

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 follows; *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 بكتيرية 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 استخدم للكشف عن 11 عزلة من جنس *Streptomyces* تم اختيار 10 حزم من الـ DNA كنتيجة للتفاعل البوليميري المتسلسل المتخصص، انتخبت العزلات المحلية المعزولة عند 1000 قاعدة نيروجينية، تم كشف عن البكتيريا قيد الاختبار باستخدام برنامج DNA Blast NCBI وكانت النتائج على النحو التالي: *Streptomyces gancidicus*, *S. werraensis*, *S. griseorubens*, *S. hawaiiensis*, *S. thermocarboxydus*, *S. cyaneus*, *S. misionensis*, *S. bellus*, *S. parvulus*, *S. labedae*,

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) μm . 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 CaCO_3 (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].

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) K₂HPO₄, (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]

Czopic 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

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 °C 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

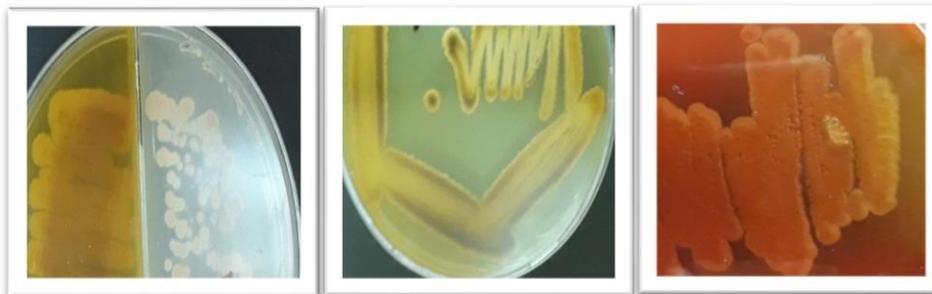


Figure 2: Streptomyces species isolated ground mycelia

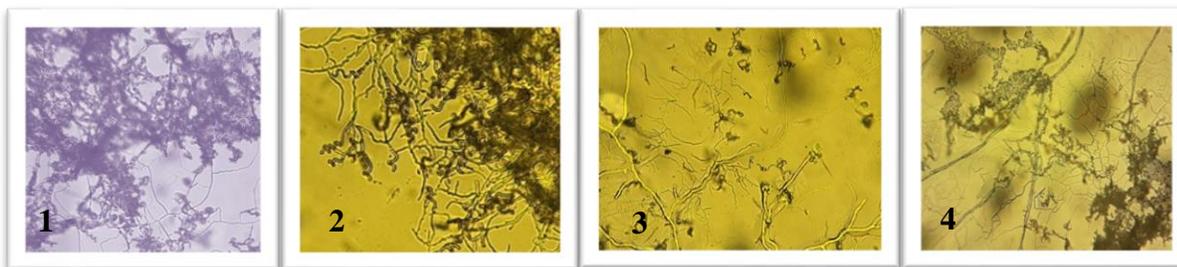


Figure 3:(1) Gram staining of isolated streptomyces under 100x magnification. (2,3,4): Glass slide technology

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]

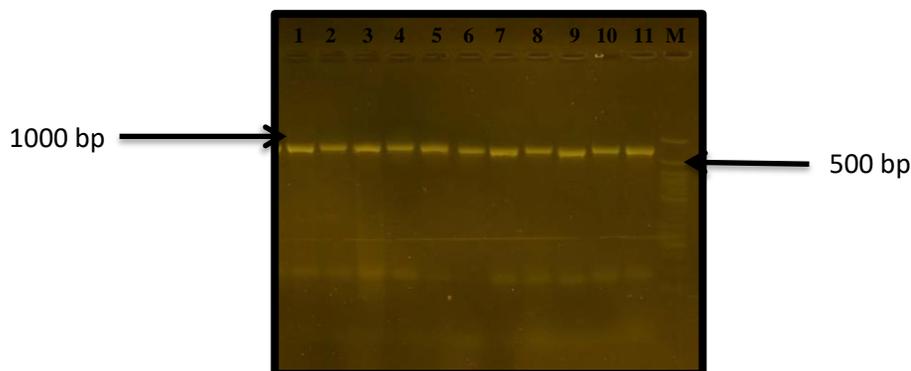


Fig.:4: The results of the bacterial samples from the region' basic polymers reaction based on primer 16s rRNA (11) *Streptomyces* isolates

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*)

```
GCCCCGCGGCCTATCAGCTTGTTGGTGAGGTAATGGCTCACCAAGGCGACGACGGGTAGC
CGGCCTGAGAGGGCGACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAG
GCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGAGGG
ATGACGGCCTTCGGGTTGTAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGTACCTG
CAGAAGAAGCGCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGT
TGTCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCGCGTTCGGTTGTGAAAGCC
CGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGTTTCGGTAGGGGAGATC
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 (MT588801.1) Fig. (5).

Download ▾ GenBank Graphics

Streptomyces gancidicus strain Kris2 16S ribosomal RNA gene, partial sequence
 Sequence ID: [MT588801.1](#) Length: 1245 Number of Matches: 1

Range 1: 190 to 665 [GenBank](#) [Graphics](#) ▾ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
865 bits(468)	0.0	472/476(99%)	0/476(0%)	Plus/Plus
Query 1	CCGCGGCCATCAGCTTGTGGTGAGGTAATGGCTCACCAAGGCGACGACGGGTAGCCGG	60		
Sbjct 190	CCGCGGCCATCAGCTTGTGGTGAGGTAATGGCTCACCAAGGCGACGACGGGTAGCCGG	249		
Query 61	CCTGAGAGGGCGACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCA	120		
Sbjct 250	CCTGAGAGGGCGACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCA	309		
Query 121	GCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCTGAGGGATG	180		
Sbjct 310	GCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCTGAGGGATG	369		
Query 181	ACGGCCTTCGGGTTGTAACCTCTTTTCAGCAGGGAAGAAGCGAAAGTGACGGTACCTGCA	240		
Sbjct 370	ACGGCCTTCGGGTTGTAACCTCTTTTCAGCAGGGAAGAAGCGAAAGTGACGGTACCTGCA	429		
Query 241	GAAGAAGCGCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGTTG	300		
Sbjct 430	GAAGAAGCGCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGTTG	489		
Query 301	TCCGGAAATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCGCGTCGGTTGTGAAAGCCC	360		
Sbjct 490	TCCGGAAATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCGCGTCGGTTGTGAAAGCCC	549		
Query 361	GGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGTTCCGGTAGGGGAGATCG	420		
Sbjct 550	GGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGTTCCGGTAGGGGAGATCG	609		
Query 421	NAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCANGAGGANCCCGGTGGCGAA	476		
Sbjct 610	GAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCANGAGGANCCCGGTGGCGAA	665		

Figure: (5) Comparison of sequences of the nitrogen base between the local isolate (MU1) and standard strain ([MT588801.1](#))

Sample MU2 (*Streptomyces werraensis*)

GGCGCACCCGCGGCCTATCAGCTTGTGGTGAGGTAATGGCTCACCAAGGCGACGACGGGT
 AGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGG
 GAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGA
 GGGATGACGGCCTTCGGGTTGTAACCTCTTTTCAGCAGGGAAGAAGCGAAAGTGACGGTA
 CCTGCAGAAGAAGCGCCGGCTAACTCCCCGCCAGCAGCCGCGGTAATACGTAGGGCGCGA
 GCGTCCCCCGAATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCGCGTCGGTTGTGAA
 AGCCCGGCCCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGTTCCGGTAGGGGAG
 ATCGGAATTCCTGGTGTAGCGGTGAAATGCGCACATATCAGGAGGAACACCGGTGGCGAA
 CGCGGATCTCTGGGCCGATACTGACGCTGAGGACCCAAAGCGTGGGGACCGAACAGGATC
 ACATCCCCTGCCACCCCGCCGCAAACGGCGGGCACTACGTGTGGGCGACCTTCCCCCCC
 CCCCCCGCCCCGCTACCCCTTAACCGCCCCCCTGGGGAGTACCGCCCCCAGGC

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 ([MN179978.1](#)) Fig. (6)

Download GenBank Graphics

Streptomyces werraensis strain S8-TSB-24 16S ribosomal RNA gene, partial sequence
 Sequence ID: [MN179978.1](#) Length: 989 Number of Matches: 1

Range 1: 177 to 823 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand				
1007 bits(545)	0.0	598/648(92%)	1/648(0%)	Plus/Plus				
Query 1	CCCCGGCC	TATCAGCTT	GTGGTGAGG	TAATGGCTC	ACCAAGGCG	AACGACG	CGGAGCCG	60
Sbjct 177	CCCCGGCC	TATCAGCTT	GTGGTGAGG	TAATGGCTC	ACCAAGGCG	AACGACG	CGGAGCCG	236
Query 61	GCCTGAGAG	GGCCGACCG	GGCCACACT	TGGGACTG	GAGACACGG	CCAGACTC	CTACGGGAG	120
Sbjct 237	GCCTGAGAG	GGCCGACCG	GGCCACACT	TGGGACTG	GAGACACGG	CCAGACTC	CTACGGGAG	296
Query 121	AGCAGTGGG	GAAATATTG	CACAATGGG	GAAAGCCT	GATGCAGCG	ACGCCCGT	GAGGGAT	180
Sbjct 297	AGCAGTGGG	GAAATATTG	CACAATGGG	GAAAGCCT	GATGCAGCG	ACGCCCGT	GAGGGAT	356
Query 181	GACGGCCTT	CGGGTTGT	AAACCTCTT	TTCAGCAGG	GAAGAAGCG	AAAGTGAC	GGTACCTGC	240
Sbjct 357	GACGGCCTT	CGGGTTGT	AAACCTCTT	TTCAGCAGG	GAAGAAGCG	AAAGTGAC	GGTACCTGC	416
Query 241	AGAAGAAGC	GCCTAACT	TNNNNGCC	AGCAGCCG	CGGTAATAC	GTAGGGCG	CAGCGTT	300
Sbjct 417	AGAAGAAGC	GCCTAACT	TNNNNGCC	AGCAGCCG	CGGTAATAC	GTAGGGCG	CAGCGTT	476
Query 301	NNNNNGAAT	TATTGGGCG	TAAAGAGCT	CGTAGGCG	GGCTTGTG	CGCGTCGG	TTGTGAAAG	360
Sbjct 477	GTCCGGAA	TATTGGGCG	TAAAGAGCT	CGTAGGCG	GGCTTGTG	CGCGTCGG	TTGTGAAAG	536
Query 361	CGGNNNTT	AAACCCGG	GCTGCAGT	CGATACGG	GCAGGCTA	GAGTTCCG	TAGGGGAG	420
Sbjct 537	CGGGGCTT	AAACCCGG	GCTGCAGT	CGATACGG	GCAGGCTA	GAGTTCCG	TAGGGGAG	596
Query 421	GGAAATTC	TGGTGTAG	CGGTGAAAT	TGCGCANAT	ATCAGGAGG	AACACCGG	TGGCGAANG	480
Sbjct 597	GGAAATTC	TGGTGTAG	CGGTGAAAT	TGCGCANAT	ATCAGGAGG	AACACCGG	TGGCGAANG	656
Query 481	GGATCTCT	TGGGCGAT	ACTGACGCT	GAGGANNA	AAAGCGTGG	GGGANC	GAACAGGAT	540
Sbjct 657	GGATCTCT	TGGGCGAT	ACTGACGCT	GAGGANNA	AAAGCGTGG	GGGANC	GAACAGGAT	716
Query 541	TNCCCTGN	NANNNCNC	GCCGNAAC	CGNGGGCAC	TANGTGTGG	GCGACNTT	CNCNNCNN	600
Sbjct 717	TACCCGTG	TAGTCCAC	GCCGTAAC	CGTGGGCG	CATAGGTGT	GGGCGAC	ATTCCACGTC	776

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

Sample MU3 (*Streptomyces griseorubens*)

GTGGATGAGCCCGCGGCCTATCAGCTTGTGGTGAGGTAATGGCTCACCAAGGCGACGACG
 GGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGAGACACGGCCAGACTCCTA
 CGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCG
 TGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACG
 GTACCTGCAGAAGAAGCGCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCG
 CGAGCGTTGTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTACGTCGGTTGT
 GAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGTTCCGGTAGG
 GGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGG
 CGAAGGCGGATCTCTGGGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAG
 GATTAGATACCCTGGTAGTCCACGCCGTAACCGGTGGGCACTAGGTGTGGGCGACATTCCA
 CGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCGCCTGGGGAGTACGGCCGCAAGGCT
 AAAACTCAAAGGATTTGACGGGGGCCCGCACAAAGCGGCGGAGCATGTGGCTTAATTCGAC
 GCAACGCGAAGAACCTTACCACGGCTTGACATACACCGGAAAGAGGGCCCCCTTGCCGCCG
 GCGACCGGCGCCCATCGGTCAGCTCCCGTCGCGAGCCGCTGGGTAAAGTCCGCAACCAGCG
 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 (MT525003.1) Fig. (7)

Score	Expect	Identities	Gaps	Strand	
1391 bits(753)	0.0	759/764(99%)	0/764(0%)	Plus/Plus	
Query 8	GATGAGCCC	CGGCCCTATCAGCTT	GTGGTGAGGTAATGGCT	CACCAAGGCGACGACGGG	67
Sbjct 164	GATGAGCCC	CGGCCCTATCAGCTT	GTGGTGAGGTAATGGCT	CACCAAGGCGACGACGGG	223
Query 68	TAGCCGGCC	TGAGAGGGGACCGGC	CACACTGGGACTGAGAC	CACGGCCAGACTCCTACG	127
Sbjct 224	TAGCCGGCC	TGAGAGGGGACCGGC	CACACTGGGACTGAGAC	CACGGCCAGACTCCTACG	283
Query 128	GGAGGCAGC	AGTGGGGAATATTGC	ACAATGGCGAAAGCCT	GATGCAGCGACGCCGCTG	187
Sbjct 284	GGAGGCAGC	AGTGGGGAATATTGC	ACAATGGCGAAAGCCT	GATGCAGCGACGCCGCTG	343
Query 188	AGGGATGAC	GGCCTTCGGGTGTAA	ACCTCTTTTCAGCAGG	GAAGGAAAGTGACGGT	247
Sbjct 344	AGGGATGAC	GGCCTTCGGGTGTAA	ACCTCTTTTCAGCAGG	GAAGGAAAGTGACGGT	403
Query 248	ACCTGCAGA	AAGCGCCCGCTAAC	TACGTGCCAGCAGCC	CGGTAATACGTAGGG	307
Sbjct 408	ACCTGCAGA	AAGCGCCCGCTAAC	TACGTGCCAGCAGCC	CGGTAATACGTAGGG	463
Query 308	AGCGTTGT	CCGGAATATTGGGCG	TAAAGAGCTCGTAGG	CGGCTTGTACGTCGGT	367
Sbjct 464	AGCGTTGT	CCGGAATATTGGGCG	TAAAGAGCTCGTAGG	CGGCTTGTACGTCGGT	523
Query 368	AAAGCCCG	GGGCTTAAACCCGGG	CTGCACTGATACGGG	CAGCTAGAGTTCCGT	427
Sbjct 524	AAAGCCCG	GGGCTTAAACCCGGG	CTGCACTGATACGGG	CAGCTAGAGTTCCGT	583
Query 428	GAGATCGG	AATTCGGTGTAGCG	GTAAATGCGCAGAT	ATCAGGAGAACACCG	487
Sbjct 584	GAGATCGG	AATTCGGTGTAGCG	GTAAATGCGCAGAT	ATCAGGAGAACACCG	643
Query 488	GAAGCGG	ATCTCTGGCCGATA	CTGACGCTGAGGAGC	GAAAGCTGGGGAGC	547
Sbjct 644	GAAGCGG	ATCTCTGGCCGATA	CTGACGCTGAGGAGC	GAAAGCTGGGGAGC	703
Query 548	ATTAGATA	CCCTGGTAGTCCAG	CGCTAAACGGTGGG	CAC TAGGTGTGGG	607
Sbjct 704	ATTAGATA	CCCTGGTAGTCCAG	CGCTAAACGGTGGG	CAC TAGGTGTGGG	763

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

Sample MU4 (*Streptomyces hawaiiensis*)

GGCGGTGCAGGATGAGCCC
 GCGGCCTATCAGCTTGTGGT
 GAGGTAGTGGCTACCAAGGC
 GACGACGGGTAGCCGGCCT
 GAGAGGGCGACCGGCCACA
 CACTGGGACTGAGACACGG
 CCCAGACTCCTACGGGAGG
 CAGCAGTGGGGAATATTGC
 ACAATGGGCGAAAGCCTG
 ATGCAGCGACGCCGCTTC
 GGGTGTAAACCTCTTTCAG
 CAGGGGAAGAAGCGAAAG
 TGACGGTACCTGCAGAAGA
 AGCGCCGGCTAACTACGT
 GCCAGCAGCCGCGGTAATA
 CGTAGGGCGCGAGCGTTG
 TCCGGAATTATTGGGCGT
 AAAGAGCTCGTAGGGCGG
 CTTGTACGTCGGTTGTG
 AAAGCCCGGGGCTTAAAC
 CCGGGTCTGCAGTCGATA
 CGGGCAGGCTAGAGTTC
 GGTAGGGGAGATCGGAAT
 TCTGGTGTAGCGGTGAA
 ATGCGCAGATATCAGGAG
 GAACACCGGTGGCGAAGG
 CGGATCTCTGGGCCGATA

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 (MT36169.1) Fig. (8)

Score	Expect	Identities	Gaps	Strand	
99.0 bits(53)	8e-17	60/66(91%)	0/66(0%)	Plus/Plus	
Query 1	CCGGNGGNC	ANGATGAGCCCGCGGC	TATCAGCTTGTGGT	GAGGNAGNGGCTCACCAA	60
Sbjct 139	CCGGCGGTG	CAGGATGAGCCCGCGGC	TATCAGCTTGTGGT	GAGGTAGTGGCTCACCAA	198
Query 61	GGGGAC				66
Sbjct 199	GGCGAC				204

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

Sample MU5 (*Streptomyces thermocarboxydus*)

CCCGCGGCCTATCAGCTTGTGGTGAGGTAATGGCTCACCAAGGCGACGACGGGTAGCCGG
 CCTGAGAGGGCGACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCA
 GCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGAGGGATG
 ACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGTACCTGCAG
 AAGAAGCGCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGCACGGCGCGAGCGTTGT
 CCGGAATTATTGGGCGTAAAGAGCTCGTAGGCCGGCTTGTCCCCTCGGTTGTGAAAGCCCGG
 GGCTTAACCCCGGGTCTGCAGTCGATACGGCCAGGCTAGAGTTCGGTAGGGGAGATCGGAC
 TTCCTGGTGTAGCGGCGAAATGCCCCATATCACGAGGACCCCCCGGTGGCGAAAGCGGAT
 CTCTGGGGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTACATAC
 CCCTGGAGCCCCCGCCACGGTGGGCCCTACGT

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 (KU158245.1) Fig. (9)



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

Sample MU6 (*Streptomyces cyaneus*)

CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGCAATCTGCCCTGCA
 CTCTGGGACAAGCCCTGGAACGGGGTCTAATACCGGATACTGATCATCTTGGGCATCCTT
 GGTGATCGAAAGCTCCGGCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTGGTGAGGT
 AATGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGA
 CTGAGACACGGCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGA
 AAGCCTGATGCAGCGACGCCGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAG
 CAGGGAAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACGTGCCAGC
 AGCCGCGGTAATACGTAGGGCGCGAGCGTTGTCCGGAATTATTGGGCGTAAAGAGCTCGTA
 GGCGGCTTGTGCGTTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACG
 GGCAGGCTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGA
 TATCACGAGGAACACCGGTGGCGAAAGCGGATCTCTGGGCCGATACTGACGCTGAGGAGC
 GAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGC
 ACTAGGTGTGGGCGACATTCCACGTCGTCGGTGC CGCAGCTAACGCATTAAGTGCCCCGCC
 TGGGGGAGTACGGCCGAAGGCTAAAACCTCAA

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 (KM215731.1) Fig. (10)

Streptomyces cyaneus strain ITD-19 16S ribosomal RNA gene, partial sequence
 Sequence ID: KM215731.1 Length: 962 Number of Matches: 1

Range 1: 20 to 836 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
1498 bits(811)	0.0	816/818(99%)	1/818(0%)	Plus/Plus
Query 1	CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGCAATCTGCCCTGCA	60		
Sbjct 20	CCTCCTTCGGGAGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGCAATCTGCCCTGCA	79		
Query 61	ACTCTGGGACAAGCCCTGGAACGGGGTCTAATACCGGATACTGATCATCTTGGGCATCC	120		
Sbjct 80	ACTCTGGGACAAGCCCTGGAACGGGGTCTAATACCGGATACTGATCATCTTGGGCATCC	139		
Query 121	TTGGTATCGAAAAGCTCCGGCGGTGCAGGATGAGCCCGCGCCTATCAGCTTGTGGTGA	180		
Sbjct 140	TTGGTATCGAAAAGCTCCGGCGGTGCAGGATGAGCCCGCGCCTATCAGCTTGTGGTGA	199		
Query 181	GGTAATGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTG	240		
Sbjct 200	GGTAATGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTG	259		
Query 241	GGACTGAGACACGGCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGG	300		
Sbjct 260	GGACTGAGACACGGCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGG	319		
Query 301	CGAAAGCCTGATGCAGCGACGCCGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTT	360		
Sbjct 320	CGAAAGCCTGATGCAGCGACGCCGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTT	379		
Query 361	TCAGCAGGGAAGAAGCGAAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACGTGC	420		
Sbjct 380	TCAGCAGGGAAGAAGCGAAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACGTGC	439		
Query 421	CAGCAGCCGCGTAATACGTAGGGCGCGAGCGTTGTCCGGAATTATTGGGCGTAAAGAGC	480		
Sbjct 440	CAGCAGCCGCGTAATACGTAGGGCGCGAGCGTTGTCCGGAATTATTGGGCGTAAAGAGC	499		
Query 481	TCGTAGGCGGCTTGTGCGCTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTC	540		
Sbjct 500	TCGTAGGCGGCTTGTGCGCTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTC	559		
Query 541	GATACGGGACGGCTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG	600		
Sbjct 560	GATACGGGACGGCTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATG	619		

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

Sample MU7 (*Streptomyces misionensis*)

AGCCCGCGGCCTATCAGCTTGTGGTGGTAAAGCCTGATGCAGCGACGCCGCGTGAGGGA
 GGCCTGAGAGGGCGACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGG
 CAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGAGGGA
 TGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGTACCTGC
 AGAAGAAGCGCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGTT
 GTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTACGTCGGTTGTGAAAGCCC
 GGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGTTTCGGTAGGGGAGATCG
 GAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGCG
 GATCTCTGGGCCGATACTGACGCTGAGGAGCGAAACCCTGGGGAGCGAACAGGATTACAT
 ACCCTGGTACTCCACGCCGTACACGGTGGGCACTAGGTGTGGGCAACATTCCACGTTGTCC
 GTGCCGACGCTAACGCATTAAGTGCCCCGCCTGGGGAGTACGGCCGCAAGGCTCACACTCC
 AAGACTCGACCGGGGCCCCCAAGCGGCGGACCATGCGGCTTACTCCACCCCCCGCCA
 AAC

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)

Score	Expect	Identities	Gaps	Strand
1242 bits(672)	0.0	691/710(97%)	0/710(0%)	Plus/Plus
Query 1	AGCCCGCGGCCTATCAGCTTGTGGTGGTAAAGCCTGATGCAGCGACGCCGCGTGAGGGA	60		
Sbjct 194	AGCCCGCGGCCTATCAGCTTGTGGTGGTAAAGCCTGATGCAGCGACGCCGCGTGAGGGA	253		
Query 61	CGGCCTGAGAGGGCGACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAG	120		
Sbjct 254	CGGCCTGAGAGGGCGACCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAG	313		
Query 121	GCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGAGGG	180		
Sbjct 314	GCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGAGGG	373		
Query 181	ATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGTACCT	240		
Sbjct 374	ATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAAGAAGCGAAAGTGACGGTACCT	433		
Query 241	GCAGAAGAAGCGCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCG	300		
Sbjct 434	GCAGAAGAAGCGCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCG	493		
Query 301	TTGTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTACGTCGGTTGTGAAAG	360		
Sbjct 494	TTGTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTACGTCGGTTGTGAAAG	553		
Query 361	CCCGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGTTCCGGTAGGGGAGA	420		
Sbjct 554	CCCGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGTTCCGGTAGGGGAGA	613		
Query 421	TCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAG	480		
Sbjct 614	TCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAG	673		
Query 481	GCCGATCTCTGGGCCGATACTGACGCTGAGGAGCGAAANNNTGGGGAGCGAACAGGATTA	540		
Sbjct 674	GCCGATCTCTGGGCCGATACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGATTA	733		
Query 541	NATACNCTGGTANTCCACGCCGTANACGGTGGGCACTAGGTGTGGGCAACATTCCACGTT	600		
Sbjct 734	GATACCTGGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGGCAACATTCCACGTT	793		

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

Sample MU8 (*Streptomyces bellus*)

AGTTTGATCATGGCTCAGGACGAACGCTGGCGGGCGTGCTTAACACATGCAAGTCGAACGAT
 GAACCACTTCGGTGGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGCAATCTGCCCTGC
 ACTCTGGGACAAGCCCTGGAAACGGGGTCTAATACCGGATACTGACCCGCTTGGGCATCCA
 AGCGGTTTCGAAAGCTCCGGCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTGGTGAGG
 TAATGGCTCACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGGCGACCGGCCACACTGGG
 ACTGAGACACGGCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCG
 AAAGCCTGATGCAGCGACGCCGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCA
 GCAGGGAAGAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACGTGCCAG
 CAGCCGCGGTAATACGTAGGGCGCGAGCGTTGTCCGGAATTATTGGGCGTAAAGAGCTCGT
 AGGCGGCTTGTACGTTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATAC
 GGCAGGCTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAG
 ATATCAGGAGGAACACCGGTGGCGAAAGCGGATCTCTGGGCCGATACTGACGCTGAGGAG
 CGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGGTGGG
 CACTAGGTGTGGGCGACATTC

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 (MT355856.1) Fig. (12)

Score	Expect	Identities	Gaps	Strand
1175 bits(636)	0.0	643/650(99%)	0/650(0%)	Plus/Plus
Query 1	GAGCCCGCGGCTATCAGCTTGTGGTGAGGTAATGGCTCACCAAGGCGACGACGGGTAG	60		
Sbjct 169	GAGCCCGCGGCTATCAGCTTGTGGTGAGGTAATGGCTCACCAAGGCGACGACGGGTAG	228		
Query 61	CCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGAGACACGGCCAGACTCCTACGGGA	120		
Sbjct 229	CCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGAGACACGGCCAGACTCCTACGGGA	288		
Query 121	GGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGAGG	180		
Sbjct 289	GGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGAGG	348		
Query 181	GATGACGGCCTTCGGGTTGTAACCTCTTTTCAGCAGGGAAGAAGCGAAAGTGACGGTACC	240		
Sbjct 349	GATGACGGCCTTCGGGTTGTAACCTCTTTTCAGCAGGGAAGAAGCGAAAGTGACGGTACC	408		
Query 241	TGCAGAAGAAGCGCCGGCTAACTACGTGCCAGCAGCCCGGTAATACGTAGGGCGCGAGC	300		
Sbjct 409	TGCAGAAGAAGCGCCGGCTAACTACGTGCCAGCAGCCCGGTAATACGTAGGGCGCGAGC	468		
Query 301	GTTGTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGGCGCTTGTACGTCGGTTGTGAAA	360		
Sbjct 469	GTTGTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGGCGCTTGTACGTCGGTTGTGAAA	528		
Query 361	GCCCGGGCTTAACCCCGGGTCTGCAGTGCATACGGGAGGCTAGAGTTTCGGTAGGGGAG	420		
Sbjct 529	GCCCGGGCTTAACCCCGGGTCTGCAGTGCATACGGGAGGCTAGAGTTTCGGTAGGGGAG	588		
Query 421	ATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAA	480		
Sbjct 589	ATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAA	648		
Query 481	GGCGGATCTCTGGGCGATACGACGCTGAGGAGCGAAAANNNTGGGGAGCGAACAGGATT	540		
Sbjct 649	GGCGGATCTCTGGGCGATACGACGCTGAGGAGCGAAAAGCGTGGGGAGCGAACAGGATT	708		
Query 541	ANATACNCTGGTANTCCAGCCGTANACGGTGGGCACTAGGTGTGGGCAACATTCACGT	600		
Sbjct 709	AGATACCTGTAGTCCACGCCGTAAACGGTGGGCACTAGGTGTGGGCAACATTCACGT	768		

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

Sample MU9 (*Streptomyces parvulus*)

GCGCCCCCGCCTATCCCCTTGTGGTGAGGCAATGGCTCACCAAGGCGACGACGGGTAGC
 CGGCCTGAGAGGGCGACCGGCCACCCTGGGACTGAGACACGGCCAGACTCCTACGGGAG
 GCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGAGGG

ATGACGGCCTTCGGGTTGTAAACCTCTTTCCCCACGGAAGAAGCGAAAGTGACGGCACCTG
 CAGAAGAAGCGCCCCCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGT
 TGCCCCAATTATTGGGCGTAAAGAGCTCCTAGGCGGCTTGTCCCGTCGGCTGTGAAAGCC
 CGGCGCTTACCCCCCCCCCCCCCCCCCTACCCCCCCC

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)

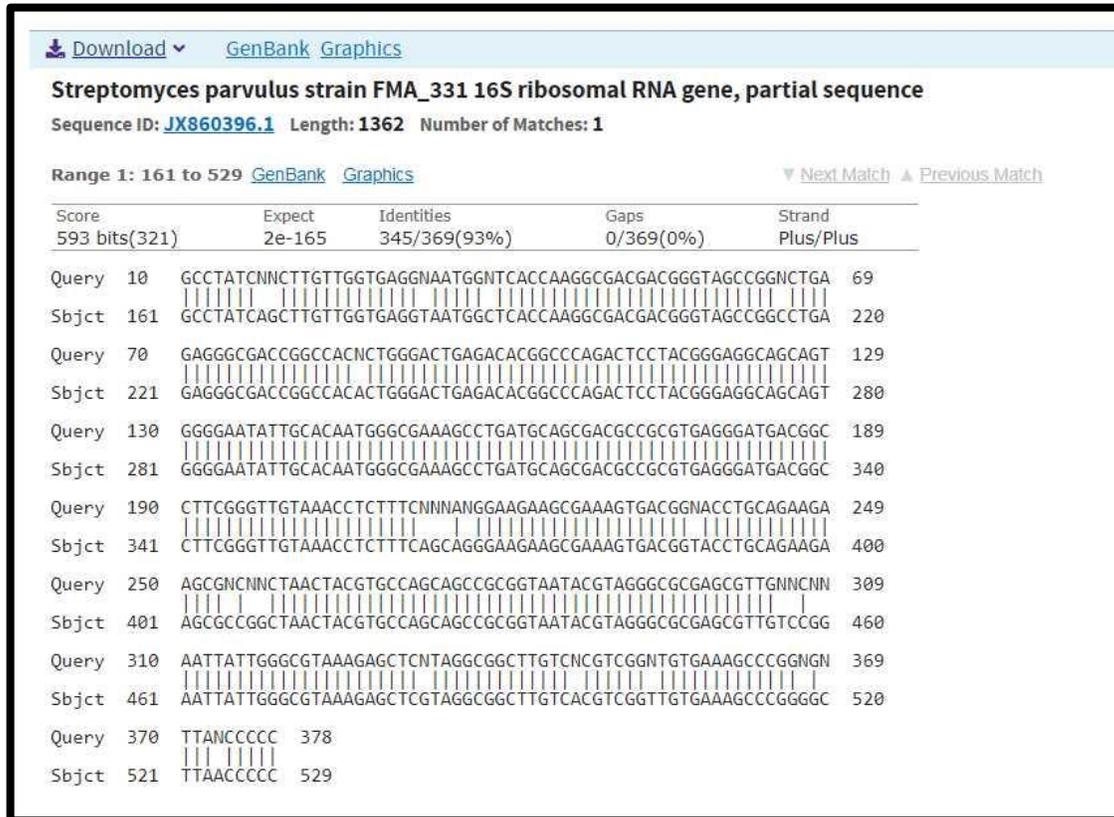


Figure: (13) Comparison of sequences the nitrogen base between the local isolate (MU9) and standard strain (JX860396.1)

Sample MU10 (*Streptomyces labedae*)

GAGCCCGCGGCCTATCAGCTTGTGGTGAGGTAATGGCTCACCAAGGCGACGACGGGTAGC
 CGGCCTGAGAGGGCGACCGGCCACACTGGGACTGAGACACGGCCAGACTCCTACGGGAG
 GCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGAGGG
 ATGACGGCCTTCGGGTTGTAAACCTCTTTTCAGCAGGGAAGAAGCGAAAGTGACGGTACCTG
 CAGAAGAAGCGCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCGAGCGT
 TGTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTACGTCGGTTGTGAAAGCC
 CGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTAGAGTTCGGTAGGGGAGATC
 GGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCAGGAGGAACACCGGTGGCGAAGGC
 GGATCTCTGGGCCGATACTGACGCTGACGAGCGAAAGCGTGGGGAGCGAACAGGATTAGA
 TACCCTGGTAGTCCACGCCGCAAACGGTGGGCACTCCCGTGGGCGACCCCCCGTCGCC

CGTGCCCGCAGCTAACGCATTAAGTGCCCCGCTGGGGAGTACGGCCGCAAGGCTAAAACCTC
 ACAGGAATTGACGGGGGCCCGCCCCACCCGCCGGACCCTGTGGCTTATTCACGCACACTC
 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 (JQ647891.1) Fig. (14)

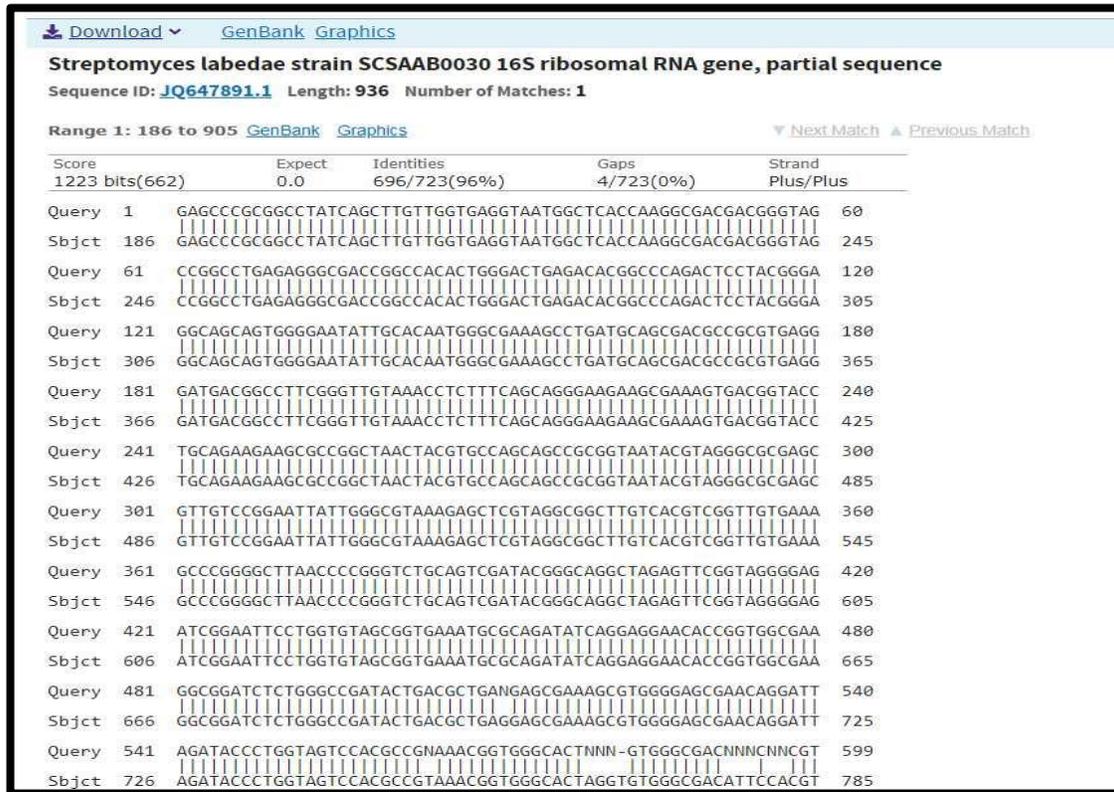


Figure: (14) Comparison of sequences the nitrogen base between the local isolate (MU10) and standard strain (JQ647891.1)

Sample MU11 (*Streptomyces variabilis*)

GGCGCACGACGAGCCCGCGGCCTATCAGCTTGTGGTGAGGTAATGGCTCCCCAAGGCGAC
 GACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGAGACACGGCCCAGACT
 CCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGC
 CGCGTGAGGGATGACGGCCTTCGGGTTGTAACCTCTTTTCAGCAGGGAAGAAGCGAAAGT
 GACGGTACCTGCAGAAGAAGCGCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAG
 GGCGCGAGCGTTGTCCGGAATATTGGGCGTAAAGAGCTCGTAGGCGGCTTGTCGCGTCGG
 TTGTGAAAGCCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAGGCTACCAGTTCGG
 TAGGGGAGATCGGAATTCCTGGTGTACCGGTGAAATGCGCAGATATCCCAGGAACACCC
 GGTGGCGAAGGCGGATCTCTGGGCCCGATACTGACGCTGAGGACCGAAAGCGTGGGGAGC
 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 (EU841660.1) Fig. (15)



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

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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