

Relationship of nanobacterium *Cupriavidus gilardii* with formation of kidney stones

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Abstract:

Fifty five kidney stones were gathered from 50 patients in Al-Sader clinical city in Al-Najaf territories. Kidney stone killed by (ESWL), (PCNL) or open an operation. The normal size of stones was under 0.5 cm and with normal load of 0.7 g. The PCR and sequencing results showed that the nanobacteria we refined is 80% like *Nanobacterium* sp. nano P 16S ribosomal RNA quality. This is a pioneer study, the first review in IRAQ that is secluded nanobacteria from kidney stone and show the connection among nanobacteria and kidney stone infection.

Keyword: nanobacterium, *Cupriavidus gilardii*, kidney stones.

Introduction:

Nanobacteria are the littlest cell-walled microscopic organisms, found in human and cow blood and in business cell culture serum. Metabolic speeds of Nanobacteria are extraordinarily lazy, they can make carbonate apatite on their cell envelope mineralizing rapidly a large portion of the accessible calcium and phosphate (National Research Council., 1999).

A few reports on clinical preliminary and serological recognition of Nanobacteria in neurotic material, principally the calcified tissues (aneurysms, carotid plaques, femoral blood vessel plaques, and cardiovascular valves) related with atherosclerosis. There are a few signs that ultrasmall microorganisms can cause or go with urinary contamination, periodontosis, and even malignant growth advancement (Miller et al., 2004 ; Laskin et al., 2005)

A few speculations have been advanced to clarify the etiology of nephrolithiasis however none has had the option to respond to completely the inquiries concerning the instrument of renal calculi arrangement. The known component of stone arrangement is the ensuing strategies like pee supersaturation, gem nucleation and collection, achieving maintenance of gems (nidi) and proceeded with development on the held crystals (Jeong et al., 2007)

The development of kidney stones could be prompted after intrarenal infusion or contamination with Nanobacteria (Ansari et al., 2017). It has as such been suggested that the biogenic apatite layer present on the cell surface may go presumably as a nidus moving the course of crystallization and improvement of calcified stores (Hu delist et al., 2004).

Bio mineralization alludes to the cycles by which organic entities structure minerals, additionally depict as portrays the testimony of mineral inside or outside the cells of living creatures (Boskey., 2003).

It field that ranges both the inorganic and the natural world. Albeit by far most of living beings don't frame mineralized stores, the wonder is still very wide spread, All five realms contain

individuals that mineralize. These organic entities are fit for framing approximately 60 distinct minerals, calcium is the cation of decision for most living beings.

The calciumbearing minerals include around half of known biominerals (Lowenstam and Weiner, 1989). Kidney stones are mineral stores in the renal calyces and pelvis that are discovered free or associated with the renal papillae. They contain clear and normal parts, Stone improvement is significantly normal with speeds of up to 14.8% and growing over the span of late years, and a recurrent speed of up to half inside the underlying 5 years of the basic stone scene (Khan et al., 2016).

The aim of study:

Isolation and identification of Nanobacteria (*Cupriavidus gilarrdii*) from kidney stones.

Materials and methods:

Materials

Polymerase chain reaction materials :

1: PCR master mix :According to Maxime PCR PreMix kit (i-Taq).

2: Molecular weight DNA marker :According to KAPA Universal Ladder kits .

3:DNA extraction from Nanobacteria :According to Protocol of G- spin DNA extraction .

4. :Agarose gel electrophoresis of DNA .

Preparation of the Agarose gel :According to Sambrook et al (1989) .

The primer used in the study :

The primer was investigated by IDT (Integrated DNA Technologies company, Canada).

Forward: 5'- AGAGTTTGATCCTGGCTCAG- 3'

Reverse: 5'- GGTTACCTGTTACGACTT- 3'

Product size
1485 base pair

Molecular detection of NB using PCR

PCR PreMix Kit (Table 3-1) is the item what is blended each part: I-Taq DNA Polymerase, dNTP combination, response cradle (Table 3-2) . Do PCR simply add a layout DNA, groundwork set, and D.W (Table 3-3). The subsequent explanation is that it has Gel stacking cradle to do electrophoresis, so we can do gel stacking with practically no treatment.

Table(3-1): The Components of the Maxime PCR PreMix kit (i-Taq)

Material	Concentration
5U/ μ l	i-Taq DNA Polymerase
2.5mM	DNTPs
1X	Reaction buffer (10X) Gel loading buffer

Table(3-2): Mixture of the specific interaction for diagnosis gene

Components	Concentration
Taq PCR PreMix	5 μ L
Forward primer	1.5 μ L (10 picomols/ μ L)
Reverse primer	1.5 μ L (10 picomols/ μ L)
DNA	5 μ L
Distill water	UP TO 20 μ L

Table(3- 3): The optimum condition of detection gene

No.	Phase	Tm (°C)	Time	No. of cycle
1 cycle	3 min	95°C	Initial Denaturation	1
40 cycle	45sec	95°C	Denaturation - 2	2
	45sec	52°C	Annealing	3
	1.5min	72°C	Extension-1	4
1 cycle	10 min.	72°C	Final Extension	5

DNA Sequencing and Sequence Alignmen

Sequencing of gene was performed by national instrumentation center for environmental management (nicem) online at (http://nicem.snu.ac.kr/main/?en_skin=index.html), biotechnology lab, machine is DNA sequencer 3730XL, Applied Biosystem), Homology search was conducted using Basic Local Alignment Search Tool (BLAST) program which is available at the National Center Biotechnology Information (NCBI) online at (<http://www.ncbi.nlm.nih.gov>) and BioEdit program.

RESULTS:-

55 kidney stones were gathered from 50 patients in Al-Sader clinical city in Al-Najaf areas. Kidney stone eliminated by extracorporeal shockwave lithotripsy (ESWL), Percutaneous

nephron lithotomy (P C N L) or open an medical procedure .The normal size of stones was under 0.5 cm and with normal load of 0.7 g .

The PCR and sequencing results showed that the band of nanobacteria is show up on 1485 bp

Initial step to guarantee that DNA isn't divided .we use electrophoresis and the outcome allude to that DNA was complet and not divided . To guarantee of the presence of DNA in examples , after extraction we tried it by Biophotometer and the aftereffect of focus between 130 ug\ml to 378 ug\ml , while the purity is between 1.59 to 1.86 (OD 260\280).

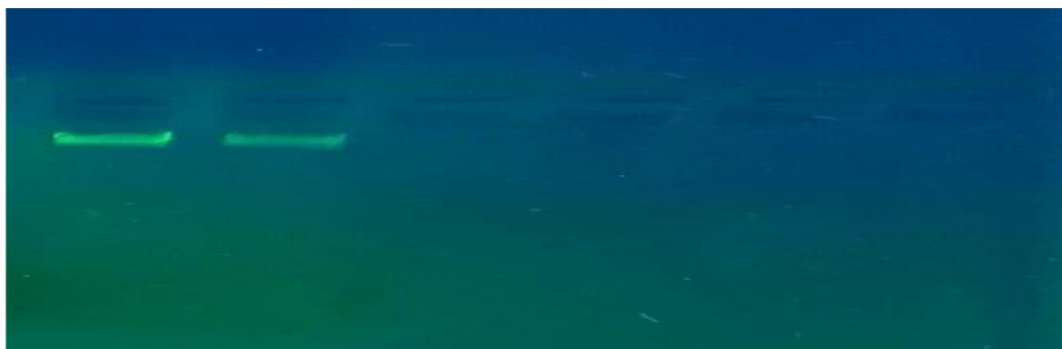


Figure (4-1): Gel electrophoresis of genomic DNA extraction from *Nanobacteria*, 1% agarose gel at 5 vol /cm for 1:15 hour

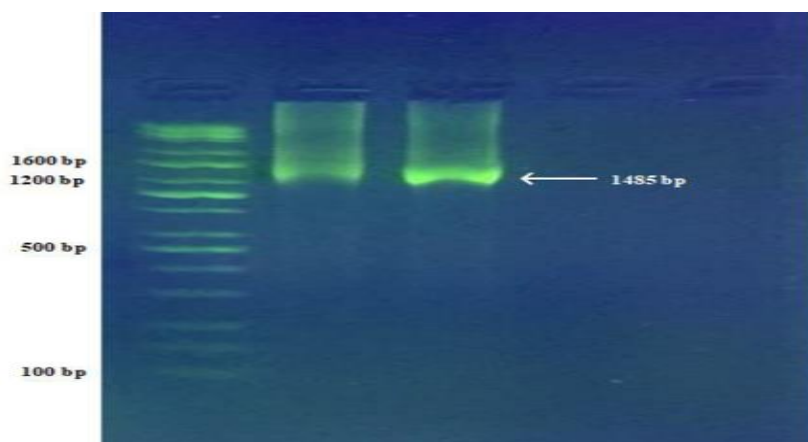


Figure (4-2): PCR product the band size 1485 bp. The product was electrophoresis on 2% agarose at 5 volt/cm. 1x TBE buffer for 1:30 hours. M: DNA ladder (100-10000).

Sequencing

The sequences producing significant alignments: 80 % identical with nanobacterium sp. Nano p 16 s rRNA (Figure 4-4 and 4-5).

The partial seguencing is :

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AACGAAGGCGGCTGCAGGCTTAACACATGCAGTCGAACGGCCCACCAGGGGGTTGCAGACGGGTT
GGTAAGTGGGGGAAAGATAGCCTAAGCTCCGAATGTGCGCGTGCGAGATCGATAACTCCGGGAAA
CTGCAATTCATACCGCATAACGAGCTACGGGGGAGAGACTGGGACCTCGGGGACTAGGATATGACCA
TGGGTTGGATTAGCTAGTTCGTGATGTTAAGGCTACCAAAGCCACGATCCATATCTGTTCTGAGAG
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GATGATGAGCCACTTGTGGAAGTGAAGTTCGGTCCAAACCCCTACGGGAGGCGGCGGTGGGGAAG
ATTGGAAAATGGGGGCATGAGCCTAATCCAGCCATACCGCTTGCCTGATTAAGGTCATAGGGTTGT
GAAGTCTTTACATCGTGAGAAGATAATGAGGAATTCGGAGAAGAGGACCAGGCTAACTTGGTGCC
ATCAGCCGTGGAAATAGAACGGGGCTAGCGTTGTTCCGGAATTTCTGGGCGTAAGCGCACGTAGGTG
GATATTTAAGTGAGGGTAAAGGTTCCAGAGCTTAACTCTGGAACACCATTGAATTACTGGGTATCTT
GGGTATGGAAAAGGTAAGTGAATTCCGAGTTTAGGGGTGGAATCCGGGATATCCGGGGGGCATA
ACTACCAGGGGGCAAGCGGCTTACTGGGGATTGCAATTTACTCGTGACACATTTATGAGGTGCGTTA
AAGGGGGGGGAACAAACAGGATTAGATATCGTTGTAGTTCCCCCCTAAACGATGAATTTTTCTT
CGGGCAGTTTACTGTTGGGGCGCAGCAGGCATTAACCTCCCCCGGGGAGTACCATCCAAAATA
AAAACCAAAGGAATTGACGGGGGTCCGCACCAGGGGTGGAGAATGTTGTTTAATTCTAAGCAACG
CGCAGAAACTTACCAGCTTTTACATTCGGGTTATGCGCGGGTGGAGAACGATGTCCTTTCATTAGG
CTGTCCACAGAACAGGTGCTGCATGGCGGTCGTCAGCTCCTGTCATTAGATTTTAGGTTAAGTCCCG
AACGACCGCCCCCCCCCTTAGTTACCCGCGTTGAGTTGAAGGCACTTTAACGCGACGTTTTTTTTGC
GGCCGGTGATACACCCGCCAGAAGATGGGGGGATGTCGTCAATTTCTCTGGCCCCACTTACAAT
TGTTTTGCTAGGCTACAACGAGACGTGTTAATCTATGGTGATTACAGAGGAAGCGAGACTGCGCTGT
CGAGCTAACTCTCCAAAAGCAATCTCAGATCGAATTGCGCTCTGCAACACAAGTGCATGAGAGTTG
AATCGCTAGTTACCGCAATCAGCATGGTGAGGTGAATCCCTTCCCGGGCCCTCTGCACACCGCACAT
CATAACAGGGGAGTCGGTTTTAACCCGAAGGTAGTGCCTAAACGCAAGGAGGAAGCTAACCGCCA
CGGGTAGGGGCAGCGACTGAGGTG
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Length = 1485 base pairs

Molecular Weight = 449932.00 Daltons, single stranded

Molecular Weight = 903269.00 Daltons, double stranded

G+C content = 51.99%

A+T content = 48.01%

Nucleotide compositions of *nanobacterium* as showed in (figure 4-28).

Nucleotide Number Mol%

A 378 25.45

C 330 22.22

G 442 29.76

T 335 22.56

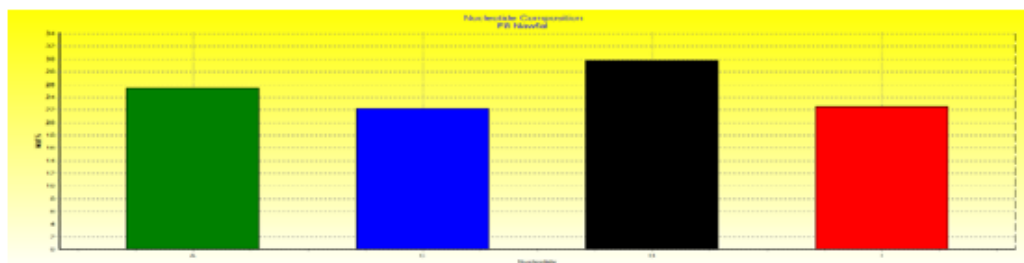


Figure (4-3): Nucleotide compositions of *nanobacterium*, which is show that : A 378 , C 330 , G 442 and T 335

Description	Max score	Total score	Query cover	E value	Ident	Accession
<input checked="" type="checkbox"/> Nanobacterium sp. nanoP 16S ribosomal RNA gene, partial sequence	1207	1207	100%	0.0	80%	JN029830.1
<input type="checkbox"/> Agrobacterium tumefaciens strain S-188E 16S ribosomal RNA gene, partial sequence	1198	1198	100%	0.0	79%	JF513176.1
<input type="checkbox"/> Agrobacterium sp. strain CIP 107444 16S ribosomal RNA gene, partial sequence	1195	1195	100%	0.0	79%	MF443190.1
<input type="checkbox"/> Uncultured bacterium clone OTU48 16S ribosomal RNA gene, partial sequence	1195	1195	100%	0.0	79%	KP975304.1

figure (4-4): the sequences producing significant alignments: 80% Identical with nanobacterium sp. Nano p 16 s rRNA.

Nanobacterium sp. nanoP 16S ribosomal RNA gene, partial sequence
Sequence ID: [JN029830.1](#) Length: 1407 Number of Matches: 1

Score	Expect	Identities	Gaps	Next Match	Previous Match
1207 bits(1338)	0.0	1196/1504(80%)	116/1504(7%)		
Query 1	AACGAAAGGC - GCCTGCAGGCTTAAACACATGCA - GTCGAAACGGCCACCAGGGG - GTTGCA				57
Sbjct 1	AACGAAAGGC - GCCTGCAGGCTTAAACACATGCA - GTCGAAACGGCCACCAGGGG - GTTGCA				60
Query 58	GACGGGTTGGTAAAGTGGGGGAAAGATAGCCTAAGCTCCGGAATGTGCGCGTGGAGATCGA				117
Sbjct 61	GACGGGTTGGTAAAGTGGGGGAAAGATAGCCTAAGCTCCGGAATGTGCGCGTGGAGATCGA				102
Query 118	TAAC TCCGGGAAACTGCAATTCATACCGCATACGAGCTACGGGGGAGAGACTGGGACCTC				177
Sbjct 103	TAGCTCCGGGAAACTGCAATTCATACCGCATACGAGCTACGGGGGAAAGATTTA - - - - TC				158
Query 178	GGGGACTAGGATATGACCATGGGTGGATTAGCTAGTTCGTGATGTTAAGGCCATACCAMA				237
Sbjct 159	GGGGA - - AGGATTGGCC - - GCGTTGGATTAGCTAGTTCGTGATGTTAAGGCCATACCMA				214
Query 238	GCCACGATCCATATCTGTTCTGAGAGGATGATGAGCCACTTGTTGGAACCTGAAACTCGGTC				297
Sbjct 215	GCCACGATCCATATCTGTTCTGAGAGGATGATGAGCCACT - TGGGACTGAGACACGGCC				273
Query 298	CAAAACCCCTACGGGAGGCCGGCGTGGGGAAGATTGGAAAAATGGGGGCATGAGCCATATCC				357
Sbjct 274	CAAACTCCTACGGGAGGCCAGCAGTGGGGAATATTGGACAAATGGGGGCA - - AGCCATGATCC				331
Query 358	AGCCATACCGCTTGCCTGATTAAGGTCATAGGGTTGTGAAGCTCTTTACATCGTGAGAAG				417
Sbjct 332	AGCCATGCCGCGTGAATGATGAAGCCCTTAGGTTGTAAAGCTCTTT - CACCG - GAGAAG				389
Query 418	ATAATGA - GGAATTCGGAGAAGAGACCAGGCCTAACCTGGTGCATCAGCCGTGGAAAAA				476
Sbjct 390	ATAATGACGGTATCCGGAGAAGAGACCAGGCCTAACCTGGTGCATCAGCCGTGGAAAAA				449
Query 477	- GAACGGGGCTAGCGTTGTTTCGGAATTTCTGGGCGTAA - GCGCACGTAGGTGGATATTTA				534
Sbjct 450	CGAACGGGGCTAGCGTTGTTTCGGAATTTACTGGGCGTAAAGCCGACCTAGGCGGATATTTA				509
Query 535	AGTGAGGTTAAAGTTCCAGAGCTTAACTCTGGAAACA - CCATTGAAATAGCTGGGTATCTT				593
Sbjct 510	AGTCAGGGTGAAATCCCAGAGCTCAACTCTGGAACTGCCTTTGA - - TACTGGGTATCTT				567
Query 594	GGGTATGGAAAAGGTAAGTGGAAATCCGAGTTTAGGGGTGGAATCCGG - GATATCCGGGG				652
Sbjct 568	GAGTATGGAAAGAGTAAAGTGGAAATCCGAGTGTAGAGGTGAAATTCGTAGATATTCGGAG				627
Query 653	GGCATAACTACCAGGGGCGAAG - CGGCTTACTGGGGATGCAATTTACTCGTGACACATT				711
Sbjct 628	G - - - - AAC - ACCAGTGGCGAAGGCGGCTTACTGG - - - - TCCA - - TACT - - - GACGCG - - -				670
Query 712	TATGAGGTGCGTTAAAAGGGGGGGAAACAAACAGGATTAGATATCGTTGTAGTTCCCCCCCC				771
Sbjct 671	- - TGAGGTGCG - - AAAGCGTGGGGAGCAAAACAGGATTAGATACCTTGTAGT - CCACGCGC				725
Query 772	cTAAACGATGAATTTT - CCTTCGGGGAGTTTACTGTT - - GGGGCGCAGC - - AGGCATTA				826
Sbjct 726	GTAAACGATGAATGTTTAGCCGTCGGGCGAGTATACTGTTTTCAGTGGCGCAGCTAACGCATTA				785
Query 827	AACCTCCCCCGGGGGAGTACCATC - CAAAAATAAAACTCAAAGGAAATGACGGGGGTCC				885
Sbjct 786	AACATTCGCGCTGGGGAGTACGATCGCAAGATTAAAACTCAAAGGAAATGACGGGGGGCC				845
Query 886	GCACCAGGGGTGGAGAAATGTTGTTTAAATCTAAGCAACCGCGCAGAAAATACCAGCTCTT				945
Sbjct 846	GCACAAGCGGTGGAGCATGTGGTTTAAATCTGAAGCAACCGCGCAGAACTTACCAGCTCTT				905
Query 946	TACATTCGGGTTATGCGCGGGTGGAGAACGATGTCCTTTCATTAGGC TGTCCACAGAACA				1005
Sbjct 906	GACATTCGGGGTATGGG - ATTGGAG - ACGATGTCCTTCAGTTAGGC TGGCCCCAGAACA				963
Query 1006	GGTGTGCATGGCGGTGCTCAGCTCCTTGCATTAGATTTTAGGTTAAGTCCCAGCAACGAC				1065
Sbjct 964	GGTGTGCATGGCTGCTGCTCAGCTCCTGCTGCTGAGATGTTGGGTTAAGTCCCAGCAACGAG				1023
Query 1066	CG - - - - - TTAGTTACCCCGGTTGAGTTGAAGGCACTTTAACCGCGACGTTTTTTT				1123
Sbjct 1024	CGCAACCTCGCCCTTAGTTAGTTGCCAGCATTTAGTTG - - GGCACCTAAGGGGA - - - - -				1073
Query 1124	ttGCGGGCGGTGATACACCCGCCAGAAAGATGGGGGATGTCGTCAATTTCTCCTGGCC				1183
Sbjct 1074	- - - CTGCGGGTGATA - - - - AGCCGAGAGGAAGGTGGGATGACGCTCAAGTCTCATGGCC				1126
Query 1184	CCACTTACAATGTTTTGCTAGGCTACAACGAGACGTGTTAATCTATGGTGATTACAG - A				1242
Sbjct 1127	- - - CTTAC - - - - - GGGCTGGGCTAC - - - - ACACGTGCTA - - CAATGGTGGTGACAGTG				1170
Query 1243	GGAAGCGAGACTGCGCTGTGAGCTAACTCTCAAAAAGCAATCTCAGATCGAATTTGCGCT				1302
Sbjct 1171	GCCAGCGAGACAGCGATGTCGAGCTAA - TC TCAAAAAGCCATCTCAGTTTCAAATGCACT				1229
Query 1303	CTGCAACACAAAGTGCATGAGAGTTTCAATCGCTAGTTACCGCA - ATCAGCATGGTGGAGT				1361
Sbjct 1230	CTGCAACTCGAGTGCATGA - AGTTGGAATCGCTAGTAATCGCAGATCAGCATGCTGCGGT				1288
Query 1362	GAATCCCTTCCGGGGCCCTCTGCACACCCGACATCATACCAGGGGAGTCGGTTTTAAACCC				1421
Sbjct 1289	GAATACGTTCCCGGGCCCTTGTGCACACCCCGTACACCATGGGAGTTGGTTTT - ACCC				1347
Query 1422	GAAGGTAGTGCCTTAAACGCAAGGAGGAAGCTAACCGCCACGGGTAGGGGCGAGGACTGA				1481
Sbjct 1348	GAAGGTAGTGCCTTAAACGCAAGGAGGAGCTAACCCAC - - - - GGTAGGGTCAGGACTGG				1403
Query 1482	GGTG 1485				
Sbjct 1404	GGTG 1407				

Figure (4-5): the partial nucleotide sequence of 16 sRNA NB. Which show 80% similarity with *nanobacterium sp.*

Discussion:

PCR results show the 1485 bp portion . in this review we have severe strategies of PCR. Nothing could be found in the negative benchmark group and there was no microscopic organisms. We support the aftereffects of PCR. Subsequently, the expansion in exact new 16S rRNA groupings and the advancement of elective gees for sub-atomic recognizable proof of certain taxa ought to additionally work on the handiness of sub-atomic ID of NB. The 16S rRNA sequencing gives unambiguous information even to uncommon separates, which are reproducible in and between labs.

16S rRNA arrangements homology investigation upholds the view that biomineralization was presence of NB distinctive strain in the diverse tissue .While most writers discovered NB in kidney stones, Drancourt neglected to separate NB in refined material from 10 models, though recognized nanoparticles in material separated by SEM (Drancourt et al., 2003). This blunder between results gained by SEM direct examination of renal stones and culture motivation is an enchanting one. When in doubt, most reports have shown that examination by SEM is more capable than culture to perceive NB . One request rises out of this finding: in the event that NB are precursors of renal stones, as affirmed by various specialists, why culture is a less useful area methodology? A single possibility is that for start creating NB it would be fundamental a base beginning number of particles which would not occur in all stones (Simonetti et al., 2012),Kumon found NB in around 60%of the urinary stone models among Japanese and Paraguayan patients(Kumon et al., 2011) .

Nucleic corrosive examination on NB has numerous issues, e.g., nucleic corrosive extraction is troublesome because of apatite and separated DNA-like material has hindered the intensification of exogenous bacterial DNA in PCR techniques. More exertion ought to be made for the portrayal of NB(Kajander et al., 2003).Conclusion: -All type of kidney stone contine nanobacteria.

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