

550.47

« »?

1* 2 1 2
2 3 4 4
1 1 4

25.11.2013

()

22.08.2013

36-

« »

()

16.09.2013

Mycobacterium

Bacillus

16S

Mycobacte-

ria

(803

)

20

GenBank®

100%

Delftia

Comamonadaceae

Burkholderiales

10

:

MYCOBACTERIUM, *DELFTIA*,

[4,

5]

[6-8].

I

Micrococcus luteum,
Mycobacterium albus, *Circinella muscae*, *Asper-*
gillus niger, *Papulaspora anomala*, *Penicillium*
notatum [9, 10]; *Bacillus simplex*, *Staphylococcus*
pasteuri, *Engyodontium album* [11]; *Deinococcus*
aetherius [12]; *Bacillus isronensis* [13].

[1],

«

»,

[2, 3],

«Gemini» [14]

(

«

»

«Exposure» [15,

16,17

],

«

» [7],

«Microbe» [18],

O/OREOS

[19]),

-

1- « », * - syroeshkin@ipg.geospace.ru

2 « »

4- « « » . . . »

3- « »

II -

() . , ,

(50) .

[20].

(50) .

Amicon Ultra-15

(Millipore), 400

() [21, - . 22,

23].

[24, 25].

6M

SiO₂. ()

0,03³

()

16S -

0,025³.

0,005³

0,02³

8,8 (25), 16,6 (NH₄)₂SO₄, 0,01%
-20, 1,5 MgCl₂, 0,2 dNTPs,

22

10

, 1,25 . Taq
16S

2013

(36)

« » ()

2-

F27/R1493.

2

« » (2)

MTG1/MTG4

(1)

MTG1/MTG4

(2).

Bacillus

2

2

« »

« "Hot start" »

γ-

Taq

: 95 - 30

« »

(30 ,

72 - 30 (1), 62

1).

2

25:36.

).

(

(GeneClean)
 (ABI 377,)
 MacVector/AssemblyLign (Oxford
 Molecular Group,).



«BLAST» 2.2.28+
<http://blast.ncbi.nlm.nih.gov/Blast.cgi>
 «DNASar», MegAlign, MacVec-
 tor/AssemblyLign (Oxford Molecular Group,
).
 ClustalV and Clus-
 talW

. 1.

« »
 « »
 « »
 « »

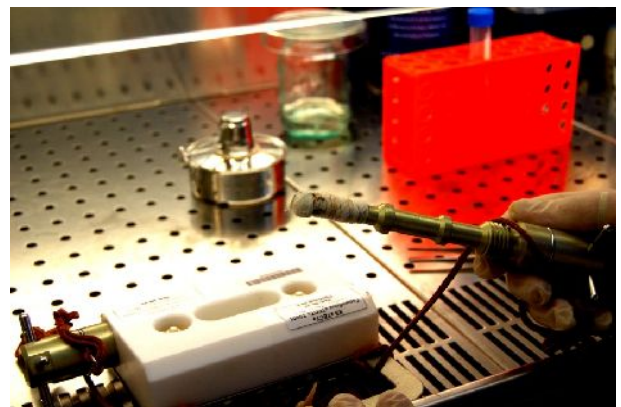
«Tanpopo»

2

[27].

«Tanpopo»

[28,
 29]. « » 2,
 « » (10.11.2009),



. 2.

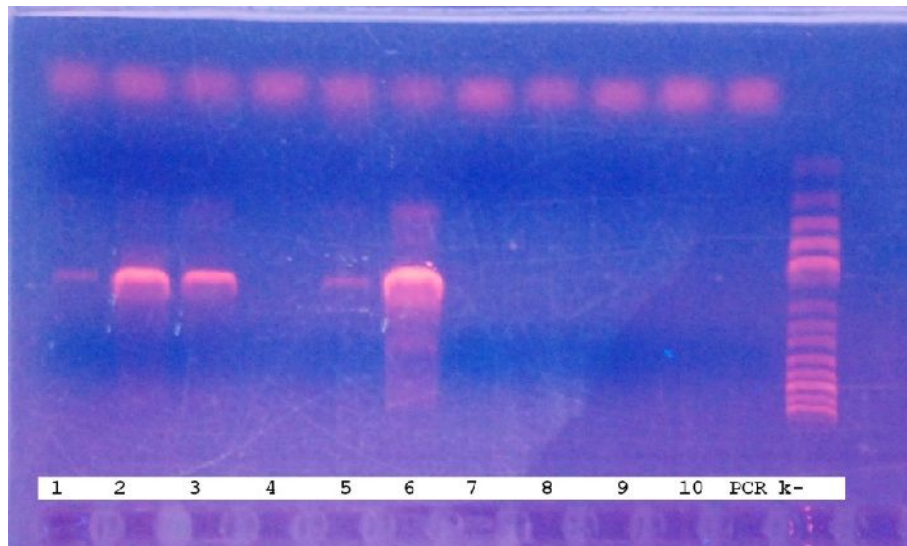
« II »

1

1.

« ».

	() / (%)			
	1	2	3	4
1	0,04 / 0,1	–	0,69 / 98	5,3 / 1,9
1	0,17 / 22	0,33 / 75	–	4,8 / 3
2	0,11 / 32	0,44 / 36	0,84 / 20	5,5 / 12
2	0,10 / 38	0,26 / 59	–	5,0 / 3



3. - , 16S- 1 - 1, 2
 - , 1, 3 - 2, 4 - 2, 5
 - 2, 6 - 2, 7 - 1, 8
 - 2, 9 - 2, 10 - 1, 11 11 (PCR k-) -
 . 12 (100 .).

AGAGTACGGTAGAGGGGGATGGAATTCCGCGTGTAGCAGTGAAATGCGTAGATATGCGGAGGAACACCGATGGCGAAGGCAAT
 CCCCTGGACCTGTACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCTAAACGAT
 GTCAACTGGTTGTTGGGAATTAGTTTTCTCAGTAACGAAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGCCGCAAGGTTG
 AAACCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGATGATGTGGTTAATTCGATGCAACGCGAAAAACCTTACCCACCTT
 TGACATGGCAGGAAGTTCCAGAGATGGATTCTGCTCGAAAGAGAACCTGCACACAGGTGCTGCATGGCTGTCGTGAGCTCGTG
 TCGTGAGATGTTGGGTTAAGTCCCAGCAACGAGCGCAACCCTTGTCATTAGTTGCTACATTGAGTTGGGCACTCTAATGAGACTGCC
 GGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAGTCTCATGGCCCTTATAGGTGGGGCTACACACGTCATACAATGGCTGG
 TACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCCATAAAACAGTCGTAGTCCGGATCGCAGTCTGCAACTCGACTGCGTG
 AAGTCGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGTCTTGACACACCCCGCTCACACCATGG
 GAGCGGGTCTCGCCAGAAGTAGGTAGCCTAACCGCAAGGA

4.

803 . . ,

16S-

Delftia

(DLS) [26].

1

[26].

(<http://www.marinespecies.org/aphia.php?p=taxdetails&id=571139>).

2

2-

()

Delftia

Mycobacteria,
40%

16S-

: . 3

(. 5).

2

803

(.)

. 4.

Delftia.

«BLAST» 2.2.28+ , 20

Mycobacteria sp.,

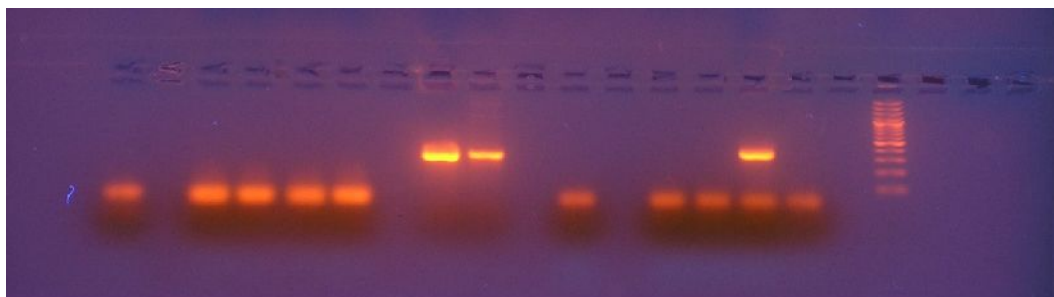
NCBI GenBank®, 100%
Delftia; *Comamonadaceae*
Burkholderiales [30].

<http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=80865&lvl=3&lin=f&keep=1&srchmode=1&unlock>.

ria sp.

Mycobacte-

. 6.



1 2 3 4 5 6 7 8 9 10 11 12 13

. 5.

Bacillus anthracis (2-6)
; 2-5 -

Mycobacteria sp. (9-12). 1
1, 2 1, 2;

6

Bacillus anthracis; 7 -

, 300 . . ; 8

2; 12 - 2; 13

, 9 - 1; 10 - 1; 11

, 100 . .

TAGATCGAGCTGGAGGATCCGTACGAGAAGATCGGCGCTGAGCTGGTCAAGGAAGTTGCCAAGAAGACTGACGACGTCGC
GGGTGACGGCACTACTACCGCCACCGTGCCTTGCCAGGCTCTGGTCAAGGAAGGTCTGCGTAACGTCGTTGCCGGCGCCA
ACCCGCTCGGCCTGAAGCGCGGCATCGAGAAGGCCGTGGAGGCCGTACCAGCTCTCTGCTGGACTCCGCCAAGGAGATC
GACACCAAGGAGCAGATCGCGGCCACCGCGGCATCTCCGCGGGTGACCAGTCCATCGG

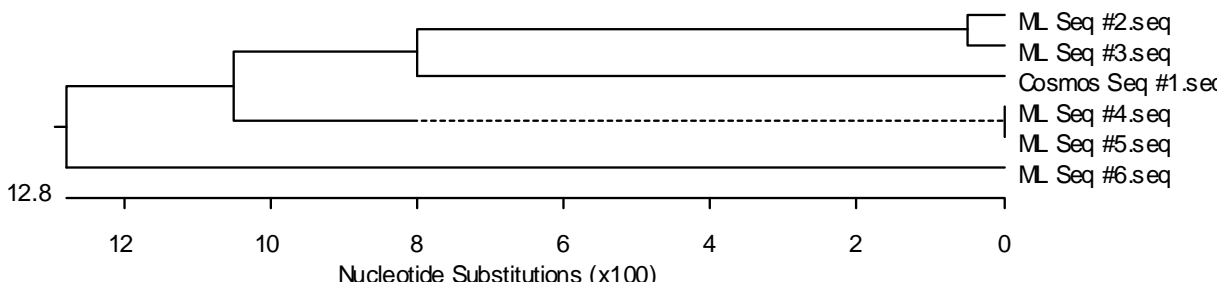
. 6.

Mycobacteria sp.

2.

2 2.

		<i>Delftia</i>	<i>Mycobacteria sp.</i>	<i>Bacillus anthracis</i>
-	1	+	-	-
	1	+	-	-
« - »	2	+	-	-
	2	+	+	-



.7.

Mycobacteria sp., Cosmos Seq #1 -

ML Seq #2 - ML Seq #6 -

Mycobacteria

sp.,

(« »)

(2006-2008).

«

»,

400

7.

92%.

II

«BLAST» 2.2.28+

20

NCBI GenBank®,

99%

M. chelonae *M. marinum*.

7)

3.

(60)	<i>Delftia</i> * ¹ , <i>Mycobacteria</i> * ²	[24,25]
(~ 12-60)	<i>Bacillus</i> [11, 13], <i>Deinococcus</i> [12], <i>Mycobacteria</i> [9, 10]	[37], [38]
(0--12)	<i>Bacillus</i> , <i>Corynebacterium</i> , <i>Microcococcus</i> , <i>Staphylocococcus</i> etc [20, 28, 32], <i>Mycobacteria</i> ² [35]	[34]. ¹ [31].

* – ; [30];
 1 – *Delftia* 92%
 2 – (), . 7.
 93% 5- (,),
 [37, 38].
Mycobacteria. (–
 . 3), [10, 20].
 [22, 23, 39]
 [24,
 25].
 [31-35]. [40-42], « »
 3
 « - ».
 [36].

Delftia *Mycobacteria*

[44, 45]

6

[46] ([34-35])

[6-8],

EXPOSURE-E

0,4

[6, 47],

[43].

Cosmic dust samples collected from the window of the International Space Station (ISS), the formation- enriched vector forward flight to the swab sampler "TEST" during spacewalk 22/08/2013 by crew member of Expedition 36 AA Misurkin. After delivery of the probe to the Earth washings with tampons and pads material (located in the sampler in vacuum) were analyzed 16.09.2013 by the presence of bacterial DNA using nested PCR using pairs of primers DNA genus *Mycobacterium*, DNA strains capsular bacteria *Bacillus* and DNA encoding 16S ribosomal RNA. Accordingly, the listed primers for amplification of the results obtained guidance on the content in the samples of cosmic dust of the bacteria genus *Mycobacteria* and unknown-kind bacteria, wherein the PCR product was sequenced. Phylogenetic analysis of the PCR product sequencing (803 bp) with more than 20 million DNA sequences from the database GenBank, showed 100% identity with the sequence of genus *Delftia* family *Comamonadaceae* order *Burkholderiales*. The presence of wild land and marine genera bacteria (not less than 10 copies per square centimeter) on the ISS indicates their possible transfer from the stratosphere into the ionosphere with the ascending branch of the global electric circuit

KEYWORDS: THE INTERNATIONAL SPACE STATION, PCR ANALYSIS OF DNA, THE GENUS MYCOBACTERIUM, THE GENUS DELFTIA, THE ASCENDING BRANCH OF THE GLOBAL ELECTRIC CIRCUIT.

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