتفاعل البوليمري المتسلسل المتخصص، انتخبت العزلات المحلية المعزولة عند 1000 قاعدة نيتروجينية ، تم كشف عن DNA Streptomyces gancidicus, S. يالنحو التالي: S. griseorubens, S. hawaiiensis, S. thermocarboxydus, S. cyaneus, S. bellus, S. parvulus, S. labedae, S. parvulus, S. labedae,

الكلمات المفتاحية: Streptomyces- البوليمر المتسلسل المتخصص - تحليل المتتابع

Introduction

The species of *streptomyces* are widely prevalent in soil, It is the largest genus of the Actinomycetes, Gram-positive bacteria. Their colors mostly are grey but few are red, green, and white, while the blue is the rarest [1]. The genus *Streptomyces* is considered from Actinomycetes diameter (0.5-2) μ m. It is also grown Aerial mycelium carrying many spores, that are arranged in chains and take different shapes, from the spiral form, Rectus- flexibilis form, Retinaculum- Apertum form [2] [3].

The *Streptomyces* genus is the most important species from the group of filaments. The Novel organisms can produce secondary metabolites (Antibiotics) and (Enzyme) production used to control many pathogenic bacteria and their inhibitory impact on harmful microbes [4] [5]. The higher rate of GC is ~70% of the content of *Streptomyces* spp. To separate *Streptomyces* from other bacterial such as Actinobacterial, there are distinguishing features such as 16S rDNA analysis and DNA-DNA hybridization [5] [6]. Geosmin, a scented substance produced by *Streptomyces* is responsible for the distinctive odor of soil.. This research aims to identify and isolate *Streptomyces* from the soil of northern Iraq (Nineveh, Duhok, Erbil) as well as diagnose them using microscopic and morphological experiments and a PCR test based on 16S rRNA to establish their genetic sequence. In addition, DNA Blast NCBI was used.

Materials and procedures

Collecting of Samples

Thirty soil samples were collected from various farm locations in Iraq's northern area, ranging in depth from 5 to 15 cm, and after being collected the samples were treated with calcium carbonate CaCO3 (1:10) and dried at 40-45 °C for four days. The samples were then placed in polyethylene bags and tightly sealed before being placed in the refrigerator until needed. (1 gm) was thoroughly mixed in tubes of 15 ml distilled water, followed by a series of dilutions until the sixth dilution was reached. On it (which was cooled to 45° C), the culture medium (starch-casein medium) was filtered. and 1ml of the last dilution was put in a sterile petri dish. This was done three times per sample. Several solitary colonies were used for re-culture in the same medium for pure culture after the plates were selected with (10-35) colonies [7] [8] [9].

Characteristics of *Streptomyces*

According to Bergy's manual of systematic bacteriology, second edition, the Actinobacteria, Part A [10]. The characteristics of *Streptomyces* are tasted based on the pattern of formation, Gram stain, and colony morphology.

Streptomyces detection

Based on the morphology and color of the colonies, the isolates were known As well as grow on Streptomyces as well as the Tryptone yeast extract glucose Agar, Glycerol Asparagine Agar, and Nutrient Agar. The aerial and medial twigs, as well as the arrangement of spores, were studied using the Slide culture technique [11].

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The media

Starch-casein medium

This medium was made by combining: (10 gm) starch, (0.3 gm) casein, (2 gm) KNO3, (2 gm) NaCl, (0.02 gm) CaCO3, (2 gm) KH2PO4, (0.05 gm) MgSO4.7H2O, (0.01 gm) FeSO4.7H2O, (18 gm) Agar, in 1 liter of distilled water, at a pH of this medium was used in isolation [12].

Tryptone-yeast extract glucose agar

The agar was made by combining (10 gm) glucose, (3gm) yeast extract, (5 gm) tryptone, (1 gm) KH2PO4, (1 gm) K2HPO4, (20 gm) agar in 1 liter distilled water with (7.2) pH, and sterilizing it in an autoclave [13]. This was the medium that was used to make the diagnosis.

Glycerol asparagine agar medium

This medium was prepared by mixing: (1 gm) asparagine, (10 gm) glycerol, (1 gm) K_2HPO_4 , (20 gm) agar, (1 ml) of trace salt solution, (0.64) gm CuSO₄.5H₂O, (0.11 gm) FeSO₄.7H₂O, (0.79 gm) MnCl₂.4H₂O, and (0.15) gm ZnSO₄.7H₂O, in (1 liter) of distilled water with 7.4 pH, The autoclave was used to sterilize items. This medium was used for diagnosis and isolation. [14]

Czapic Dox Agar_Dox agar medium

This medium was made by combining (30) gm sucrose, (3) gm NaNO3, (1) gm K2HPO4, (0.5 gm MgSO4, (0.5 gm KCl), (0.01) gm FeSO4, (15 gm agar) in 1 liter distilled water with a pH of 7.3, and sterilizing everything in the autoclave. [15]. This medium was used to isolate and identify the species.

Nutrient agar medium

This medium was made by melting (23 gm) of nutrient agar in (1 liter) of distilled water with a pH of 7.2 and sterilizing everything in the autoclave, as directed by the supplier company (Lab M Neogen Culture media). This medium was used in the isolation and identification of bacteria.

DNA from Streptomyces purification and acquisition

The DNA from the Streptomyces samples was extracted using Geneaid's kit analysis.

PCR Reactions

The Tri-EDTA (TE buffer) solution was used to fine-tune the DNA concentration in all of the isolated samples in order to achieve the optimal concentration for PCR reactions, and it worked well (50 nanogram per microliter). The master reaction for each PCR reaction was made by combining the DNA sample, the gene's specific primer, and the appender pre-mix in a (0.2ml) Eppendorf tube provided by the British company (bio). Using distilled water, the reaction volume was reduced to 20 microliters, and the components were then combined in a microfuge for (3-5) seconds. After that, the tubes were put in a thermal cycler to perform the polymer reactions, which were regulated by special software for each reaction. After that, the samples were electrophoresed in wells of a 2 percent agarose gel for 60-70 minutes. [3][4][16].

DNA Sequencing analysis

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The most common and important method for detecting single nucleotide polymorphism (SNP) mutations and variations in DNA samples is DNA sequence analysis. On the other hand, the results of PCR reactions are used to determine the sequence of the amplified parts of DNA that will be used to find and study mut. DNA sequencing findings have recently been found to be extremely accurate in identifying mutations [5].

Furthermore, if the PCR reaction yielded more than one strand, it was purified and the desired fragment of DNA was extracted by the gel; however, if the reaction yielded just one strand, it was the main strand, and it was used to evaluate the sequences [17].

Using the method of DNA sequencing to determine the nucleotide sequences of the amplified section

The results of the PCR reaction for the samples mentioned earlier, as well as the primers, were read by a Hitachi 3130 Genetic Analyzer device, indicating that the samples used in the study are diagnosis. The genetic sequence data was linked to the National Center Biotechnology Information NCBI database., The BLAST software was used to examine the findings.

Results and Discussion

Thirty soil samples were collected from various locations in Iraq's northern region, and 50 *Streptomyces* samples were isolated. The samples were chosen based on the colonies' chalky appearance in the media and the wet soil (earthy odor) the smell of rain. [18][19]. The addition of CaCO3 to the soil at a ratio of 1:10 and a temperature of 40-45 0C has a significant impact drying the soil inhibits the growth of vegetative bacteria, and adding CaCO3 raises the pH, inhibiting the growth of fungi, enabling thread-like bacteria (*Streptomyces*) to thrive in the primary isolation [20][21][22].



Figure 1: Morphology colonies of Streptomyces , which isolated aerial

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Figure 2: Streptomyces species isolated ground mycelia



Figure 3:(1) Gram staining of isolated *streptomyces* under 100x magnification. (2,3,4): Glass slide technology

Diagnosis

The slide culturing method was used to diagnose *Streptomyces* samples, which is thought to be one of the best ways (on a genus level) to expose substrate and aerial hyphae, which are the distinguishing features that differentiate thread-like bacteria from one another. [8]

Strongly branched, unsegmented, and spore-free hyphae are present in the substrate. The threads of aerial hyphae are darker, thicker, and less branched than those of substrate hyphae. [3]. The sporophore, which can be erect (rectus), spiral (spiral), straight with a bent end (retinaculum-a cum), or straight with waves (rectus) (rectus-flexibilis), surrounds a long chain of spores in aerial hyphae [23]. When the isolates were cultured on different types of media, they displayed numerous colors, were incapable of forming melanin and other pigments, and the gray-colored colonies were the most visible (figure 1,2,3). These findings are close to those of [18].

Genomic DNA polymer reaction

Under the Geneaid procedure, a particular DNA reaction to Purified DNA was obtained from species collected from local samples.

Forward primer: [AAG CCC TGG AAA CGG GGT] And the revers: [CGT GTG CAG CCC AAG ACA] [17][22]

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Fig.:4: The results of the bacterial samples from the region' basic polymers reaction based on primer 16s rRNA (11) *Streptomyces* isolates

In (Fig. 4) The samples with a similar length (1000 base) pairs generated from the *Streptomyces* reaction DNA-specific polymer show 11 strands of purified DNA. The presence of these strands demonstrates that these isolates' genomic DNA contains shared sequences of nitrogenous bases that can join with the primer and continue the reaction, resulting in new DNA strands of the same length. These findings are similar to those of [23]. As the sequences were obtained from the nitrogenous bases of the DNA samples as follows:

Sample MU1 (Streptomyces gancidicus)

GCCCCCGCGCCTATCAGCTTGTTGGTGAGGTAATGGCTCACCAAGGCGACGACGGGTAGC CGGCCTGAGAGGGCGACCGGCCACACTGGGACTGAGACACGGCCAGACTCCTACGGGAG GCAGCAGTGGGGAATATTGCACAATGGGCCGAAAGCCTGATGCAGCGACGCCGCGTGAGGG ATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGTACCTG CAGAAGAAGCGCCGGCTAACTACGTGCCAGCAGCCGCGGGTAATACGTAGGGCGCGAGCGT TGTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGCCGGGCTAGGGGCGCGAGGCT CGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGTTCGGTAGGGGAGATC GCAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCACGAGGACCCCCGGTGGCGAACCCG GATCTCTGGGCCGATACTG

These sequences were entered into a program DNA BLAST to show their types and how close they are to sequences in the Gene Bank, as the result of the analysis showed a similarity of (99%) between these sequences and the sequences of bacterial isolates registered in the Gene Bank with the number (<u>MT588801.1</u>) Fig. (5).

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Figure: (5) Comparison of sequences of the nitrogen base between the local isolate (MU1) and standard strain (<u>MT588801.1</u>)

Sample MU2 (Streptomyces werraensis)

GGCGCACCCGCGGCCTATCAGCTTGTTGGTGAGGTAATGGCTCACCAAGGCGACGACGGGG AGCCGGCCTGAGAGGGCGACCGGCCACACTGGGGACTGAGACACGGCCAGACTCCTACGG GAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGA GGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGTA CCTGCAGAAGAAGCGCCGGCTAACTCCCCGCCAGCAGCCGCGGTAATACGTAGGGCGCGA GCGTTCCCCCGAATTATTGGGCGTAAAGAGCTCGTAGGCGGCGCTTGTCGCGTCGGTTGTGAA AGCCCGGCCCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGTTCGGTAGGGGAG ATCGGAATTCCTGGTGTAGCGGTGAAATGCGCACATATCAGGAGGAACACCGGTGGCGAA CGCGGATCTCTGGGCCGATACTGACGCTGAGGACCCAAAGCGTGGGGAACCGGAGCC ACATCCCCTGCCACCCCCGCCGCAAACGGCGGGCACTACGTGTGGGGCGACCTTCCCCCC CCCCCCGCCCCCGCTACCCCTTAACCGCCCCCCTGGGGAGTACCGCCCCCAGGC

The result of the program DNA BLAST analysis showed a similarity of (92%) between sequences of bacterial isolates registered in the Gene Bank with the number (<u>MN179978.1) Fig. (6)</u>

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L Dow	nload	✓ GenBank G	raphics			
Strept	omy	ces werraensis s	train S8-TSB-24 16	S ribosomal RNA ger	ne, partia	al sequence
Sequen	ce ID: 1	MN179978.1 Leng	th: 989 Number of Ma	tches: 1		
Range	1: 177	7 to 823 GenBank	Graphics		Vext	Match 🔺 Previous Match
Score 1007 b	its(54	Expect 5) 0.0	Identities 598/648(92%)	Gaps 1/648(0%)	Strand Plus/Plu	us
Query	1	CCCGCGGCCTATCA	GCTTGTTGGTGAGGTAAT	GGCTCACCAAGGCGACGACG	GTAGCCG	60
Sbjct	177	CCCGCGGCCTATCA	SCTTGTTGGTGAGGTAAT	GCTCACCAAGGCGACGACG	GTAGCCG	236
Query	61	GCCTGAGAGGGCGA		AGACACGGCCCAGACTCCTAG	GGGAGGC	120
Sbjct	237	GCCTGAGAGGGGCGA	CGGCCACACTGGGACTG	AGACACGGCCCAGACTCCTAC	GGGAGGC	296
Query	121	AGCAGTGGGGAATA	TGCACAATGGGCGAAAG	CTGATGCAGCGACGCCGCG	GAGGGAT	180
Sbjct	297	AGCAGTGGGGGAATA	ttocacaatooocoaaao	CTGATGCAGCGACGCCGCG	GAGGGAT	356
Query	181	GACGGCCTTCGGGT	TGTAAACCTCTTTCAGCA	GGAAGAAGCGAAAGTGACG	TACCTGC	240
Sbjct	357	GACGGCCTTCGGGT	tgtaaacctctttcagca	GGAAGAAGCGAAAGTGACGO	TACCTGC	416
Query	241	AGAAGAAGCGCCGG	TAACTNNNNGCCAGCAG	CCGCGGTAATACGTAGGGCG	GAGCGTT	300
Sbjct	417	AGAAGAAGCGCCGG	ĊŦĂĂĊŦACGŦĠĊĊĂĠĊĂĠ	cccccctatatacctacccc	ĠĂĠĊĠŦŦ	476
Query	301	NNNNNGAATTATTG	GCGTAAAGAGCTCGTAG	GCGGCTTGTCGCGTCGGTTG	GAAAGCC	360
Sbjct	477	GTCCGGAATTATTG	GCGTAAAGAGCTCGTAG	******	GAAAGCC	536
Query	361	CGGNNNTTAACCCC	GGGTCTGCAGTCGATACG	GCAGGCTAGAGTTCGGTAG	GGAGATC	420
Sbjct	537	ĊĠĠĠĠĊŦŦĂĂĊĊĊĊ	sőgtétésékétégétésétésé	SGCAGGCTAGAGTTCGGTAGO	GĠĠĂĠĂŦĊ	596
Query	421	GGAATTCCTGGTGT	AGCGGTGAAATGCGCANA	TATCAGGAGGAACACCGGTGC	CGAANGN	480
Sbjct	597	GGAATTCCTGGTGT	AGCGGTGAAATGCGCAGA	TATCAGGAGGAACACCGGTGG	scgaagc	656
Query	481	GGATCTCTGGGCCG	ATACTGACGCTGAGGANNI	VAAAGCGTGGGGGANCGAACAC	GATNANA	540
Sbjct	657	ĠĠĂŦĊŦĊŦĠĠĠĊĊĠ	ATÁCTGÁCGCTGÁGGÁGCO	SÁAAGCGTGGGGGAGCGAACAG	GÁTTÁGÁ	716
Query	541	TNCCCTGNNANNNCI	VCGCCGNAAACGGNGGGC	ACTANGTGTGGGGGGACNTTCC		600
Sbjct	717	TACCCTGGTAGTCC	ACGCCGTAAACGGTGGGC	ACTAGGTGTGGGGGGGACATTC	ACGTCGT	776

Figure: (6) Comparison of sequences the nitrogen base between the local isolate (MU2) and standard strain (MN179978.1)

Sample MU3 (Streptomyces griseorubens)

GTGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATGGCTCACCAAGGCGACGACG GGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTA CGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCG TGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACG GTACCTGCAGAAGAAGCGCCGGCTAACTACGTGCCAGCAGCGCGCGGTAATACGTAGGGCG CGAGCGTTGTCCGGAATTATTGGGCGTAAACGTGCCAGCAGCCGCGGTAATACGTAGGGCG CGAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGTTCGGTAGG GGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGG CGAAGGCGGATCTCTGGGGCCGATACTGACGCTGAGGGGAGCGAAAGCGTGGGGAGCGAACAG GATTAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGGCACTAGGTGTGGGCGACATTCCA CGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCGCCTGGGGAGTACGGCCGCAAGGCT AAAACTCAAAGGATTTGACGGGGGCCCGCACAAGCGGCGGAGCATGTGGCTTAATTCGAC GCAACGCGAAGAACCTTACCACGGCTGACATACACCGGAAGAGGCCCCCTTGCCGCCG GCGACCGGCGCCCATCGGTCAGCTCCCGTCGCGAGCCGCTGGGTTAAGTCCGCAACCAGCG CGAACGCGAAGAACCTTACCACGCTTGACATACACCGGAAAGAGGCCCCCTTGCCGCCG GCGACCGGCGCCCATCGGTCAGCTCCCGTCGCGAGCCGCTGGGTTAAGTCCGCAACCAGCG CACCCTTG

The result of the program DNA BLAST analysis showed a similarity of (99%) between sequences of bacterial isolates registered in the Gene Bank with the number (<u>MT525003.1) Fig. (7)</u>

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strept	omy	ces griseorub	ens strain	K5 16S ribos	omal RNA ge	ene, partia	l sequ	lence
equen	ce ID:	41525003.1 Le	ingth: 1286	Number of Mat	ches: 1			
lange	1: 164	to 927 GenBar	nk Graphics			1	V Next I	Match A Previous Matc
5core 1391 b	its(75	Exp 3) 0.0	ect Ident 759/	ities 764(99%)	Gaps 0/764(0	%) F	strand Plus/Plu	IS
uery	8	GATGAGCCCGCG	GCCTATCAGC	TTGTTGGTGAGG	TAATGGCTCACC	AAGGCGACGA	CGGG	67
bjct	164	GATGAGCCCGCG	GCCTATCAGC	TGTTGGTGAGG	TAATGGCTCACC	AAGGCGACGA	CGGG	223
Jery	68	ТАБССБЕСТБА	GAGGGCGACC	GGCCACACTGGG	ACTGAGACACGG	CCCAGACTCC	TACG	127
bjct	224	TAGCCGGCCTGA	GAGGGCGACC	GGCCACACTGG	ACTGAGACACGG	CCCAGACTCC	TACG	283
uery	128	GGAGGCAGCAGT	GGGGAATATT	GCACAATGGGCG	AAAGCCTGATGC	AGCGACGCCG	CGTG	187
bjct	284	GGAGGCAGCAGT	GGGGAATATT	GCACAATGGGCG	AAAGCCTGATGC	AGCGACGCCG	CGTG	343
uery	188	AGGGATGACGGC	сттерертте	таласстстттс	AGCAGGGAAGAA	GCGAAAGTGA	CGGT	247
bjct	344	AGGGATGACGGC	cttccccttc	TAAAcctctttc	AGCAGGGAAGAA	GCGAAAGTGA	CGGT	403
Juery	248	ACCTGCAGAAGA	AGCGCCGGCT	AACTACGTGCCA	GCAGCCGCGGTA	ATACGTAGGG	CGCG	307
bjct	404	ACCTGCAGAAGA	AGCGCCGGCT	AACTACGTGCCA	GCAGCCGCGGTA	ATACGTAGGG	CGCG	463
luery	308	AGCGTTGTCCGG	AATTATTGGG	CGTAAAGAGCTC	GTAGGCGGCTTG	TCACGTCGGT	TGTG	367
bjct	464	AGCGTTGTCCGG	AATTATTGGG	CGTAAAGAGCTC	GTAGGCGGCTTG	TCACGTCGGT	toto	523
uery	368	AAAGCCCGGGGGC	TTAACCCCGG	GTCTGCAGTCGA	TACGGGCAGGCT	AGAGTTCGGT	AGGG	427
bjct	524	AAAGCCCGGGGGC	TTAACCCCGG	GTCTGCAGTCGA	TACGGGCAGGCT	AGAGTTCGGT	AGGG	583
uery	428	GAGATCGGAATT	CCTGGTGTAG	CGGTGAAATGCG	CAGATATCAGGA	GGAACACCGG	TGGC	487
bjct	584	GAGATCGGAATT	ccteetetae	CGGTGAAATGCG	CAGATATCAGGA	GGAACACCGG	TGGC	643
uery	488	GAAGGCGGATCT	CTGGGCCGAT	ACTGACGCTGAG	GAGCGAAAGCGT	GGGGAGCGAA	CAGG	547
bjct	644	GAAGGCGGATCT	CTGGGCCGAT	ACTGACGCTGAG	GAGCGAAAGCGT	GGGGAGCGAA	CAGG	703
luery	548	ATTAGATACCCT	GGTAGTCCAC	GCCGTAAACGGT	GGGCACTAGGTG	TGGGCGACAT	TCCA	607
bjct	704	ATTAGATACCCT	GGTAGTCCAC	GCCGTAAACGGT	GGGCACTAGGTG	TGGGCGACAT	tcca	763

Figure: (7) Comparison of sequences the nitrogen base between the local isolate (MU3) and standard strain (<u>MT525003.1)</u>

Sample MU4 (Streptomyces hawaiiensis)

GGCGGTGCAGGATGAGCCCGCGGGCCTATCAGCTTGTTGGTGAGGTAGTGGCTCACCAAGGC GACGACGGGTAGCCGGCCTGAGAGGGGCGACCGGCCACACTGGGACTGAGACACGGCCAG ACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGA CGCCGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAA AGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACGTGCCAGCAGCCGCGGGAAAGAAGCGAA AGTGACGGCGCGAGCGTTGTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGCGCGGGCTTGTCACGT CGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGTTC GGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACAC CGGTGGCGAAGGCGGATCTCTGGGCCGATAC

The result of the program DNA BLAST analysis showed a similarity of (91%) between sequences of bacterial isolates registered in the Gene Bank with the number (<u>MT36169.1) Fig. (8)</u>

Formon		LC J HCIVVC	illensis str	ain SER1 16S ribos	omal RNA gene,	partial sec	juence	9
Sequen	ce ID:	MT361619	.1 Length:	835 Number of Match	es: 1			
Range	1: 139) to 204 🤤	enBank Gra	aphics		▼ Next I	Match 🛛	Previous Match
Score			Expect	Identities	Gaps	Strand		-
99.0 b	its(53)	1	8e-17	60/66(91%)	0/66(0%)	Plus/Plus		
Query	1	CCGGNGGN	IGCANGATGA	GCCCGCGGCCTATCAGCT	TGTTGGTGAGGNAGNGG		60	
Sbjct	139	cccccc	FGCAGGATGA	GCCCGCGGCCTATCAGCT	TGTTGGTGAGGTAGTGG	GCTCACCAA	198	
Ouerv	61	GGGGAC	66					
A								

Figure: (8) Comparison of sequences the nitrogen base between the local isolate (MU4) and standard strain (<u>MT36169.1)</u>

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Sample MU5 (*Streptomyces thermocarboxydus*)

The result of the program DNA BLAST analysis showed a similarity of (96%) between sequences of bacterial isolates registered in the Gene Bank with the number (<u>KU158245.1) Fig. (9)</u>

🛓 Dow	nload	✓ GenBank G	raphics			
Strept	omyc	es thermocarb	oxydus strain BPS	SEAC5 16S ribosomal	RNA gene	e, partial sequence
Sequen	ce ID: K	U158245.1 Leng	th: 855 Number of M	atches: 1		
Range	1:160	to 738 GenBank	Graphics		▼ Next	Match A Previous Match
Score 931 bit	s(504)	Expect 0.0	Identities 557/582(96%)	Gaps 5/582(0%)	Strand Plus/Plu	us
Query	1	CCCGCGGCCTATCA	GCTTGTTGGTGAGGTAA	TGGCTCACCAAGGCGACGACG	GGTAGCCG	60
Sbjct	160	CCCGCGGCCTATCA	GCTTGTTGGTGAGGTAA	TGGCTCACCAAGGCGACGACG	GGTAGCCG	219
Query	61	GCCTGAGAGGGCGA	CCGGCCACACTGGGACT	GAGACACGGCCCAGACTCCTA	CGGGAGGC	120
Sbjct	220	GCCTGAGAGGGCGA	CCGGCCACACTGGGACT	GAGACACGGCCCAGACTCCTA	CGGGAGGC	279
Query	121	AGCAGTGGGGAATA	TTGCACAATGGGCGAAA	GCCTGATGCAGCGACGCCGCG	TGAGGGAT	180
Sbjct	280	AGCAGTGGGGGAATA	TTGCACAATGGGCGAAA	GCCTGATGCAGCGACGCCGCG	TGAGGGAT	339
Query	181	GACGGCCTTCGGGT	TGTAAACCTCTTTCAGC	AGGGAAGAAGCGAAAGTGACG	GTACCTGC	240
Sbjct	340	GACGGCCTTCGGGT	TGTAAACCTCTTTCAGC	AGGGAAGAAGCGAAAGTGACG	GTACCTGC	399
Query	241	AGAAGAAGCGCCGG	CTAACTACGTGCCAGCA	GCCGCGGTAATACGCACGGCG	CGAGCGTT	300
Sbjct	400	AGAAGAAGCGCCGG	CTAACTACGTGCCAGCA	GCCGCGGTAATACGTAGGGCG	CGAGCGTT	459
Query	301	GTCCGGAATTATTG	GGCGTAAAGAGCTCGTA	GGCGGCTTGTCCCGTCGGTTG	TGAAAGCC	360
Sbjct	460	GTCCGGAATTATTG	GCGTAAAGAGCTCGTA	GCGGCTTGTCGCGTCGGTTG	TGAAAGCC	519
Query	361	CGGGGCTTAACCCC	GGGTCTGCAGTCGATAC	GGCCAGGCTAGAGTTCGGTAG	GGGAGATC	420
Sbjct	520	CGGGGCTTAACCCC	GGTCTGCAGTCGATAC	GGGCAGGCTAGAGTTCGGTAG	GGGAGATC	579
Query	421	GGACTTCCTGGTGT	AGCGGCGAAATGCCCCC	ATATCACGAGGACCCCCCGGT	GGCGAAAG	480
Sbjct	580	GGAATTCCTGGTGT	AGCGGTGAAATGCGCAG	ATATCAGGAGGAACA-CCGGT	GGCGAAGG	638
Query	481	CGGATCTCTGGGGGC	CGATACTGACGCTGAGG	AGCGAAAGCGTGGGGGAGCGAA	CAGGATTA	540
Sbjct	639	CGGATCTCT-GGGC	CGATACTGACGCTGAGG	AGCGAAAGCGTGGGGAGCGAA	CAGGATTA	697
Query	541	CATACCCCTGG-AG	cccc-ccGCCCACGGT	GGGCCCTACGT 580		
Sbjct	698	GATACCC-TGGTAG	TCCACGCCGTAAACGGT	GGGCACTACGT 738		

Figure: (9) Comparison of sequences the nitrogen base between the local isolate (MU5) and standard strain (<u>KU158245.1)</u>

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Sample MU6 (Streptomyces cyaneus)

CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGCAATCTGCCCTGCA CTCTGGGACAAGCCCTGGAAACGGGGTCTAATACCGGATACTGATCATCTTGGGCATCCTT GGTGATCGAAAGCTCCGGCGGTGCAGGATGAGCCGGCGGCCTATCAGCTTGTTGGTGAGGT AATGGCTCACCAAGGCGACGACGGGTAGCCGGCCGGGCGAGGGGCGACCGGCCACACTGGGA CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGA AAGCCTGATGCAGCGACGCCGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAG CAGGGAAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACGTGCCAGC AGCCGCGGTAATACGTAGGGCGCGAGCGTTGTCCGGAATTATTGGGCGTAAACGTCGTA GGCGGCTTGTCGCGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACG GGCAGGCTAGAGTTCGGTAGGGGAGATCGGAATTCTGGGCGTAACTGACGCCGAGA TATCACGAGGAACACCGGTGGCGAAAGCGGATCTCTGGGCCGATACTGACGCTGAGGAGC GAAAGCGTGGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGC ACTAGGTGTGGGCGACATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCGCC TGGGGGAGTACGGCCGCAAGGCTAAAACTCAAA

The result of the program DNA BLAST analysis showed a similarity of (99%) between sequences of bacterial isolates registered in the Gene Bank with the number (<u>KM215731.1</u>) Fig. (10)

🛓 Dow	nload	✓ <u>GenBank</u> Gr	aphics			
Strept	tomy	ces cyaneus stra	in ITD-19 16S ribo	osomal RNA gene, par	tial sequ	ence
Sequen	ce ID: I	(M215731.1 Leng	n: 962 Number of M	atches: 1		
Range	1: 20	to 836 GenBank	raphics		V Next	Match A Previous Match
Score 1498 b	oits(81	1) Expect	Identities 816/818(99%)	Gaps 1/818(0%)	Strand Plus/Pl	us
Query	1	CCTCCTTCGGGAGGG	GATTAGTGGCGAACGGG	TGAGTAACACGTGGGCAATC	GCCCTGC	60
Sbjct	20	CCTCCTTCGGGAGGG	GATTAGTGGCGAACGGG	TGAGTAACACGTGGGCAATC	GCCCTGC	79
Query	61	ACTCTGGGACAAGCC	CTGGAAACGGGGTCTAA	ATACCGGATACTGATCATCTTC	GGCATCC	120
Sbjct	80	ACTCTGGGACAAGCC	CTGGAAACGGGGTCTAA	TACCGGATACTGATCATCTTC	GGCATCC	139
Query	121	TTGGTGATCGAAAGC	TCCGGCGGTGCAGGATG	AGCCCGCGGCCTATCAGCTTC	TTGGTGA	180
Sbjct	140	TTGGTGATCGAAAGC	TCCGGCGGTGCAGGATG	GAGCCCGCGGCCTATCAGCTTC	STTGGTGA	199
Query	181	GGTAATGGCTCACCA	AGGCGACGACGGGTAGC	CGGCCTGAGAGGGCGACCGG	CACACTG	240
Sbjct	200	GGTAATGGCTCACCA	AGGCGACGACGGGTAGC	CGGCCTGAGAGGGCGACCGGC	CACACTG	259
Query	241	GGACTGAGACACGGC	CCAGACTCCTACGGGAG	GCAGCAGTGGGGGAATATTGCA	CAATGGG	300
Sbjct	260	GGACTGAGACACGGC	CCAGACTCCTACGGGAG	GCAGCAGTGGGGGAATATTGC4	ACAATGGG	319
Query	301	CGAAAGCCTGATGCA	GCGACGCCGCGTGAGGG	ATGACGGCCTTCGGGTTGTA	ACCTCTT	360
Sbjct	320	CGAAAGCCTGATGCA	GCGACGCCGCGTGAGGG	GATGACGGCCTTCGGGTTGTA	ACCTCTT	379
Query	361	TCAGCAGGGAAGAAG	CGAAAGTGACGGTACCT	GCAGAAGAAGCGCCGGCTAAG	TACGTOC	420
Sbjct	380	TCAGCAGGGAAGAAG	CGAAAGTGACGGTACCT	GCAGAAGAAGCGCCGGCTAAC	TACGTGC	439
Query	421	CAGCAGCCGCGGTAA	TACGTAGGGCGCGAGCG	TTGTCCGGAATTATTGGGCG1	AAAGAGC	480
Sbjct	440	CAGCAGCCGCGGTAA	TACGTAGGGCGCGAGCG	TTGTCCGGAATTATTGGGCG	TAAAGAGC	499
Query	481	TCGTAGGCGGCTTGT	CGCGTCGGTTGTGAAAG	SCCCGGGGCTTAACCCCGGGT	TGCAGTC	540
Sbjct	500	TCGTAGGCGGCTTGT	CGCGTCGGTTGTGAAAG	SCCCGGGGCTTAACCCCGGGTC	TGCAGTC	559
Query	541	GATACGGGCAGGCTA	GAGTTCGGTAGGGGAGA	TCGGAATTCCTGGTGTAGCGG	TGAAATG	600
Sbjct	560	GATACGGGCAGGCTA	GAGTTCGGTAGGGGAGA	ATCGGAATTCCTGGTGTAGCGC	TGAAATG	619

Figure: (10) Comparison of sequences the nitrogen base between the local isolate (MU6) and standard strain (<u>KM215731.1)</u>

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Sample MU7 (Streptomyces misionensis)

The result of the program DNA BLAST analysis showed a similarity of (97%) between sequences of bacterial isolates registered in the Gene Bank with the number (MT515826.1) Fig. (11)

Ł Dow	nload	✓ GenBan	<u>k</u> <u>Graphic</u>	<u>s</u>			
Strept	omy	ces misioner	isis straii	SA20 16S rib	osomal RNA gen	e, partial sec	quence
Sequen	ce ID: 1	AT515826.1	ength: 143	88 Number of M	atches: 1		
Range	1: 194	to 903 GenB	ank Graph	ics		V Next	Match 🔺 Previous Mate
Score 1242 b	its(67	Ex 2) 0.	pect Io 0 6	entities 91/710(97%)	Gaps 0/710(0%)	Strand Plus/Pl	us
Query	1	AGCCCGCGGCC	TATCAGCT	GTTGGTGAGGTAA	TGGCTCACCAAGGCGA	CGACGGGTAGC	60
Sbjct	194	AGCCCGCGGCC	TATCAGCT	GTTGGTGAGGTAA	TGGCTCACCAAGGCGA	ACGACGGGTAGC	253
Query	61	CGGCCTGAGAG	GGCGACCG	CCACACTGGGACT	GAGACACGGCCCAGAC	TCCTACGGGAG	120
Sbjct	254	CGGCCTGAGAG	GGCGACCG	SCCACACTGGGACT	GAGACACGGCCCAGAC	TCCTACGGGAG	313
Query	121	GCAGCAGTGGG	GAATATTGO	ACAATGGGCGAAA	GCCTGATGCAGCGACG	CCGCGTGAGGG	180
Sbjct	314	GCAGCAGTGGG	GAATATTGO	ACAATGGGCGAAA	GCCTGATGCAGCGACG	GCCGCGTGAGGG	373
Query	181	ATGACGGCCTT	CGGGTTGT	AACCTCTTTCAGC	AGGGAAGAAGCGAAAG	TGACGGTACCT	240
Sbjct	374	ATGACGGCCTT	CGGGTTGT	AACCTCTTTCAGC	AGGGAAGAAGCGAAAG	TGACGGTACCT	433
Query	241	GCAGAAGAAGC	GCCGGCTA	CTACGTGCCAGCA	GCCGCGGTAATACGTA	GGGCGCGAGCG	300
Sbjct	434	GCAGAAGAAGC	GCCGGCTA	ACTACGTGCCAGCA	I I I I I I I I I I I I I I I I I I I	AGGGCGCGAGCG	493
Query	301	TTGTCCGGAAT	TATTGGGC	TAAAGAGCTCGTA	GGCGGCTTGTCACGTC	GGTTGTGAAAG	360
Sbjct	494	TTGTCCGGAAT	TATTGGGCO	TAAAGAGCTCGTA	GGCGGCTTGTCACGTC	GGTTGTGAAAG	553
Query	361	CCCGGGGCTTA	ACCCCGGG	CTGCAGTCGATAC	GGGCAGGCTAGAGTTC	GGTAGGGGAGA	420
Sbjct	554	CCCGGGGGCTTA	ACCCCGGG	CTGCAGTCGATAC	GGGCAGGCTAGAGTTC	GGTAGGGGAGA	613
Query	421	TCGGAATTCCT	GGTGTAGCO	GTGAAATGCGCAG	ATATCAGGAGGAACAC	CGGTGGCGAAG	480
Sbjct	614	TCGGAATTCCT	GGTGTAGCO	GTGAAATGCGCAG	ATATCAGGAGGAACAC	CGGTGGCGAAG	673
Query	481	GCGGATCTCTG	GGCCGATAG	TGACGCTGAGGAG	CGAAANNNTGGGGAGG	GAACAGGATTA	540
Sbjct	674	GCGGATCTCTG	GGCCGATAC	TGACGCTGAGGAG	CGAAAGCGTGGGGAGC	GAACAGGATTA	733
Query	541	NATACNCTGGT	ANTCCACGO	CGTANACGGTGGG	CACTAGGTGTGGGCAA	CATTCCACGTT	600
Sbjct	734	GATACCCTGGT	AGTCCACGO	CGTAAACGGTGGG	CACTAGGTGTGGGCAA	CATTCCACGTT	793

Figure: (11) Comparion of sequences the nitrogen base between the local isolate (MU7) and standard strain (MT515826.1

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Sample MU8 (Streptomyces bellus)

The result of the program DNA BLAST analysis showed a similarity of (99%) between sequences of bacterial isolates registered in the Gene Bank with the number (<u>MT355856.1) Fig. (12)</u>

Ł Dow	nload	✓ <u>GenBank</u> Grap	<u>phics</u>			
Strept	tomy	ces bellus strain S	A312 16S ribosom	al RNA gene, partia	al sequen	ce
Sequen	ce ID:	MT355856.1 Length:	1401 Number of Mat	ches: 1		
Range	1: 16	9 to 818 GenBank G	raphics		V Next	Match 🔺 Previous Match
Score 1175 b	oits(63	Expect 6) 0.0	Identities 643/650(99%)	Gaps 0/650(0%)	Strand Plus/Plu	IS
Query	1	GAGCCCGCGGCCTATCA	AGCTTGTTGGTGAGGTAA	TGGCTCACCAAGGCGACG	ACGGGTAG	60
Sbjct	169	GAGCCCGCGGCCTATCA	AGCTTGTTGGTGAGGTAA	TGGCTCACCAAGGCGACG	ACGGGTAG	228
Query	61	CCGGCCTGAGAGGGCGA	ACCGGCCACACTGGGACT	GAGACACGGCCCAGACTC	CTACGGGA	120
Sbjct	229	CCGGCCTGAGAGGGCGA	ACCGGCCACACTGGGACT	GAGACACGGCCCAGACTC	CTACGGGA	288
Query	121	GGCAGCAGTGGGGAATA	ATTGCACAATGGGCGAAA	GCCTGATGCAGCGACGCC	GCGTGAGG	180
Sbjct	289	GGCAGCAGTGGGGGAATA	ATTGCACAATGGGCGAAA	GCCTGATGCAGCGACGCC	GCGTGAGG	348
Query	181	GATGACGGCCTTCGGGT	TTGTAAACCTCTTTCAGC	AGGGAAGAAGCGAAAGTG	ACGGTACC	240
Sbjct	349	GATGACGGCCTTCGGGT	TTGTAAACCTCTTTCAGC	AGGGAAGAAGCGAAAGTG	ACGGTACC	408
Query	241	TGCAGAAGAAGCGCCGG	<u>SCTAACTACGTGCCAGCA</u>	ĢÇÇĞÇĞĞTAATAÇĞTAĞĞ	ĢÇĢÇĢAĢÇ	300
Sbjct	409	TGCAGAAGAAGCGCCGG	GCTAACTACGTGCCAGCA	GCCGCGGTAATACGTAGG	GCGCGAGC	468
Query	301	GTTGTCCGGAATTATTC	бөөсөтааарарстсета	GGCGGCTTGTCACGTCGG	TTGTGAAA	360
Sbjct	469	GTTGTCCGGAATTATTC	GGCGTAAAGAGCTCGTA	GGCGGCTTGTCACGTCGG	TIGTGAAA	528
Query	361	GCCCGGGGGCTTAACCCC	GGGTCTGCAGTCGATAC	GGGCAGGCTAGAGTTCGG	TAGGGGAG	420
Sbjct	529	GCCCGGGGGCTTAACCCC	CGGGTCTGCAGTCGATAC	GGGCAGGCTAGAGTTCGG	TAGGGGAG	588
Query	421	ATCGGAATTCCTGGTGT	ТАĞÇĞĞTĞAAATĞÇĞÇAĞ	ATATCAGGAGGAACACCG	GTGGCGAA	480
Sbjct	589	ATCGGAATTCCTGGTGT	TAGCGGTGAAATGCGCAG	ATATCAGGAGGAACACCG	GTGGCGAA	648
Query	481	GGCGGATCTCTGGGCCC	GATACTGACGCTGAGGAG	CGAAANNNTGGGGAGCGA	ACAGGATT	540
Sbjct	649	GGCGGATCTCTGGGCCG	GATACTGACGCTGAGGAG	CGAAAGCGTGGGGGAGCGA	ACAGGATT	708
Query	541	ANATACNCTGGTANTCO	ACGCCGTANACGGTGGG	CACTAGGTGTGGGGCAACA	TTCCACGT	600
Sbjct	709	AGATACCCTGGTAGTCC	CACGCCGTAAACGGTGGG	CACTAGGTGTGGGGCAACA	TTCCACGT	768

Figure: (12) Comparison of sequences the nitrogen base between the local isolate (MU8) and standard strain (<u>MT515826.1</u>)

Sample MU9 (Streptomyces parvulus)

GCGCCCCCGCCTATCCCCTTGTTGGTGAGGCAATGGCTCACCAAGGCGACGACGGGTAGC CGGCCTGAGAGGGCGACCGGCCACCCTGGGACTGAGACACGGCCCAGACTCCTACGGGAG GCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGAGGG

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The result of the program DNA BLAST analysis showed a similarity of (93%) between sequences of bacterial isolates registered in the Gene Bank with the number (JX860396.1) Fig. (13)

Coguon	omyc	es parvulus strain Fl	MA_331 16S ribo	somal RNA gene,	partial se	equence
Range	1: 161	to 529 GenBank Graph	nics	103. 1	V Next	Match 🛦 Previous Match
Score 593 bit	s(321	Expect Id 2e-165 3	dentities 45/369(93%)	Gaps 0/369(0%)	Strand Plus/Plu	JS
Query	10	GCCTATCNNCTTGTTGGTG	AGGNAATGGNTCACCA	AGGCGACGACGGGTAGC	CGGNCTGA	69
Sbjct	161	GCCTATCAGCTTGTTGGTG	AGGTAATGGCTCACCA	AGGCGACGACGGGTAGC	CGGCCTGA	220
Query	70	GAGGGCGACCGGCCACNCT	GGGACTGAGACACGGC	CCAGACTCCTACGGGAG	GCAGCAGT	129
Sbjct	221	GAGGGCGACCGGCCACACT	GGGACTGAGACACGGC	CCAGACTCCTACGGGAG	GCAGCAGT	280
Query	130	GGGGAATATTGCACAATGG	GCGAAAGCCTGATGCA	GCGACGCCGCGTGAGGG	ATGACGGC	189
Sbjct	281	GGGGAATATTGCACAATGG	GCGAAAGCCTGATGCA	GCGACGCCGCGTGAGGG	ATGACGGC	340
Query	190	CTTCGGGTTGTAAACCTCT	TTCNNNANGGAAGAAG	CGAAAGTGACGGNACCT	GCAGAAGA	249
Sbjct	341	CTTCGGGTTGTAAACCTCT	TTCAGCAGGGAAGAAG	CGAAAGTGACGGTACCT	GCAGAAGA	400
Query	250	AGCGNCNNCTAACTACGTG	CCAGCAGCCGCGGTAA	TACGTAGGGCGCGAGCG	TTGNNCNN	309
Sbjct	401	AGCGCCGGCTAACTACGTG	CCAGCAGCCGCGGTAA	TACGTAGGGCGCGAGCG	TTGTCCGG	460
Query	310	AATTATTGGGCGTAAAGAG	CTCNTAGGCGGCTTGT	CNCGTCGGNTGTGAAAG	CCCGGNGN	369
Sbjct	461	AATTATTGGGCGTAAAGAG	CTCGTAGGCGGCTTGT	CACGTCGGTTGTGAAAG		520
Query	370	TTANCCCCC 378				
Sbjct	521	TTAACCCCC 529				

Figure: (13) Comparison of sequences the nitrogen base between the local isolate (MU9) and standard strain (JX860396.1)

Sample MU10 (Streptomyces labedae)

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CGTGCCGCAGCTAACGCATTAAGTGCCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTC ACAGGAATTGACGGGGGCCCCGCCCACCCGCCGGACCCTGTGGCTTATTCACGCACACTC CGCT

The result of the program DNA BLAST analysis showed a similarity of (96%) between sequences of bacterial isolates registered in the Gene Bank with the number (<u>JQ647891.1) Fig. (14)</u>

Streptomyces labedae strain SCSAAB0030 16S ribosomal RNA gene, partial sequence Sequence ID: JQ647891.1 Length: 936 Number of Matches: 1 Range 1: 186 to 905 GenBank Graphics V NextMatch & Previous Matches: 1 Score Expect Identities Gaps Strand 1223 bits(662) 0.0 696/723(96%) Gaps Strand Query 1 GAGCCCCGCGCCCTATCAGCTTGTTGGTGAGGTAATGGCTCACCAAGGCGACGAGCGGGTAG 60 Sbjct 186 GAACCCCGCGGCCTATCAGCTTGTTGGTGAGGGAAATGGCTCACCAAGGCGACGAGCGGGCTAG 245 Query 61 CCGGCCTGAGAAGGGCGACCGGCCAACTGGGACACGGCGCGAGCGGGCGAGCGGGCGAGGGGGGAA 245 Sbjct 246 CCGGCCTGAGAAGGGCGAACCGGCCAACTGGGACGGAGCGGGCGAACGGGCCGGGGGGGA 305 Query 121 GGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGCCGCGGTGGGG 305 Sbjct 306 GGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCCAGCGGCGGGGGGGG	L Dow	nload	✓ <u>GenBank</u>	<u>Graphics</u>				
Sequence ID: JQ647891.1 Length: 936 Number of Matches: 1 Range 1: 186 to 905 GenBank Graphics Score Expect Identities 696/723(96%) Gaps 4/723(0%) Plus/Plus 1223 bits(662) 0.0 696/723(96%) Gaps 4/723(0%) Plus/Plus Ouery 1 GAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATGGCTCACCAAGGCGAGCAGGGGGGTAG 60 60 Sbjct 186 GAGCCCGGGGCCTATCAGCTTGTTGGTGAGGTAATGGCTCACCAAGGCGAGCAGGGGGGGG	strept	tomy	ces labedae sti	ain SCSAAB	0030 16S rib	osomal RNA g	gene, partia	l sequence
Range 1: 186 to 905 GenBank Graphics MextMatch Previous Mathematical Strand Score Expect Identifies Gaps Strand 1223 bits(662) 0.0 696/723(96%) 4/723(0%) Plus/Plus Query 1 GAGCCCCGCGGCCTATCAGCTTGTTGGTGGAGGTAATGGCTCACCAAGGGGAGAGGGGGGGG	Sequen	ce ID:	IQ647891.1 Len	gth: 936 Num	ber of Matches:	1		
ScoreExpectIdentifiesGapsStrand1223 bits(662)0.0696/723(96%):4/723(0%)Plus/PlusQuery1GAGCCCGCGGCCTATCAGCTTGTTGGTGGGGGGAATATGGCTCACCAAGGGCGACGACGGCGG60Sbjct186GAGCCCGCGGCCTATCAGCTTGTTGGTGGGGGGAATATGGCTCACCAAGGCGACGACGGCGGGGA245Query61CCGGCCTGAGAGGGCGACCGGCCACACTGGGACCTGAGACCGGCCCAGACCGCCCGGGCAG120Sbjct246CCGGCCTGAGAGGGCGACCGGCCACACTGGGCAAAGCCTGAGACCGGCCCAGACTCCTACGGGA395Sbjct246CCGGCCTGAGAGGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGGCGCCGCGCGGTGAGG386Sbjct396GGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCCGCGTGAGG385Sbjct396GGCAGCAGTGGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGGTGAGG385Sbjct396GGCAGCAGTGGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGGTGGGGAACGGTACC240Sbjct396GATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGCGGAACGGGTGCG386Sbjct326GATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAGCGCGGGTAATACGTAGGGCGCGGGG380Sbjct426TGCAGAAGAAAGCGCCGGGCTAACTACGTGCCAGCAGCCGCGGGTAATACGTAGGGCGGCGGGGGGGG	Range	1: 180	5 to 905 GenBan	Graphics			Vext	Match 🛦 Previous Match
1223 Dits(662) 0.0 696/723(96%) 4/723(0%) Pils/Pils Query 1 GAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATGGCTCACCAAGGCGACGGCGGGGAG 60 Sbjct 186 GAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATGGCTCACCAAGGCGACGGCGACGGGGGAG 245 Query 61 CCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGAGACACGGCCCAGCCCACGGCCCAGCACTCCTACGGGA 120 Sbjct 246 CCGGCCTGAGGAGGGCGACCGGCCACACTGGGACTGAGACACGGCCCAGCGCCGGCGAGC 305 Query 121 GGCAGCAGTGGGGAATATTGCACAATGGCGGAAAGCCTGATGCAGCGACGACCGCGCGTGAGG 380 Sbjct 306 GGCAGCAGTGGGGGAATATTGCACAATGGCGGAAAGCCTGATGCAGCGACGCCGGGTGAGG 365 Query 181 GATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGGAAGAAGCGAAAGCGAAAGTGAAGGTACC 240 Sbjct 366 GATGACGGCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGC 300 Sbjct 426 TGCAGAAGAAGGCCCCGGCTAAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGAGC 485 Query 301 GTTGTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGCGCGGTAATACGTAGGGCGAGC 360 Sbjct 426 TTGCAGAAATATTGGGCGTAAAGAGCTCGTAGGCGGCGGGGTAATACGTAGGGCGAGC 485 Query 301 GTTGTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGGCGGCGCGGCTAAACGGCTGGGAGGAG 420 <td< th=""><th>Score</th><th></th><th>Expe</th><th>ct Identities</th><th></th><th>Gaps</th><th>Strand</th><th></th></td<>	Score		Expe	ct Identities		Gaps	Strand	
Query1GAGCCCGCGGCCTATCAGCTTGTTGGTGGAGGTAATGGCTCACCAAGGCGACGACGACGACGGCTAG60Sbjct186GAGCCCGCGGCCTATCAGCTTGTTGGTGGAGGTAATGGCTCACCAAGGCGACGACGACGACGGCTAG245Query61CCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGAGACTGAGACACGGCCCAGACTCCTACGGGA120Sbjct246CCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGA305Query121GGCAGCAGTGGGGAATATTGCACAATGGCCGAAAGCCTGATGCAGCGACGCCCGCGTGAGG180Sbjct306GGCAGCAGTGGGGAATATTGCACAATGGCCGAAAGCCTGATGCAGCGACGCCCGCGTGAGG365Query181GATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAGCGAAAGTGACGGTACC240Sbjct366GATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAGCGAAAGTGACGGTACC425Query181GATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAGCGAAAGTGACGGTACC425Query241TGCAGAAGAAGCGCCGGCTAACTACGTGCCAGCAGCGGCGGGAAAAGCGAAAGTGAGGGCGCGAGC300Sbjct426GTTGTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGCGTTGTCACGTCGGTTGTGAAA360Sbjct486GTTGTCCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGAAA360Sbjct486GTTGTCCCGGAATTATTGGGCGTAAAGAGCTCGTAGGGCGCAGGCTTGTCACGTCGGTGGGAAG420Sbjct546GCCCGGGGCTTAACCCCGGGTCTGCCACACGCGGCAGGCCTAGCGTTGGTAGGGGGG420Sbjct546GCCCGGGGCTTAACCCCGGGTGGAAATGCGCAGGCAGGCA	1223 0	its(66	2) 0.0	696/723	3(96%)	4/723(0%)	Plus/Plu	us
Sbjet186GAGCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATGGCTCACCAAGGCGACGACGACGGACG	Query	1	GAGCCCGCGGCCT	ATCAGCTTGTTG	GTGAGGTAATGG	GCTCACCAAGGCGA	CGACGGGTAG	60
Query61CCGGCCTGAGAGGGCGACCGGCCACACTGGGCACTGAGACGGCCCAGGCTCCTACGGGA120Sbjct246CCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGAGACCGGCCCAGACTCCTACGGGA305Query121GGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGAGG180Sbjct306GGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACCGCGCGCG	Sbjct	186	GAGCCCGCGGCCT	ATCAGCTTGTTG	GTGAGGTAAŤĠŎ	GCTCACCAAGĠĊĠĂ	CGACGGGTÁG	245
Sbjet246ćććśćććtášáčćśćććáčććáččćáččáčáčáčáčáčáčáčáčáčáčáč	Query	61	CCGGCCTGAGAGG	GCGACCGGCCAC	ACTGGGACTGAG	ACACGGCCCAGAC	TCCTACGGGA	120
Query121GGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGCGAGG180Sbjct306GGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGGGGG365Query181GATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAGCGAAAGTGACGGTACC240Sbjct366GATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAGCGAAAGTGACGGTACC425Query241TGCAGAAAGAAGCGCCGGCTAACTACGTGCCAGCCAGCGGCGGTAATACGTAGGGCGCGAGC300Sbjct426TGCAGAAAGAAGCGCCGGCTAACTACGTGCCAGCAGCGGCGGTATACGTAGGGCGCGAGC485Query301GTTGTCCGGAATTATTGGGCGTAAAAGAGCTCGTAGGCGGCGTGTTGTCACGTGGGTGTGGAAA360Sbjct486GTTGTCCGGAATTATTGGGCGTAAAAGAGCTCGTAGGCGGCGTTGTCACGTCGGTTGTGAAA545Query361GCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGTAGGGCGCAGCCTAGGGGGAG420Sbjct546GCCCGGGGCTTAACCCCGGGGTCTGCAGTCGATACGGGCAGGCTAGAGTTCGGTAGGGGGAG420Sbjct546GCCCGGGGCTTAACCCCCGGGTCTGCAGTCGATACGGCAGGCTAGAGTTCGGTAGGGGAGG420Sbjct546GCCCGGGGCTTAACCCCGGGGTCGCAAGTCGATACGGGCAGGCTAGAGTTCGGTAGGGGGAG420Sbjct546GCCCGGGGCTTAACCCCGGGGTGGAAATGCGCCAGATATCAGGAGGAACACCGGTGGCGAA480Sbjct606ATCGGAATTCCTGGTGTAGCGGTGAAATGCGCCAGATATCAGGAGGAACACCGGTGGCGAA665Query481GGCGGATCCTGGGGCGATACTGACCGCGTGAGAGCGAAACGCGTGGGGAACCGAGGGAACCAGGATT540Sbjct666GGCGGATCCTCGGGCGATACTGACCGCCGAAACGGTGGGGCACTNNN-GTGGGGGAACCAGGATT725Query541AGATACCCTGGTAGCCGCCGAAACGGCGGAAACGGTGGGGCACTNNN-GTGGGCGACNNNNCNNCGT599	Sbjct	246	ĊĊĠĠĊĊŦĠĂĠĂĠĠ	ĠĊĠĂĊĊĠĠĊĊĂĊ	ACTGGGACTGAG	ACACGGCCCAGAC	TCCTACGGGA	305
Sbjct 306 GdCAGCAGCAGCAGCAGCAGAAAAAAAAAAAAAAAAAA	Query	121	GGCAGCAGTGGGG	AATATTGCACAA	TGGGCGAAAGCC	TGATGCAGCGACG	CCGCGTGAGG	180
Query181GATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGTACC240Sbjct366GATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGGAA	Sbjct	306	GGCAGCAGTGGGG	AATATTGCACAA	téééééé	TGATGCAGCGACG	CCGCGTGAGG	365
Sbjct 366 GATGACGGCCTTCGGGCTGAAACCTCTTTCAGCAGGGAAGAAGGAAG	Query	181	GATGACGGCCTTC	GGGTTGTAAACC	TCTTTCAGCAGG	GAAGAAGCGAAAG	TGACGGTACC	240
Query241TGCAGAAGAAGCGCCGGCTAACTACGTGCCAGCAGCCGCGGGTAATACGTAGGGCGCGAGC300Sbjct426TGCAGAAGAGCGCCGGCTAACTACGTGCCAGCAGCCGCGGGGAATACGTAGGGCGCGAGC485Query301GTTGTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGCGGTGTGTGAAAA360Sbjct486GTTGTCCGGAATTATTGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGAAA545Query361GCCCGGGGCTTAACCCCGGGTCTGCAGTCGATAGGGCGGCTAGGGCGGCTGGCGGAGGGGGGG420Sbjct546GCCCGGGGCTTAACCCCGGGTCTGCAGTCGATAGGGCAGGCTAGAGTTCGGTAGGGGAG605Query421ATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAA480Sbjct606ATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAA665Query481GGCGGATCTCTGGGCCGATACTGACGCTGANAGGCGAAAAGCGTGGGGAACACCGGTGGCGAAA665Query481GGCGGATCTCTGGGCCGATACTGACGCTGANAGAGCGCAAAAGCGTGGGGAACAACCGGTGGGGAAC540Sbjct666GGCGGATCTCTGGGCCGATACTGACGCTGANAGAGCGAAAAGCGTGGGGAACAACAGGATT725Query541AGATACCCCGGTAGTAGCCGCGAAAAGGGGGGGCACTNNN-GTGGGCGACNNNNNNGT599	Sbjct	366	GATGACGGCCTTC	GGGTTGTAAACC	TCTTTCAGCAGO	GAAGAAGCGAAAG	TGACGGTACC	425
Sbjct 426 TGCAGAAAGAAGCGCCGGCTAACTACTGCGCGCCGCGCGCG	Query	241	TGCAGAAGAAGCG	CCGGCTAACTAC	GTGCCAGCAGCO	GCGGTAATACGTA	GGGCGCGAGC	300
Query 301 GTTGTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGAAA 360 Sbjct 486 GTTGTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCACGTCGGTTGTGAAA 545 Query 361 GCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGCCAGGCTAGGCTGCGGTTGTGAGAA 545 Sbjct 546 GCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGCCAGGCTAGAGTTGCGATAGGGGAG 605 Sbjct 546 GCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGCAGGCTAGAGTTCGGTAGGGGAG 605 Query 421 ATCGGAATTCCTGGTGTAGCGGTGAAATGCCCAGATATCAGGAGGAACACCGGTGGCGAA 480 Sbjct 606 ATCCGGAATTCCTGGTGTGAGCGGTGAAATGCCCAGATATCAGGAGGAACACCGGTGGCGAAA 665 Query 481 GGCGGATCTCTGGGCCGATACTGACGCTGANAGCGCTAAAGGCAAACACCGGTGGGGAACCAGGATT 540 Sbjct 666 GGCGGATCTCTGGGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAACCAGGATT 725 Query 541 AGATACCCTGGTAGTCGCCGNAAACGGTGGGGCACTNNN-GTGGGCGACNNNCNNCGT 549	Sbjct	426	TGCAGAAGAAGCG	CCGGCTAACTAC	GTGCCAGCAGCO	GCGGTAATACGTA	GGGCGCGAGC	485
Sbjct 486 GTTGTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGCGTGTGCACGGTTGGGAAA 545 Query 361 GCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGCGGCTAGAGCTCGGTAGGGGAG 420 Sbjct 545 GCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGCAGGCTAGAGTTCGGTAGGGGAG 605 Query 421 ATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATACGGCAGGATACCGGGGAACACCGGTGGCGAA 480 Sbjct 606 ATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAAACACCGGTGGCGAAA 665 Query 421 ATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGCAAA 665 Sbjct 606 ATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAAACACCGGTGGCGCAAA 665 Query 481 GGCGGATCTCTGGGCCGATACTGACGCTGANAGCGCTGAAGGCGAAAGCGTGGGGAACAACGGTGGGGAACCAGGATT 540 Sbjct 666 GGCGGATCTCTGGGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT 725 Query 541 AGATACCCTGGTAGTGCCGCGNAAACGGTGGGGCACTNNN-GTGGGCGCACNNNCNNCGT 599	Query	301	GTTGTCCGGAATT	ATTGGGCGTAAA	GAGCTCGTAGG	GOCTTOTCACOTC	GGTTGTGAAA	360
Query 361 GCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGCAGGCTAGAGTTCGGTAGGGGAG 420 Sbjct 546 GCCCGGGGCTTAACCCGGGTCTGCAGTCGATCGGTACGGGCAGGCTAGAGTTCGGTAGGGGAG 605 Query 421 ATCGGAATTCCTGGTGTAGCGGTGAAATGCGCCAGATATCAGGAGGAACACCGGTGGCGAA 480 Sbjct 606 ATCGGAATTCCTGGTGTAGCGGTGAAATGCGCCAGATATCAGGAGGAACACCGGTGGCGAA 665 Query 481 GGCGGATCTCTGGGCCGATACTGACGCTGANGAGCGAAAGCGGTGGGGAGCGAACAGCGATT 540 Sbjct 666 GGCGGATCTCTGGGCCGATACTGACGCTGANGAGCGAAAGCGTGGGGAGCGAACAGGATT 540 Sbjct 666 GGCGGATCTCTGGGCCGATACTGACGCTGANGGAGCGAAAGCGTGGGGAGCGAACAGGATT 725 Query 541 AGATACCCTGGTAGTCGCACGCCGNAAACGGTGGGGCACATNNN-GTGGGCGACNNNCNNCGT 599	Sbjct	486	GTTGTCCGGAATT	ATTGGGCGTAAA	GAGCTCGTAGGC	GGCTTGTCACGTC	GGTTGTGAAA	545
Sbjet 546 GCCCGGGGCTTAACCCCCGGGTCTGCAGTCGAATGCCGAGGGAGG	Query	361	GCCCGGGGCTTAA	ссссбебтствс	AGTCGATACGGG	CAGGCTAGAGTTC	GGTAGGGGAG	420
Query 421 ATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAA 480 Sbjct 606 ATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAA 665 Query 481 GGCGGATCTCTGGGCCGATACTGACGCTGANGAGCGAAGGCGAAGGGGGAGCGAACAGCGATT 540 Sbjct 666 GGCGGATCTCTGGGCCGATACTGACGCTGAGGGAGCGAAGCGTGGGGAGCGAACAGGATT 540 Sbjct 666 GGCGGATCTCTGGGCCGATACTGACGCTGAGGGAGCGAAGCGTGGGGAGCGAACAGGATT 725 Query 541 AGATACCCTGGTAGTGCACCGCCGAAAAGGGTGGGCACATNNN-GTGGGCGACNNNCNNCGT 599	Sbjct	546	GCCCGGGGCTTAA	CCCCGGGTCTGC	AGTCGATACGG	CAGGCTAGAGTTC	GGTAGGGGAG	605
Sbjet 606 ATCGGAATTCCTGGGTGTAGCGGTGAAATGCGCAGAATATCAGGAGGAACACCGGTGGCGAA 665 Query 481 GGCGGATCTCTGGGCCGATACTGACGCTGANGAGCGAAAGCGTGGGGAGCGAACAGGATT 540 Sbjet 666 GGCGGATCTCTGGGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT 725 Query 541 AGATACCCTGGTAGCGCCGAAACGGTGGGGCACCANAACGGTGGGCAACAGGATT 725 Query 541 AGATACCCTGGTAGTGCCCGCGAAAACGGTGGGCACANNN-GTGGGCGACNNNCNNCGT 599	Query	421	ATCGGAATTCCTG	GTGTAGCGGTGA	AATGCGCAGATA	TCAGGAGGAACAC	CGGTGGCGAA	480
Query 481 GGCGGATCTTTGGGCCGATACTGACGCTGANGAGCGAAAGCGTGGGGAGCGAACAGGATT 540 Query 481 GGCGGATCTTGGGCCGATACTGACGCTGANGAGCGAAAGCGTGGGGAGCGAACAGGATT 540 Sbjct 666 GGCGGATCTTGGGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATT 725 Query 541 AGATACCCTGGTAGTCCACGCCGNAAACGGTGGGGCACTNNN-GTGGGCGACNNNCNNCGT 599	Sbjct	606			AATGCGCAGATA		CGGTGGCGAA	665
Sbjct 666 GGCGGATCTCTGGGCCCGATACTGACGCTGAGGAGCCGAACGCGGGGGCGAACAGGATT 725 Juery 541 AGATACCCCTGGTAGTCCACGCCGNAAACGGTGGGCACATNNN-GTGGGCCGACNNNCNNCGT 599	Juery	481	GGCGGATCTCTGG	GCCGATACTGAC	GCTGANGAGCGA	AAGCGTGGGGAGC	GAACAGGATT	540
Query 541 AGATACCCTGGTAGTCCACGCCGNAAACGGTGGGCGCACTNNN-GTGGGCGGACNNNCNNCGT 599	Shict	666					GAACAGGATT	725
	Juony	5/1	AGATACCCTEGTA	STCCACGCCGNA	AACGGTGGGCAG		CNNNCNNCGT	500
	Chiet	736						795

Figure: (14) Comparison of sequences the nitrogen base between the local isolate (MU10) and standard strain (JQ647891.1)

Sample MU11 (Streptomyces variabilis)

GGCGCACGACGAGCCCGCGGGCCTATCAGCTTGTTGGTGAGGTAATGGCTCCCCAAGGCGAC GACGGGTAGCCGGCCTGAGAGGGGCGACCGGCCACACTGGGACTGAGACACGGCCCAGACT CCTACGGGAGGCAGCAGTGGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGC CGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAGAG GACGGTACCTGCAGAAGAAGCGCCGGCTAACTACGTGCCAGCAGCCGCGGGTAATACGTAG GGCGCGAGCGTTGTCCGGAATTATTGGGCCGTAAAGAGCTCGTAGGCGGCGGCTTGTCGCGTCGG TTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTACCAGTTCGG TAGGGGAGATCGGAATTCCTGGTGTACCGGTGAAATGCGCAGGACGCGAGGCTACCAGTTCGG GGTGGCGAAGGCGGATCTCTGGGCCCGATACTGACGCTGAGGACCGAAAGCGTGGGGAAC C

The result of the program DNA BLAST analysis showed a similarity of (97%) between sequences of bacterial isolates registered in the Gene Bank with the number (<u>EU841660.1) Fig. (15)</u>

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strept	omy	ces variabilis strai	IN HBUM174064 16	5S ribosomal RNA go	ene, par	tial sequence
sequent	Le ID.	.0041000.1 Length.	1447 Number of Mat	cries. 1		
Range	1: 169	to 709 GenBank G	raphics		▼ Next	Match 🔺 Previous Match
Score 926 bit	s(501	Expect	Identities 524/543(97%)	Gaps 2/543(0%)	Strand Plus/Plu	us
Query	1	GGNGCANGANGAGCCC	GCGGCCTATCAGCTTGTT	GGTGAGGTAATGGCTNNNG	AAGGCGA	60
Sbjct	169	GGTGCAGGATGAGCCC	GCGGCCTATCAGCTTGT	GGTGAGGTAATGGCTCAC	AAGGCGA	228
Query	61	CGACGGGTAGCCGGCC	TGAGAGGGGCGACCGGCCA	CACTGGGACTGAGACACG	SCCCAGAC	120
5bjct	229	CGACGGGTAGCCGGCC	TGAGAGGGCGACCGGCCA	CACTGGGACTGAGACACG	SCCCAGAC	288
Query	121	TCCTACGGGAGGCAGC	AGTGGGGAATATTGCACA	ATGGGCGAAAGCCTGATGC	AGCGACG	180
bjct	289	TCCTACGGGAGGCAGC.	AGTGGGGAATATTGCACA	ATGGGCGAAAGCCTGATGC	AGCGACG	348
Query	181	CCGCGTGAGGGATGAC	GGCCTTCGGGTTGTAAAC	CTCTTTCAGCAGGGAAGAA	GCGAAAG	240
Sbjct	349	CCGCGTGAGGGATGAC	GGCCTTCGGGTTGTAAAC	CTCTTTCAGCAGGGAAGA	GCGAAAG	408
Query	241	TGACGGTACCTGCAGA	AGAAGCGCCGGCTAACTA	CGTGCCAGCAGCCGCGGTA	ATACGTA	300
Sbjct	409	TGACGGTACCTGCAGA	AGAAGCGCCGGCTAACTA	ACGTGCCAGCAGCCGCGGT/	ATACGTA	468
Query	301	GGGCGCGAGCGTTGTC	CGGAATTATTGGGCGTAA	AGAGCTCGTAGGCGGCTTG	TCGCGTC	360
Sbjct	469	GGGCGCGAGCGTTGTC	CGGAATTATTGGGCGTAA	AGAGCTCGTAGGCGGCTTG	TCACGTC	528
Query	361	GGTTGTGAAAGCCCGG	GGCTTAACCCCGGGTCTG	CAGTCGATACGGGNAGGN	ANNAGTT	420
Sbjct	529	ĠĠŦŦĠŦĠĂĂĂĠĊĊĊĠĠ	ĠĠĊŦŦĂĂĊĊĊĊĠĠĠŦĊŦĠ	scágtcgatácgggcággci	AG-AGTT	587
Query	421	CGGTAGGGGGAGATCGG	AATTCCTGGTGTANNGGT	GAAATGCGCAGATATCNNG	AGGAACA	480
bjct	588	ĊĠĠŦĂĠĠĠĠĠĠĊĊĠĠ.	AATTCCTGGTGTAGCGGT	GAAATGCGCAGATATCAG	AGGAACA	647
Query	481	CCCGGTGGCGAAGGNG	GATCTCTGGGCCCGATAC	TGACGCTGAGGANNGAAAG	GCGTGGGG	540
Sbjct	648	ċċċĠġţġġċġĂġġċġ	ĠĂŦĊŦĊŦĠĠĠ-ĊĊĠĂŦĂĊ	tigacigic tigagigago gadad	CGTGGGG	706
Query	541	AGC 543				
Sbjct	707	ÁGC 709				

Figure: (15) Comparison of sequences the nitrogen base between the local isolate (MU11) and standard strain (<u>EU841660.1)</u>

The partial 16S rRNA sequences deposited in GenBank were analyzed using DNA Blast (Figure 5,6,7,8,9,10,11,12,13,14,15). It was discovered in that all isolates belong to a *Streptomyces* species with (77-99%) resemblance to the 16S rRNA series of closely related species. 16S rRNA, bacterial genetic maker often In chromosomal DNA, there is a multigene family or operons. The role of this gene has changed dramatically over time, and its size is now large enough for informatics purposes. [24].

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