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KEGG (Kyoto Encyclopedia of Genes and Genomes) (*Pathway maps*) [2], *ENTREZ Genome Database*, *Pseudomonas Genome Database V2*.

(NCBI) *ENTREZ Genome Database*,

[3],   *Pseudomonas Genome DatabaseV2 (Database Search)* [4].   -   *Genome Statistics - Candida*.

•

,   *Pseudomonas, Burkholderia, Corynebacterium*

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(1).

,   ,   *Pseudomonas, Burkholderia, Corynebacterium, Ralstonia, Bdellovibrio*
(nahF, doxA, nahW, phnE, ndoB, ndoA)

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n-   (C$_2$-C$_7$)   *Pseudomonas sp.,*
(cnbR, orf1, cnbCb, cnbI).

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[5].

Pseudomonas sp., Sphingomonas sp.   Brevibacterium sp.   ,
(ndoA, dbfA). *Pseudomonas sp.*
Staphylococcus auricularis DBF63

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Pseudomonas   .

                                                                        ,

                            .

                        (*bphB*).
                                    Pseudomonas   sp

                .   ,

Pseudomonas aeruginosa,

                                                                [6].   36,8   %
                                                                [6].
                                                    (*arB,   arA*)   *Pseudomonas sp.,*
Sphingomonas   sp.,   Escherichia   coli   -

                                                                                    ,

                            .

                                        Burkholderia, Nocardia, Rhodococcus, Mycobacterium
            Pseudomonas

                                                    ,   ,   .

                                                                                ,

                                                                        Pseudomonas.

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1	2	3	4	5
Pseudomo-nas putida	-		*nahAa*	
			nahAb	
	NAH7		*nahB*	*cis-* -
		,	*nahF*	-
		2-	*nahC*	1,2- -
			nahG	c
Pseudomo-nas putida NCIB9816	-		*ndoA*	
			ndoB	
			ndoC	
Pseudomo-nas sp. strain U2	-		*nagB*	*cis-* -
			nagF	
Burkhold-eria sp.	-	,	*phnF*	

		, ,	*phnE*	-
		,	*phnB*	
Pseudomo- nas putida OUS82	-	,	*pahAa*	
		,	*pahB*	*cis-* -
		,	*pahE*	-
Pseudomo- nas stutzeri AN10	-		*nahG*	-1-
	2- -		*nahW*	-1-
Noca rdio-des sp. strain KP7	-		*phdA*	-
			phdB	-
			phdD	
			phdK	2-
Rhododoc- cus sp. strain 124	-	,	*nidA*	
		,	*nidB*	
		,	*nidC*	*cis-* -
Mycobacte- rium sp. PYR-1	-		*nidD*	
			nidB	*nidB* -
Sphingomo- nas paucimobil- is var.	-		*pbhA*	
		,	*pbhB*	
			pbhC	-
		,	*pbhD*	
Pseudomon as putida HS12/pNB1	-	4- -	*cnbR*	
		4- -	*orf1*	
		4- -	*cnbCb*	2- -1,6-
		4- -	*cnbE*	2- -4-
		4- - -	*cnbI*	2- -4-

3

Pseudomonas aeruginosa UCBPP-PA14	-	,	*cyp23 (picK)*	*cyp23* - 450-
	- -	,	*adhC (fdh)*	
P. aeruginosa PAO1		,		450-
Corynebacterium sp. (7E1C)	-	-	*CYP153*	*CYP153* - 450-
Acinetobacter sp. EB104	-	-	*CYP153*	*CYP153* - 450-
Corynebacterium glutamicum ATCC	-	,	*cgl0553*	*cgl0553* - 450-
Corynebacterium jeikeium	-	,	*cypX*	*cypX* - 450-
Pseudomonas sp			*ndoA*	-1,2-
			dbfA	- 9-
Pseudomonas sp. strain LB400				-1,2-
			bphB	2,3- -2,3- -
Pseudomonas aeruginosa	-		*ST1118*	-
			adh	
Pseudomonas sp. CA10			*arA*	-1,9 -
Pseudomonas sp. CA10			*arB*	2- -2,3- - 1,2-

10^- 20 [7].

450.

450 -

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Candida   ,   (. *guilliermondii*, .
tropicalis,   . *lipolytica*)   ,
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[8].

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[9].

ENTREZ Genome Database,
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450   (*alk1(CYP52A1), alk2(CYP52A2), alk3(CYP52A3),
alk4 (CYP52A4), CYP52A14, CaALK8*)
Candida tropicalis, Candida maltosa, Candida albicans   Yarrowia lipolytica (.
2).

2 -   ,
-

1	2	3	4
Candida maltosa	- , - , -	*alk1(CYP52A1)*	P450alk-
	-	*alk2(CYP52A2)*	*CYP52A2* - P450alk-
	- ,	*alk5(CYP52A5)*	*CYP52A5* - P450alk-
	- (C_{10}- C_{16})	*NCP*	NADPH- P-450
Candida tropicalis	- (C_{10}- C_{16})	*CT-T3A*	
	- (C_{10}- C_{16})	*CT-T1B*	
	- (C_{10}- C_{16})	*NCP*	NADPH- P-450
	- (C_{10}- C_{16})	*CYP52A12*	*CYP52A12* - P450
Yarrowia lipolytica	- , - , - ,	*alk1*	P450alk-

	- , - , - ,	*YAS2*	,
			alk1
	- , - , - ,	*alk2*	P450alk-
Candida albicans	- (C_{10}-C_{16})	*CaALK8(CYP52A21)*	CYP52A21- - P450
	- (C_{10}-C_{16})	*CYP52 3 (ALK3)*	CYP52A3- P450

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         : *Actinomyces, Arthrobacter, Bacillus, Corynebacterium, Desulfotomaculum, Micrococcus, Pseudomonas, Sarcina, Sphingomonas, Mycobacterium Burkholderia, Rhodococcus, Alcaligenes, Marinobacter, Alcanivorax, Sphingomonas,   .   Pseudomonas.*

     ,   ,
Phanerochaete, Penicillium, Aspergillus, Trichoderma, Fusarium, Candida, Yarrowia, Pichia.

          Pseudomonas, Burkholderia, Corynebacterium
Candida, Yarrowia.

1. *Vinas M., Sabate J., Espuny M.J., Solanas A.M.* Bacterial community dynamics and polycyclic aromatic hydrocarbon degradation during bioremediation of heavily creosote-contaminated soil //Appl. Environ. Microbiol. – 2005. -   71(11). -   . 7008-7018.

2. http://www.genome.jp/kegg/

3. http: //www.ncbi.nlm.nih.gov

4. http://www.pseudomonas.com

5. *Van Hamme D.J., Singh A., Ward O.P.* Recent Advances in Petroleum Microbiology // Microbiology and Molecular. Biology Reviews. - 2003. - V. 67. -   4. - P. 503.

6. *Kulkarni R. S., Kanekar P.P.* Bioremediation of -Caprolactam from Nylon-6 Waste Water by Use of *Pseudomonas aeruginosa* MCM B-407 // Current Microbiology. - 1998. - V. 37. (3).- P.191-194.

7. *Fell J., Uden N.* Yeast in marine environments // J. Marine microboilogy. – 1960. -   2. – P. 853.

8. *Walker S., Austin H., Colwell R.* Utilization of mixed hydrocabon substrate b petroleum-degrading microorganisms // J. Gen. And Appl. Microbiology. -1975. - V. 21. -   21. - . 27-39.

9. *Braun B.R.* et al.   A human-curated annotation of the *Candida albicans* genome // PLoS Genet 1. – 2005. -   1. - . 36-57

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KEGG, Pseudomonas Genome Database v2, NCBI, Genome Statistics - Candida   .

.   *Actinomyces, Arthrobacter, Bacillus, Corynebacterium, Micrococcus, Pseudomonas, Sphingomonas, Burkholderia, Rhodococcus*   *Penicillium, Aspergillus*, *Candida, Yarrowia, Pichia*   .

Pseudomonas, Burkholderia, Corynebacterium
Candida, Yarrowia   .

Summary

In the methods of computer analysis was carried out screening for the presence of oxidizing microbial genomes of genes encoding enzymes of degradation of petroleum hydrocarbons and petroleum products.

Computer analysis showed that the degradation of petroleum hydrocarbons and petroleum uchastvtsuyut large number of microorganisms. The most common belong to: *Actinomyces, Arthrobacter, Bacillus, Corynebacterium, Micrococcus, Pseudomonas, Sphingomonas, Burkholderia, Rhodococcus* and other fungi that can aerobically destroy these compounds belong to *Penicillium, Aspergillus, Candida, Yarrowia, Pichia*.

We have shown that the destruction of hydrocarbons involves a large number of microorganisms. The highest hydrocarbon potential is typical for bacteria of *Pseudomonas, Burkholderia, Corynebacterium*, and yeasts of *Candida, Yarrowia.*