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A Complete Sequence of the 16S rRNA Gene of a Novel *Streptomyces coelicolor* (AB588124) (QU66c-2002) Isolated from the Soil of Qatar

[1]I.A. Mahasneh, [2]R.F. Al-Thani, [1]M.A. Abuannadi and [1]M.A. Qandil
[1]Biotechnology and Genetic Engineering Research Laboratory, Department of Biological Sciences, Faculty of Sciences, AL al-Bayt University, Mafraq City, P.O. Box 130040, Jordan
[2]Department of Biological and Environmental Sciences, College of Arts And Sciences, Qatar University, P.O. Box 2713, Doha City, Qatar

Abstract: The aim of this study was to determine the sequence of the 16S rRNA gene and thus to conduct the phylogenic position of the naturally occurring wild type strain of *Streptomyces* QU66C. Here we show conclusively the full sequence of the 16S rRNA gene of a novel wide type strain of *Streptomyces coelicolor* which has been isolated from the soil of Qatar and thus characterized on the basis of its phenotypic and genotypic features. In comparison with the homologous strains in GeneBanks, the phylogenic position of the isolate is in between *S. coelicolor* A3 (2) (Y00411) (NC003888) and *S. coelicolor* (C) (EF371438). The sequence of present strain has been deposited in the International Nucleotide Sequence Databases) (INSD) in the GenBanks/DDBJ/EMBL/NCBI) and assigned an accession number of AB588124 and thus the strain is being known as *Streptomyces coelicolor* (AB588124) (QU66C-2002). Present strain shows a similarity and identities of 99.40, 99.40, 99.40, 99.33 and 99.31% with a score value of 2693, 2693, 2687, 2673 and 2673 bits for *Streptomyces coelicolor* A3(2) (Y00411) (NC003888), *S. violaceoruber* AF503494 (ancient name for *S. coelicolor* and *S. lividans*), *S. lividans* AF503498, *S. lividans* AB184826 and *S. coelicolor* (C) (EF371438), respectively. In comparison with the *S. coelicolor* clones in Sanger database the strain shows a positive high scoring alignment similarity of 99.4% with score of 6907 with five clones of *S. coelicolor* A3 (2) (AL939116, AL939119, AL939124, AL939114, AL939108) and a 99% similarity with a score of 6889 for AL939110. Similarly, the BLAST search on EMBL GeneBAnk shows a 99.40% similarity with 2 strains of *S. violaceoruber* (AF503494, AF503492) with high score of 2738.

Key words: Antibiotic production, *Streptomyces coelicolor* , 16S rRNA sequencing, streptomyces phylogeny, *S.coelicolor* (ab588124) (qu66c-2002) strain

INTRODUCTION

There is a world wide growing demand for production of a new generation of antibiotics particularly due to the increase of resistant pathogens, evolution of novel diseases and toxicity of the currently used compounds (Silbergeld *et al*., 2008; Hakvag *et al*., 2008). The problem of multi-resistance is being progressively increasing due to the misuse of the available antibiotics (Harrison and Svec, 1998; Larson, 2007; Marino, 2008; Hawkey, 2008). The *Streptomyces* genus is the most diversified groups of Eubacteria, widely spread around all environments particularly in the desert soil where most common habitats occurs (Dunbar *et al*., 1999). The biotechnological importance of *Sterptomyces* as producers for the majority of antibiotics in use today keeps them as the main natural stock for screening programs (Berdy, 2005; Bull and Stach, 2007; El-Sherbiny *et al*., 2009; Akanji *et al*., 2011; Sinha *et al*., 2011). In addition, empirical screening using various assays has revealed that Streptomyces are capable to produce antibiotics with a broad spectrum activity in both human and veterinary medicine such as antibacterial, antifungal, anti-cancer, anti-parasitic and anti-viral (Atta and Ahmad, 2009; Morakchi *et al*., 2009) as well as some immune-suppressants (Watve *et al*., 2001) and several enzymes important in the food and other industries. There are two main approaches being used for discovery of new antibiotics; screening programs for natural strains and mutation protocols (Busti *et al*., 2006; Fiedler *et al*., 2008). As a result of this, more than 500 species of *Streptomyces* have been isolated (Zaitlin *et al*., 2003; Euzeby, 2008; Hakvag *et al*., 2008; Morakchi *et al*., 2009). Among those

Corresponding Author: Ihsan Mahasneh, Biotechnology and Genetic Engineering Research Laboratory, Department of Biological Sciences, Faculty of Sciences, Al-al-Bayt University, Mafraq City, P.O. Box 130040, Jordan Tel: 962-6397000, +962795902513

was the model organism *Streptomyces coelicolor* A3 (2) of which its complete genome was published (Bentley *et al*., 2002) making the species as the most studied member of the genus world-wide and is becoming the a genetic paradigm for the actinomycetes (Swiercz *et al*., 2008; O'Rourke *et al*., 2009; Xu *et al*., 2010). Further more, biotechnology researchers have begun using *Streptomyces* species for heterologous expression of proteins over the traditionally known *Escherichia coli,* as the latter was not capable of protein glycosylation or folding (Payne *et al*., 1990; Brawner *et al*., 1991; Hopwood, 1999; Hu *et al*., 2000; Sioud *et al*., 2009).

Recently there have been world wide interest on the molecular techniques (Abu Bakar *et al*., 2010; Onasanya *et al*., 2010; Sifour *et al*., 2010; Zolgharnein *et al*., 2010) particularly the 16S rRNA phylogenic analysis which provides a great impact on *Streptomyces* systematic and minimizing wrong identification (Anderson and Wellington, 2001; Kim *et al*., 2004; Jiang *et al*., 2007; Singh *et al*., 2009). Taxonomically, *S. coelicolor* A3 (2) belongs to the species of *S. violaceoruber* and not a validly described separate species which should not to be mistaken for the actual *S. coelicolor* (Muller). The present *Streptomyces* strain QU66C has been isolated from the soil of Qatar during screening program and was selected as presumable strain of *S. coelicolor*. The aim of this study was to determine the phylogenetic position of the naturally occurring wild type strain of *Streptomyces* QU 66C which has proven to have high potential of production a novel antibiotic.

MATERIALS AND METHODS

Bacterial strain and culture conditions: The investigated strain was isolated from desert soil of Qatar (Abu-Smra area) during a screening program for a novel antibiotic during the year 2002. The strain was then deposited in the Qatar University Culture Collection (QUCC) as strain QU66C and later on (during the partial sequence of the 16S rRNA gene) it was deposited in the NCIMB Ltd, Aberdeen, Scotland, UK as strain NCSQ 17869 during 2003. Phenotypic characteristics of the strain were determined after examination as described previously (Garrity, 2010; Williams *et al*., 1983a, b). Cultures of strain from different growth stages were examined using both phase-contrast microscope and electron microscope.

The screening for optimum growth of the strain revealed that the Nutrient Agar (NA) and Nutrient Broth (NB) (each supplemented with 1% starch) were the optimum media, known hereinafter as NAS and NBS, respectively. The pure culture was then maintained in NBS medium at 37°C and culture conditions were kept as described previously (Kieser *et al*., 2000).

Assay for antibiotics: The antimicrobial assay for the strain antibiotics was conducted using both of inhibition zone method and the minimum inhibition concentration. The production of antibiotics by present strain was determined as described earlier (Kieser *et al*., 2000) and as follows: The Actinorhodin (Act) was extracted using the 1 N KOH for pH adjustment to 8.0 before A640 was measured. The undecylprodigiosin (Red) was extracted using 0.5 M HCl for acidification before A530 was measured. The calcium-dependent lipopeptide antibiotics (CDA) was detected as normally assayed (Kieser *et al*., 2000). For production of the antibiotic droplets on the surface of the colonies, strain was cultured on Potato Dextrose Agar (PDA) and incubated for several days.

Analysis of 16S rRNA gene: During 2007, the 16S rRNA gene sequence was determined. The genomic DNA of the *Streptomyces* QU66C strain was extracted using the PrepMan Ultra Sample Preparation Reagent kit (No: 4367554) according to the protocol stated by manufacturer (Applied Biosystem, USA). The 16S rRNA gene was amplified using the MicroSeq full gene 16S rRNA Bacterial Identification kit (No: 4349155) and the PCR Amp system 9700 according to the manufacturer protocol (Applied Biosystem, USA). The PCR program consisted of an initial denaturation at 95°C for 10 min to activate the AmpliTaq DNA polymerase, then 30 cycles (30 sec at 95°C, 30 sec at 60°C , 45 sec at 72°C for denaturation, annealing and extension, respectively), followed by 10 min at 72°C for final extension. Then, the PCR product was purified using wizard PCR preps DNA purification system kit (No: A7231) according to the manufacturer (Promega, USA). The sequencing mix then were mixed and run on the PCR for 25 cycles (10 sec at 96°C, 5 sec at 50°C, 4 min at 60°C for denaturation, annealing and extension, respectively). The reaction was terminated with a final extension at 72°C for 5 min. The excess dye terminators and primer were removed from the sequencing mix using DyeEX® 2.0 spin kit (No: 63204) according to the manufacturer (Qiagen, USA).

The 16S rRNA gene sequence was conducted using the genetic analyzer (ABI Prism GA310, Applied Biosystem, USA). The GA310 analyzer is equipped with a compatible a data collecting software (v 3.0) and a Microbial Identification Software MicroSEQ® ID (v 2.0). The software allows the user to create consensus sequences and to compare it with the microbial library of

the full gene of 16S rRNA, available in the Applied Biosystem (http://www.appliedbiosystems.com).

Pairwise sequence alignment: The full gene sequence of present strain QU66C was aligned automatically using the BLAST against the gene library available for *Streptomyces* species in the NCBI (www.ncbi nlm. nih. gov), Sanger Institute (http://www.sanger.ac.uk), DDBJ (http://www.ddbj.nig.ac.jp) and EMBL-EBI GeneBank (http://www.ebi.ac.uk).

Multiple sequence alignment: The phylogenetic analysis was constructed using Nighbor-Joinin tree (Saitou and Nei, 1987; Dopazo, 1994; Tamura *et al*., 2007) of the isolated strain using the BLAST and CLUSTAL W (1.83) available in the DDBJ GeneBank. The closely related homologous strains were identified, retrieved and compared to the sequence of the strain QU66C, using CLUSTAL W (version 3.2) available on the Biology StudyBench (http:/woekbench.sds.edu).

Statistical criteria for species identification: Identification of species through sequence similarity was determined based on the criteria used by Bosshard *et al*. (2003) where if the difference between the query and the compared strain is 1-1.5% (14-22 bp), 1.5-5.0% (23-72 bp) and 5.-0-7.0% (72-98 bp), then the query strain should be given to the same species, genus or a different genus, respectively.

Genebank accession number: The complete sequence (1404 bp) of the 16S rRNA gene of QU66C strain has been deposited in the International Nucleotide Sequence Databases (INSD) (DDBJ GenBank), EMBL-EBI Bank (European Bioinformatics Institute and the European Molecular Biology Laboratory) and the National Center for Biotechnology Information (NCBI).

RESULTS

Physiological and biochemical features: The physiological and biochemical characteristics of the isolate are given in Table 1. The examined features of the investigated strain QU66C showed the typical morphology of *Streptomyces* on various agar plates, aerobic, gram-positive, non-motile, non-acid fast.

The morphology of colonies were typically similar to that of *S. coelicolor* where it showed the actinorhodin production and then its conspicuous red color diffusion in the media after 48 h of growth. The isolate was exposed to the most notable test for the *S. coelicolor* is that the red-blue acid-base indicator. Thus the colonies that become red-purple because of actinorhodin production will rapidly turn blue on fuming the colonies with ammonia, consistent with the known pH indicator properties of the compounds.

Table 1: Physio-biochemical features and antimicrobial profile of the isolate strain streptomyces coelicolor AB588124 (QU66C-2202). Bacterial strains used as control (*)

Feature	Presence (+)/Absence (-)
Growth on sole carbon source	
D-Glucose	+
D-Xylose	+
D-Arbinose	+
D-Manitol	+
D-Lactose	+
D-Succurose	+
D-Sorbitol	+
D-Starch	+
Biochemical tests	
Catalase	+
Amylase	+
Gelatin	+
Nitrate reductase	+
Casein	+
Ornithine	-
Indole	-
Urease	-
H_2S production	-
Antibacterial activity	
Echererichia coli ATCC 25922*	+
Staphylococcus aureus ATCC 25923*	+
Pseudomonas aeruginosa ATCC 27853*	+
Escherichia coli	+
Staphylococcus aureus	+
Staphylococcus epidermidis	+
Pseudomonas aeruginosa	+
Bacillus cereus	+
Micrococcus luteus	+
Klebsiella sp.	+
Antifungal activity	
Candida albicans	+
Penicillium strain IM 56	-
Penicillium strain IM 65/3	-

The screening for optimum growth of the strain revealed that the NAS and NBS were the optimum solid and liquid media respectively. For production of the antibiotic droplets on the colonies surface, isolate was cultured on Potato Dextrose Agar (PDA) for 5 days before several droplets (3-5) appeared on the top of each colony.

The isolate has the ability to utilize all tested carbon sources (D-glucose, D-xylose, D-arbinose, D-manitol, D-lactose, D-succurose, D-sorbitol, D-starch). The isolate showed a positive for catalase, amylase, nitrate reductase, starch hydrolyses, gelatin hydrolyses, casein break down but was negative for ornithine, indole and urease as well as hydrogen sulfide production.

Antimicrobial profile of strain QU66C: The antimicrobial profiles of the isolate is given in Table 1. The antibiotic of the strain showed antimicrobial activity against some local medical isolates (all brought from Hamad Hospital, Qatar) such as: *Escherichia coli*, *Bacillus cerus*,

GGACGAACGC	TGGCGGCGTG	CTTAACACAT	GCAAGTCGAA	CGATGAACCA	50
CTTCGGTGGG	GATTAGTGGC	GAACGGGTGA	GTAACACGTG	GGCAATCTGC	100
CCTGCACTCT	GGGACAAGCC	CTGGAAACGG	GGTCTAATAC	CGGATACTGA	150
CCCTCTTGGG	CATCTGCGAG	GTTCGAAAGC	TCCGGCGGTG	CAGGATGAGC	200
CCGCGGCCTA	TCAGCTAGTT	GGTGAGGTAA	TGGCTCACCA	AGGCGACGAC	250
GGGTAGCCGG	CCTGAGAGGG	CGACCGGCCA	CACTGGGACT	GAGACACGGC	300
CCAGACTCCT	ACGGGAGGCA	GCAGTGGGGA	ATATTGCACA	ATGGGCGAAA	350
GCCTGATGCA	GCGACGCCGC	GTGAGGGATG	ACGGCCTTCG	GGTTGTAAAC	400
CTCTTTCAGC	AGGGAAGAAG	CGAAAGTGAC	GGTACCTGCA	GAAGAAGCGC	450
CGGCTAACTA	CGTGCCAGCA	GCCGCGGTAA	TACGTAGGGC	GCAAGCGTTG	500
TCCGGAATTA	TTGGGCGTAA	AGAGCTCGTA	GGCGGCTTGT	CACGTCGGTT	550
GTGAAAGCCC	GGGGCTTAAC	CCCGGGTCTG	CAGTCGATAC	GGGCAGGCTA	600
GAGTTCGGTA	GGGGAGATCG	GAATTCCTGG	TGTAGCGGTG	AAATGCGCAG	650
ATATCAGGAG	GAACACCGGT	GGCGAAGGCG	GATCTCTGGG	CCGATACTGA	700
CGCTGAGGAG	CGAAAGCGTG	GGGAGCGAAC	AGGATTAGAT	ACCCTGGTAG	750
TCCACGCCGT	AAACGGTGGG	CACTAGGTGT	GGGCAACATT	CCACGTTGTC	800
CGTGCCGCAG	CTAACGCATT	AAGTGCCCCG	CCTGGGGAGT	ACGGCCGCAA	850
GGCTAAAACT	CAAAGGAATT	GACGGGGGCC	CGCACAAGCG	GCGGAGCATG	900
TGGCTTAATT	CGACGCAACG	CGAAGAACCT	TACCAAGGCT	TGACATACAC	950
CGGAAAGCAT	CAGAGATGGT	GCCCCCCTTG	TGGTCGGTGT	ACAGGTGGTG	1000
CATGGCTGTC	GTCAGCTCGT	GTCGTGAGAT	GTTGGGTTAA	GTCCCGCAAC	1050
GAGCGCAACC	CTTGTCCCGT	GTTGCCAGCA	AGCCCTTCGG	GGTGTTGGGG	1100
ACTCACGGGA	GACCGCCGGG	GTCAACTCGG	AGGAAGGTGG	GGACGACGTC	1150
AAGTCATCAT	GCCCCTTATG	TCTTGGGCTG	CACACGTGCT	ACAATGGCCG	1200
GTACAATGAG	CTGCGATACC	GCGAGGTGGA	GCGAATCTCA	AAAAGCCGGT	1250
CTCAGTTCGG	ATTGGGGTCT	GCAACTCGAC	CCCATGAAGT	CGGAGTCGCT	1300
AGTAATCGCA	GATCAGCATT	GCTGCGGTGA	ATACGTTCCC	GGGCCTTGTA	1350
CACACCGCCC	GTCACGTCAC	GAAAGTCGGT	AACACCCGAA	GCCGGTGGCC	1400
CAAC					1404

Fig. 1: The full sequence of 16S rRNA gene of the novel streptomyces coelicolor AB588124 (isolate QU66C) with a length of 1404 bp. IUPAC codes: R (A or G), Y (C or T), M (A or C), S (G or C), W (A or T), K (G or T)

Micrococcus luts, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *S. epidermis* and *Klebsilla* sp. It also showed antibacterial activity against the control organisms (brought from the Central Laboratory, Ministry of Health, Jordan) such as: *Staphylococcus aureus* MRSA ATCC 25023, *Pseudomonas aeruginosa* ATCC 27853, *Escheria coli* ATCC 25922. The isolate showed an activity against *Candida albicans* but not against *Penicillum* IM56, *Penicillium* IM 65/3).

The antibiotics production by present strain was determined as described above in the Materials and Methods section. The stain showed a high potential for antibiotics production (data in preparation for the coming study). The strain is capable of production of all antibiotics known for the *S. coelicolor*.

Comparative analysis 16S rRNA sequence of QU66C strain: A full sequence (1404 bp) of the gene which is given in Fig. 1. Initially a partial sequence of the gene (480 bp) was determined (data not shown) in the National Institute for Multicultural Competence (NIMC, UK) during 2002 but the library search-report at that time was not enough to determine the species level, therefore we have waited seven years until we have imported the GA310 sequencer. The full sequence (1404) of present strain was BLASTED with the microbial genome library of the full gene of 16S rRNA, available in the Applied Biosystem (http:// www. appliedbio systems.com). The library search report for the top 20 matching strains were obtained and thus the phylogenetic tree of the top 5 homologous was conducted (Fig. 3). The phylogenetic destination of the strain QU66C is in between *S. coelicolor* A3 (2) (Y00411) (NC003888) and *S. coelicolor* (C) (EF371438) (Fig. 3). The summary of the BLAST given in Table 2 shows that the query strain QU66C has a similarity and identities of 99.40, 99.40, 99.40, 99.33 and 99.31% with variable score value of 2693, 2693, 2687, 2673 and 2673 bits for *Streptomyces coelicolor* A3 (2) (Y00411) (NC003888), *S. violaceoruber* AF503494 (ancient name for *S. coelicolor* and *S. lividans*), *S. lividans* AF503498, *S. lividans* AB184826 and *S. coelicolor* (C) (EF371438), respectively. The positions of the mismatched between the strain QU66C and the compared strains *S. violaceoruber* AF503494 are given in Table 3.

The graphical BLAST and summary of the 16S rRNA sequence of the isolate QU66C are given in Fig. 2 and Table 2, respectively. The searching report out of the *S. coelicolor* database shows that the strain QU66C has a positive high scoring alignment similarity of 99.40% with score of 6907 with five clones of *S. coelicolor* A3 (2) (AL939116, AL939119, AL939124, AL939114, AL939108); whilst shows a 99.00% similarity with a score of 6889 for AL939110. A similar results was obtained when BLAST

Table 2: Library search report of the top 5 high-scoring strains to our isolate streptomyces coelicolor AB588124 (QU66C) as BLASTED in sanger institute (http://www.sanger.ac.uk), DDBJ (http://www.ddbj.nig.ac.jp), applied biosystem (http://www.appliedbiosystems.com), EMBL-EBI Bank (http://www.ebi.ac.uk) and the NCBI (www.ncbi nlm.nih.gov)

Entry name	Accession number	Entry length (bp)	Score	Similarity (%)
S. coelicolor A3 (2)	Y00411 (NC003888)	Full sequence	2693	99.4
S. violaceoruber	AF503494	1531	2693	99.4
S. lividans	AF503498	1507	2687	99.4
S. lividans	AB184826	1457	2673	99.33
S. colicolor (C)	EF371438	1493	2673	99.31

Table 3: Locations of the different 17 base pairs between the full sequence of 16S rRNA gene of the *Streptomyces coelicolor* AB588124 (QU66C) and that of *S. violaceoruber* AF503494. IUPAC codes: R (A or G), Y (C or T), M (A or C), S (G or C), W (A or T), K (G or T)

Entry name	39	103	152	153	155	156	157	164	165	166	168	169	171	190	216	1222	1402
S. coelicolor AB588124 (QU66C)	R	G	M	K	T	T	G	Y	W	W	M	K	K	C	A	G	R
S. violaceoruber AF503494 Similarity (99.4 %)	A	T	C	T	G	C	A	T	G	C	A	G	T	A	T	A	A

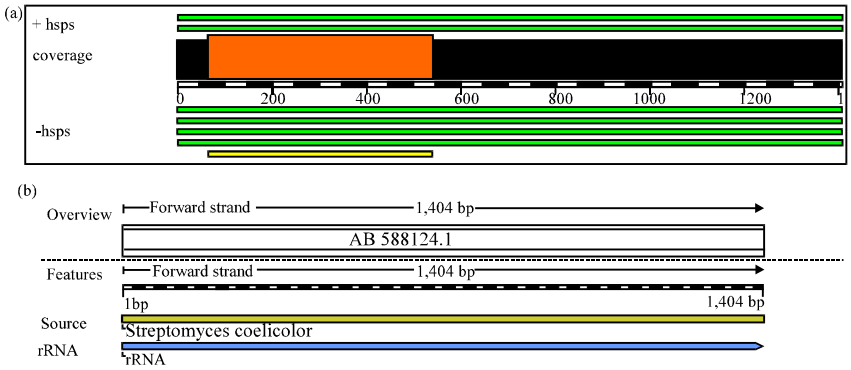

Fig. 2 (a-b): Graphical BLAST of QU66C (1404 bp) as compared to the *S. coelicolor* complete sequence (8, 668, 907 bp) available in Sanger database (http://blast.wustl.edu, webmaster@sanger.ac.uk) (b) The visible feature range of the 16S rRNA of the isolate QU66C as appeared in EMBL-EBI Bank (http://www.ebi.ac.uk)

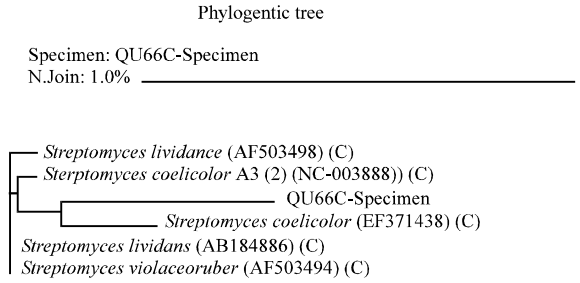

Fig. 3: The inferred phylogenetic tree of the isolate strain (specimen) Streptomyces coelicolor AB588124 (QU66C-2002) using the Neighbor-Joining method

search was carried out on EMBL BLAST in addition to 2 strains of *S. violaceoruber* (AF503494, AF503492) with high score of 2738. Furthermore when the sequence of QU66C was BLASTED with the DDBJ database using the CLUSTAL W (1.83), the strains showed a similarity of 99.40% for the closest 3 strains of *S. coelicolor* EF371438, *S. violaceoruber* AB184833 and *S. lividans* AB 184695.

We have therefore, shown conclusively that on the basis of both phenotypic and genotypic features and according to the criteria reported earlier (Bosshard *et al*., 2003), the strain isolate QU66C should be assigned as *Streptomyces coelicolor* (QU66C-2002). The complete sequence of the 16S rRNA gene of *S. coelicolor* (QU66C) strain has been deposited in the International Nucleotide Sequence Databases (INSD) in the GenBank/DDBJ (connected with GeneBank/EMBL/NCBI) and assigned an accession number of AB588124 under a voucher specimen (Professor Ihsan Mahasneh QU66C-2002). The strains is therefore, hereinafter, known as *Streptomyces coelicolor* (AB588124) (QU66C-2002).

DISCUSSION

The present strain *S. coelicolor* AB588124 (QU66C-2002) has showed a marked and conspicuous phenotypic and genotypic features of *S. coelicolor* compared with homologous strains in different GeneBanks (Fig. 1-3; Table 2, 3) which support present results. The strain was highly (99.40%) identical to *S. coelicolor* A3 (2),

S. violaceoruber and *S. lividans*. This is in full agreement with a previous result reported earlier using the 16S rRNA on the molecular taxonomy of *Streptomyces* collected from different GeneBanks and collections (ATCC, DSM, JCM) where both species *S. lividans* and *S. coelicolor* has given a possibility to be classified as *S. violaceoruber* (Chistova *et al*., 1995). The taxonomy of *S. lividans* is closely related to *S. coelicolor* because it produces the same four types of antibiotics but the Act and Red genes are normally poorly expressed under usual growth condition (Hosoya *et al*., 1998). The majority of the members of this group share highly similar phenotypes and 16S rRNA sequences and thus the biosynthetic gene clusters required for production of this antibiotic must be transferred from *S. coelicolor* into the *S. lividans* (Lai *et al*., 2002; Haifing *et al*., 2002).

Historically, it has been known for many years that the most notable indicator for the *S. coelicolor* is that the red-blue acid-base test (Kieser *et al*., 2000). Present strain started to release its pigments that are blue/green in alkali and red in acidic conditions, thereby giving the bacterial colonies/culture those colors under the respective conditions. Thus the colonies of present isolate that become red-purple because of actinorhodin production have rapidly turned blue on fuming with ammonia which is consistent with the known pH indicator properties of the compounds (Kieser *et al*., 2000). Based on phenotypic and genotypic data, it has been shown conclusively that the isolate QU66C is a novel wild type strain for Qatar and has been given the its name and accession of *S. coelicolor* AB588124 (QU66C-2002) which to be used in antibiotic production. The *S. coelicolor* produces pigments, complex lipids, signal molecules and four kinds of antibiotics including the cyclopentanon methylenomycin, lipoptide Calcium-Dependent Antibiotic (CDA), blue polyketide Actinorhodin (Act) and red tripyrcol undecylprodigiosin (Feitelson *et al*., 1986; Liu *et al*., 2005). The 16S rRNA sequence data provide a conclusive evidence that present isolate is phylogenetically identical to *S. coelicolor* A3 (2), *S. violaceoruber* and *S. lividans*.

CONCLUSION

The present results shows that the present strain is a novel wide type strain capable of antibiotics production without any genetic alteration as it appeared in other strains. Moreover, the present results provides a better understanding of the role of RNase III gene (AbsB) encoded the mRNA for the AdpA transcription factor on regulation of antibiotic production (Lee *et al*., 2006; O'Rourke *et al*., 2009; Anderson and Wellington, 2001; Payne *et al*., 1990).

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